

CC with cellular growth and division. The sequences of the invention may be
CC useful for gene therapy. The protein kinase or the nucleic acid encoding
CC the protein is useful for modulating cellular growth, differentiation
CC and/or development, and for modulating cellular metabolic pathways,
CC particularly for regulating one or more proteins involved in growth and
CC metabolism. The invention may also be useful for development of
CC therapeutics for the treatment of viral infections (for example hepatitis
CC B), cellular growth related disorders (for example heart failure,
CC hypertension, atrial fibrillation, dilated and idiopathic cardiomyopathy
CC or angina), proliferative or differentiative disorders such as cancer
CC (for example liver, melanoma, prostate, cervical, breast, colon or
CC sarcoma), disorders related with programmed cell death (for example
CC Alzheimer's disease, Parkinson's disease or epilepsy), or autoimmune
CC disorders (for example systemic lupus erythematosus). The present
CC sequence is the amino acid sequence of the novel human kinase protein
CC 14171 of the invention.

XX Sequence 784 AA;

Query Match 100.0%; Score 4078; DB 7; Length 784;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGDGTWALALRTFDAGEPTMEKVGSGGFGQVYKRVHMKMTALAKCPSLAVDD 60
DB 1 MEGDGTWALALRTFDAGEPTMEKVGSGGFGQVYKRVHMKMTALAKCPSLAVDD 60
QY 61 RERMLLEAKKMEAKFRYILPVYIGREPVGLVMEYTGSLLEKLASPLPMDLFR 120
DB 61 RERMLLEAKKMEAKFRYILPVYIGREPVGLVMEYTGSLLEKLASPLPMDLFR 120
QY 121 ITHETAVGMNPLHCAAPPLHLDLKPAHLLDAHNVKISPGKACKGSHSHDLSMDG 180
DB 121 ITHETAVGMNPLHCAAPPLHLDLKPAHLLDAHNVKISPGKACKGSHSHDLSMDG 180
QY 181 LFGTAVYPPERIRKESRLFTKHDVGFAYIWMGVLTQCKPFADEKIMLIHMVAVVGH 240
DB 181 LFGTAVYPPERIRKESRLFTKHDVGFAYIWMGVLTQCKPFADEKIMLIHMVAVVGH 240
QY 241 RPELPVCRARPRACSHLIRLMQRCWQDPRVRPTFOBITSETEDLCRPPDEVEKETAHD 300
DB 241 RPELPVCRARPRACSHLIRLMQRCWQDPRVRPTFOBITSETEDLCRPPDEVEKETAHD 300
QY 301 LDVKSPPPRSEVVARLKRAAPFPDNDYSISLISQDGVGVQAVGPELSSESSES 360
DB 301 LDVKSPPPRSEVVARLKRAAPFPDNDYSISLISQDGVGVQAVGPELSSESSES 360
QY 361 KLPSGSGKRLSGVSDSAFSSRGLSISFEREPSTDLGTTTRPEEBACGCHVRDTS 420
DB 361 KLPSGSGKRLSGVSDSAFSSRGLSISFEREPSTDLGTTTRPEEBACGCHVRDTS 420
QY 421 KLMKTLIQDQVDLALDSGASLIHLAVEAGQECACMLLNANPNLSNRSGSTPLHMAVE 480
DB 421 KLMKTLIQDQVDLALDSGASLIHLAVEAGQECACMLLNANPNLSNRSGSTPLHMAVE 480
QY 481 RRVAVVELLARKTSVNAKDQMTALHFAQNGDESTRLLLEKNASVNVDEGRTP 540
DB 481 RRVAVVELLARKTSVNAKDQMTALHFAQNGDESTRLLLEKNASVNVDEGRTP 540
QY 541 MHVACQHQENIVRILRRGVDSIQKDAWLPVHYAAWQGLPIVKLLAKQPVSVNAQ 600
DB 541 MHVACQHQENIVRILRRGVDSIQKDAWLPVHYAAWQGLPIVKLLAKQPVSVNAQ 600
QY 601 TLDSGTPLHLAAQRGHYVARILLIDCSGVNCSLLAQPLHVAAREGHTSTARILLRG 660
DB 601 TLDSGTPLHLAAQRGHYVARILLIDCSGVNCSLLAQPLHVAAREGHTSTARILLRG 660
QY 661 AKKEAVTSQGTATLHAAANGHLATYKLLVEEKADVLARGPILNORALHAAHGSVEYE 720
DB 661 AKKEAVTSQGTATLHAAANGHLATYKLLVEEKADVLARGPILNORALHAAHGSVEYE 720
QY 721 ELVSAVDVIDLFDQGLSALHLAAQGRHAQTVETLLRHGAHINLSLKFQGGHGPATLLR 780
DB 721 ELVSAVDVIDLFDQGLSALHLAAQGRHAQTVETLLRHGAHINLSLKFQGGHGPATLLR 780

Db 721 ELVSAVDVIDLFDQGLSALHLAAQGRHAQTVETLLRHGAHINLSLKFQGGHGPATLLR 780
QY 781 RSKT 784
Db 781 RSKT 784
RESULT 2
ADL67198
ID ADL67198 standard; protein: 784 AA.
XX
XX ADL67198;
AC
AC 03-JUN-2004 (first entry)
DT
XX
XX Human 14171 protein kinase.
XX
XX Human; 14171 protein kinase; cancer; immunological disorder;
KW inflammation; heart failure; hypertension; atrial fibrillation;
KW viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
KW predictive medicine; forensic biology; enzyme.
XX
XX Homo sapiens.
OS
XX
XX Key
FX Modified-site
FT 6..11
FT /note= "N-myristoylation site"
FT 22..279
FT /note= Protein kinase domain
FT 23..26
FT /note= "Casein kinase II phosphorylation site"
FT 153..168
FT /note= "N-myristoylation site"
FT 169..174
FT /note= "N-myristoylation site"
FT 180..185
FT /note= "N-myristoylation site"
FT 202..205
FT /note= "Casein kinase II phosphorylation site"
FT 218..220
FT /note= "Protein kinase C phosphorylation site"
FT 275..278
FT /note= "Casein kinase II phosphorylation site"
FT 281..284
FT /note= "Casein kinase II phosphorylation site"
FT 297..300
FT /note= "Casein kinase II phosphorylation site"
FT 305..308
FT /note= "Casein kinase II phosphorylation site"
FT 319..322
FT /note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
FT 331..334
FT /note= "Casein kinase II phosphorylation site"
FT 337..340
FT /note= "Casein kinase II phosphorylation site"
FT 342..347
FT /note= "N-myristoylation site"
FT 356..359
FT /note= "Casein kinase II phosphorylation site"
FT 365..368
FT /note= "Glycosaminoglycan attachment site"
FT 367..370
FT /note= "Amidation site"
FT 367..369
FT /note= "Protein kinase C phosphorylation site"
FT 369..372
FT /note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
FT 375..378
FT /note= "Casein kinase II phosphorylation site"
FT 382..384
FT /note= "Protein kinase C phosphorylation site"

FT Modified-site 396..399
 /note="Casein kinase II phosphorylation site"
 FT Modified-site 402..404
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 419..421
 /note="Protein kinase C phosphorylation site"
 FT Active-site 433..444
 /note="Eukaryotic and viral aspartyl protease active site"
 FT Domain 437..766
 /note = Ankyrin repeat domain
 FT Modified-site 449..454
 /note="N-myristoylation site"
 FT Modified-site 465..468
 /note="Glycosylation site"
 FT Modified-site 467..469
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 469..472
 /note="CAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 493..496
 /note="CAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 519..521
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 527..530
 /note="Glycosylation site"
 FT Modified-site 529..532
 /note="Casein kinase II phosphorylation site"
 FT Modified-site 560..565
 /note="N-myristoylation site"
 FT Modified-site 594..599
 /note="N-myristoylation site"
 FT Modified-site 652..654
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 685..687
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 703..706
 /note="Glycosylation site"
 FT Modified-site 758..763
 /note="N-myristoylation site"
 FT Modified-site 765..767
 /note="Protein kinase C phosphorylation site"
 FT US2004048305-A1.
 PN 11-MAR-2004.
 PD 10-SEP-2003; 2003US-00658904.
 PF 11-FEB-2000; 2000US-0182096P.
 PR 12-FEB-2001; 2001US-00781882.
 XX (MILL-) MILLENNITUM PHARM INC.
 PA Kapeller-Libermann R;
 PI WPI: 2004-226195/21.
 XX N-PSDB; ADL67197, ADL67199.
 DR New 14171 protein kinase and nucleic acid, useful for diagnosing or
 PT treating diseases with aberrant expression of the 14171 protein kinase,
 PT such as cancer, an immunological disorder, inflammation, heart failure
 PT and hypertension.
 XX Claim 5; SEQ ID NO 2; 62bp; English.
 PS The invention provides novel human 14171 protein kinase polypeptides and
 CC polynucleotides. The methods and compositions of the present invention
 CC are useful for the diagnosis and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of a 14171 protein kinase
 CC such as cancer, immunological disorder, inflammation, heart failure,
 CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.

CC The invention can also be used in chromosome mapping, tissue typing,
 CC predictive medicine, forensic biology and prognostic assays. The present
 CC sequence is human 14171 protein kinase.

SQ Sequence 784 AA;

Query Match 100.0%; Score 4078; DB 8; Length 784;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGDGTFWALALRTFDAGEFTGMEKVGSGGFGQVTVKRVHVMKWTALAKCSPLAYDD	60
DB	1	MEGDGTFWALALRTFDAGEFTGMEKVGSGGFGQVTVKRVHVMKWTALAKCSPLAYDD	60
QY	61	RERRELLERAKMEAKRYTLIPYVGCREBVGIVMEKMGSLKTLASEPLPDLRFR	120
DB	61	RERRELLERAKMEAKRYTLIPYVGCREBVGIVMEKMGSLKTLASEPLPDLRFR	120
QY	121	IIHETAVGMNPLHCAAPPLHLDLKPANILDAHYHVKISDFGLAKCNGLSHSHDLSMDG	180
DB	121	IIHETAVGMNPLHCAAPPLHLDLKPANILDAHYHVKISDFGLAKCNGLSHSHDLSMDG	180
QY	181	LFGTIAVLPERRIREKSRLPFTKHDVYSFAIVIGVLTQKKPFADKNIILHMKVYVGH	240
DB	181	LFGTIAVLPERRIREKSRLPFTKHDVYSFAIVIGVLTQKKPFADKNIILHMKVYVGH	240
QY	241	RPELPVCRAPRACSHILRMQRCWQDPRVPRFQGITSETBTLCEKPDDEVETAMD	300
DB	241	RPELPVCRAPRACSHILRMQRCWQDPRVPRFQGITSETBTLCEKPDDEVETAMD	300
QY	301	LDVKSPPRPSRVVPARLKRAAPTFDNDYLSLQLSDGVSQAVGPEELSRSSSES	360
DB	301	LDVKSPPRPSRVVPARLKRAAPTFDNDYLSLQLSDGVSQAVGPEELSRSSSES	360
QY	361	KLPSGSGKRLSGVSVDSAFSSRGLSLSPEREBSIDLGTRRPEEBACGCHRVDT	420
DB	361	KLPSGSGKRLSGVSVDSAFSSRGLSLSPEREBSIDLGTRRPEEBACGCHRVDT	420
QY	421	KLMKTLQPDVDLADSGASLIHLAVEGQERCAWLLNNANPMLSRRGSTPLHMAVE	480
DB	421	KLMKTLQPDVDLADSGASLIHLAVEGQERCAWLLNNANPMLSRRGSTPLHMAVE	480
QY	481	RRVRGVVELLARKISVNAKEDQWTLHPAQNQDSESTRLLKKNASVNEVDEGRTP	540
DB	481	RRVRGVVELLARKISVNAKEDQWTLHPAQNQDSESTRLLKKNASVNEVDEGRTP	540
QY	541	MHVACQHQENIVRILRRGVDSLOGKDAMLPLHYAAMQGHLPVVKLLAKQPGVSVNAQ	600
DB	541	MHVACQHQENIVRILRRGVDSLOGKDAMLPLHYAAMQGHLPVVKLLAKQPGVSVNAQ	600
QY	601	TLDGRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPLHVAEFTGHTSTARILLHRG	660
DB	601	TLDGRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPLHVAEFTGHTSTARILLHRG	660
QY	661	AKGEAVTSQGYTALHAARNGHLATVKLLVEKQAVLARGPLNQTALHAAHGSVEYE	720
DB	661	AKGEAVTSQGYTALHAARNGHLATVKLLVEKQAVLARGPLNQTALHAAHGSVEYE	720
QY	721	ELVSAVDVIDLFDQGLSALHLAQRHAQVETTLRHGHINILQSLKFGGSHGPAATLLR	780
DB	721	ELVSAVDVIDLFDQGLSALHLAQRHAQVETTLRHGHINILQSLKFGGSHGPAATLLR	780
QY	781	RKST 784	
DB	781	RKST 784	

RESULT 3
 ABP58154
 ID ABP58154 standard; protein; 784 AA.
 XX
 AC ABP58154;
 XX

DT 18-MAR-2003 (first entry)
 XX Death associated kinase containing ankyrin repeats (DAKAR) variant.
 XX Death associated kinase containing ankyrin repeats; DAKAR; human;
 KW protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;
 KW antiproliferative; cytostatic.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Domain 22..302
 FT /note="catalytic or kinase domain"
 FT 142..148
 FT Region /note="serine/threonine catalytic loop motif"
 FT 160..162
 FT /note="serine/threonine catalytic loop motif"
 FT Cleavage-site 433..437
 FT /note="caspase cleavage site"
 FT 469..482
 FT /note="putative nuclear localisation site"
 FT Region
 FT
 FN WO200298894-A1.
 XX
 XX 12-DEC-2002.
 PD
 XX
 XX 04-JUN-2002; 2002WO-US018039.
 PF
 XX 04-JUN-2001; 2001US-0295959P.
 PR 29-NOV-2001; 2001US-0334362P.
 XX
 PA (IMMUNEX CORP.
 XX
 P1 Bird TA, Holland PM, Peschon JJ, Virca GD;
 XX
 DR WPI; 2003-148648/14.
 XX
 PT New isolated human death associated kinase containing ankyrin repeats
 PT polypeptide and polynucleotide, useful for treating psoriasis, melanoma
 PT or squamous cell carcinoma.
 FT
 PS Example 1; Page; 154pp; English.
 XX
 CC The present sequence is the protein sequence of a naturally occurring
 CC variant of human death associated kinase containing ankyrin repeats
 CC (DAKAR, see ABP4150). The variant has a valine for methionine
 CC substitution at amino acid 666. DAKAR is a novel member of the
 CC serine/threonine protein kinase family. DAKAR is a mediator of apoptosis
 CC and putative modulator of cellular differentiation, proliferation, cell
 CC cycle and/or senescence. Human DAKAR includes a catalytic domain has
 CC similarity to the receptor interaction protein (RIP) family of apoptosis-
 CC inducing kinases, and contains 9 ankyrin repeats in its C-terminal
 CC regulatory domain. It also includes a number of putative protein kinase C
 CC phosphorylation sites. The invention provides DAKAR nucleic acids and
 CC polypeptides, as well as recombinant vectors, transfected host cells and
 CC methods of producing DAKAR polypeptides. The polypeptides are used in a
 CC claimed method of identifying candidate compounds that modulate DAKAR
 CC activity. DAKAR agonists can be used to treat psoriasis, melanoma and
 CC squamous cell carcinoma (claimed). Note: The present sequence is not
 CC shown in the specification but is derived from the human DAKAR sequence
 CC given in the sequence listing (see ABP58150)
 XX
 SQ Sequence 784 AA;
 Query Match 97.6%; Score 3980; DB 6; Length 784;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MEGDGTTPALALLTPDAGETGWEKSGSGFGQVYKRRHNMKTWLAIKSPSLHVD 60
 DB 1 MEGDGTTPALALLTPDAGETGWEKSGSGFGQVYKRRHNMKTWLAIKSPSLHVD 60
 QY 61 RRMWELBEAKKEMAKFRYILPYVGI CREPVGVLWMEYMGSLKLLASBPDPMDLRF 120

DB 61 RRMWELBEAKKEMAKFRYILPYVGI CREPVGVLWMEYMGSLKLLASBPDPMDLRF 120
 QY 121 ITHETAVGNMFLHOMAPPLHLHLDKPANILLDAHNYKISDFGLAKKNGSHSIDLSMDG 180
 DB 121 ITHETAVGNMFLHOMAPPLHLHLDKPANILLDAHNYKISDFGLAKKNGSHSIDLSMDG 180
 QY 181 LFGTIAVLPERIEREKSLPDTKHDVYSFAIVIMGVLTKKKPFADENKILHIMKVYKG 240
 DB 181 LFGTIAVLPERIEREKSLPDTKHDVYSFAIVIMGVLTKKKPFADENKILHIMKVYKG 240
 QY 241 RPELPVVCARAPRACSHLIRLMORCWQGDPRVREPTFOEITSETBDCPKDDEVEKETAMD 300
 DB 241 RPELPVVCARAPRACSHLIRLMORCWQGDPRVREPTFOEITSETBDCPKDDEVEKETAMD 300
 QY 301 LDVKSPEPSPSEVTPALUKRASAPTFPNQDYSLSLSLQDQSVQAVEGPELSRSSSES 360
 DB 301 LDVKSPEPSPSEVTPALUKRASAPTFPNQDYSLSLSLQDQSVQAVEGPELSRSSSES 360
 QY 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPEREPTSDGTTTRPREBACGCHRVDT 420
 DB 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPEREPTSDGTTTRPREBACGCHRVDT 420
 QY 421 KLAKTIQPOVDLALDSGASLHLAVEAGOECAKWLILNNANENLSNRRGTEPLMAVE 480
 DB 421 KLAKTIQPOVDLALDSGASLHLAVEAGOECAKWLILNNANENLSNRRGTEPLMAVE 480
 QY 481 RRVNGVVELLARKISVNAQDEQWTLHFAAQNQDSSSTRLLKRAVSVEVDPEGRTP 540
 DB 481 RRVNGVVELLARKISVNAQDEQWTLHFAAQNQDSSSTRLLKRAVSVEVDPEGRTP 540
 QY 541 MHVACQGOENIVAILRGGVDSLOGKDAMLPHYVAMOGHLPIYKLLAKOPGVVNAQ 600
 DB 541 MHVACQGOENIVAILRGGVDSLOGKDAMLPHYVAMOGHLPIYKLLAKOPGVVNAQ 600
 QY 601 TLDRTPHLAAGHYRVARILLDQSDVNVCSLAQTPHLVAETGHTSTABILLHRG 660
 DB 601 TLDRTPHLAAGHYRVARILLDQSDVNVCSLAQTPHLVAETGHTSTABILLHRG 660
 QY 661 AGKNAVSDGTALHLAARNCHLATVGLVBEKADVLAAGLNTALHLAAHGHSEVVE 720
 DB 661 AGKNAVSDGTALHLAARNCHLATVGLVBEKADVLAAGLNTALHLAAHGHSEVVE 720
 QY 721 ELVSADVIDLDFDEQSLSLHLAAGRAQVETLLRHGAHINLSLFGQSGHAPATLLR 780
 DB 721 ELVSADVIDLDFDEQSLSLHLAAGRAQVETLLRHGAHINLSLFGQSGHAPATLLR 780
 QY 781 RSKT 784
 DB 781 RSKT 784
 RESULT 4
 ADE38377
 ID ADE38377 standard; protein; 784 AA.
 XX
 XX ADE38377;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human protein 14171 amino acid sequence.
 XX
 XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;
 KW aberrant protein activity; cytostatic; antitumor; antidiabetic;
 KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
 KW prostatic cancer; Grave's disease; diabetic retinopathy; protein 14171.
 OS Homo sapiens.
 XX
 XX WO2003065006-A2.
 PD 07-AUG-2003.
 XX

PF 30-JAN-2003; 2003WO-US002588.
 XX 31-JAN-2002; 2002US-0353600P.
 PR 15-MAR-2002; 2002US-0364517P.
 PR 09-APR-2002; 2002US-0371075P.
 PR 10-APR-2002; 2002US-0371507P.
 PR 16-APR-2002; 2002US-0372984P.
 PR 19-APR-2002; 2002US-0374194P.
 PR 24-MAY-2002; 2002US-0382995P.
 PR 31-MAY-2002; 2002US-0385023P.
 PR 14-JUN-2002; 2002US-0388653P.
 PR 17-JUN-2002; 2002US-0389395P.
 PR 25-JUN-2002; 2002US-0391324P.
 PR 15-JUL-2002; 2002US-0395944P.
 PR 22-JUL-2002; 2002US-0397726P.
 PR 13-AUG-2002; 2002US-0403046P.
 PR 22-AUG-2002; 2002US-0405155P.
 PR 27-AUG-2002; 2002US-0406361P.
 PR 25-OCT-2002; 2002US-0421195P.
 PR 12-NOV-2002; 2002US-0425456P.
 PR 19-NOV-2002; 2002US-0427626P.
 PR 10-DEC-2002; 2002US-0432122P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES,
 PI Williamson MW, Rudolph-Owen LA;
 XX WPI: 2003-646176/61.
 DR N-PSDB; ADE38376.
 XX
 PT Treating subject having tumorigenic disorder or angiogenic disorder
 PT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
 PT acid, by administering a modulator.
 XX
 XX Disclosure; SEQ ID NO 38; 454pp; English.
 PS
 XX
 CC This invention relates to a novel method of treating a human subject
 CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant
 CC gene expression or activity of an isolated protein, by administering a
 CC modulator. The modulator may have cytostatic, antihypertoid, antidiabetic
 CC or ophthalmologic activity. The method is useful for treating a subject
 CC having a tumorigenic or angiogenic disorder, in particular for treating
 CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic
 CC cancer) and, for example, Grave's disease and diabetic retinopathy. The
 CC present sequence is the amino acid sequence of the novel isolated human
 CC protein 14171 of the invention.
 CC
 XX
 XX Sequence 784 AA;
 SQ
 Query Match 97.6%; Score 3980; DB 7; Length 784;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 301 LDVSPPEPRSEVYPARLKRAAPTPFNDYSLSELSQLDSGVSAVEGPEELSRSSSES 360
 DB 301 LDVSPPEPRSEVYPARLKRAAPTFNDYSLSELSQLDSGVSAVEGPEELSRSSSES 360
 QY 361 KLPSGSGKRLSGVSVDSAFSSRGLSLSPEREPTSDIGTTRPPEEACGCHRVDTLS 420
 DB 361 KLPSGSGKRLSGVSVDSAFSSRGLSLSPEREPTSDIGTTRPPEEACGCHRVDTLS 420
 QY 421 KLMTILOPOVDVLDLDSGASLHLAVBAGQBECAKMLLNANPRLSNRSGSTPLHMAVE 480
 DB 421 KLMTILOPOVDVLDLDSGASLHLAVBAGQBECAKMLLNANPRLSNRSGSTPLHMAVE 480
 QY 481 RRVGVVELLARKISVNAKEDQMTALHPAONGDSSSTRLLEKNASVNEVPEGRTP 540
 DB 481 RRVGVVELLARKISVNAKEDQMTALHPAONGDSSSTRLLEKNASVNEVPEGRTP 540
 QY 541 MHVACQHQENIVHLLRQGVDSLOQKDAWLPHTYAMQGHLPVKKLAKQGVSVNAQ 600
 DB 541 MHVACQHQENIVHLLRQGVDSLOQKDAWLPHTYAMQGHLPVKKLAKQGVSVNAQ 600
 QY 601 TLDEGTPHLAAQGRHVRVANILDLCSGVVCSLLAQTPLHVAEFGHTSTARLLHRG 660
 DB 601 TLDEGTPHLAAQGRHVRVANILDLCSGVVCSLLAQTPLHVAEFGHTSTARLLHRG 660
 QY 661 AGKEAVTSDGYTALHLAARNGHILATVKLVBEKADVLRGPINOTALHMAAHGSEVVE 720
 DB 661 AGKEAVTSDGYTALHLAARNGHILATVKLVBEKADVLRGPINOTALHMAAHGSEVVE 720
 QY 721 ELVSADVIDLDFDEQGLSALHLAAGRHQVETLLRHGAHINTLSLKEQGGHPATLLR 780
 DB 721 ELVSADVIDLDFDEQGLSALHLAAGRHQVETLLRHGAHINTLSLKEQGGHPATLLR 780
 QY 781 RSKT 784
 DB 781 RSKT 784
 DB 781 RSKT 784
 RESULT 5
 ABW02412
 ID ABW02412 standard; protein; 784 AA.
 XX
 AC ABW02412;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human protein kinase C-associated kinase (PKC) protein.
 XX
 KW Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK;
 KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 173..177
 FT /note= "Activation loop motif"
 PN US2003199462-A1.
 XX
 PD 23-OCT-2003.
 XX
 PR 23-APR-2002; 2002US-00128174.
 XX
 PR 23-APR-2002; 2002US-00128174.
 XX
 PA (NUNEZ/) NUNEZ G.
 PA (INOH/) INOHARA N.
 PA (MUTO/) MUTO A.
 PI Nunez G, Inohara N, Muto A;
 XX
 DR WPI: 2003-852808/79.
 DR N-PSDB; AAD64329.

XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKC induced NF-KB activation for treating hyperglycemia.
XX Claim 20; SEQ ID NO 12; Opp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKC induced NF-kappaB activation for treating hyperglycemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK protein
XX
XX Sequence 784 AA;
SQ
Query Match 97.6%; Score 3980; DB 7; Length 784;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 MEGDGTWALALATPTPAGEFTGWEKVGSGGFGVYVRHVHMTWLAIKCPSLAHDD 60
DB 1 MEGDGTWALALATPTPAGEFTGWEKVGSGGFGVYVRHVHMTWLAIKCPSLAHDD 60
QY RERRELLBEAKKMEAKFRYIIPVYGICREPVGLVMEWETGSLKLAASEPLPMDLFR 120
DB RERRELLBEAKKMEAKFRYIIPVYGICREPVGLVMEWETGSLKLAASEPLPMDLFR 120
QY 121 IIEHRAVAGNPLFHCAAPPLHLHDLPANILDAHYHVTSDPKLAKNGLSHSHLSMDG 180
DB 121 IIEHRAVAGNPLFHCAAPPLHLHDLPANILDAHYHVTSDPKLAKNGLSHSHLSMDG 180
QY 121 IIEHRAVAGNPLFHCAAPPLHLHDLPANILDAHYHVTSDPKLAKNGLSHSHLSMDG 180
DB 121 IIEHRAVAGNPLFHCAAPPLHLHDLPANILDAHYHVTSDPKLAKNGLSHSHLSMDG 180
QY 161 LFGTIAVLPERRIRKESRLFTDKHDVSPAIYIVGVLTKCKPFADEKNILHIMVYVKGH 240
DB 161 LFGTIAVLPERRIRKESRLFTDKHDVSPAIYIVGVLTKCKPFADEKNILHIMVYVKGH 240
QY 241 RPELPVVCGRAPRACSHLIRLMQRCWQDPPRPFPFOETSTETDLCEKPDDEVKETAHD 300
DB 241 RPELPVVCGRAPRACSHLIRLMQRCWQDPPRPFPFOETSTETDLCEKPDDEVKETAHD 300
QY 241 RPELPVVCGRAPRACSHLIRLMQRCWQDPPRPFPFOETSTETDLCEKPDDEVKETAHD 300
DB 241 RPELPVVCGRAPRACSHLIRLMQRCWQDPPRPFPFOETSTETDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPPEPRSEVVPARLKRASAPTFDNDYSLSELLSOLDSGVSAVAGPEELSRSSSES 360
DB 301 LDVKSPPPEPRSEVVPARLKRASAPTFDNDYSLSELLSOLDSGVSAVAGPEELSRSSSES 360
QY 361 KLPSSGSGKRLSGVSDSAFSSRSGLSLSPFERPSTDLGTTTRRBEEDACGCHRVDTLS 420
DB 361 KLPSSGSGKRLSGVSDSAFSSRSGLSLSPFERPSTDLGTTTRRBEEDACGCHRVDTLS 420
QY 421 KLMKLIQDQDVLADSGASLIHLAVEAGQEECAWILLNANPNLSNRGSTPLHMAVE 480
DB 421 KLMKLIQDQDVLADSGASLIHLAVEAGQEECAWILLNANPNLSNRGSTPLHMAVE 480
QY 481 RRVGVVELLLARKISVNAKDEDMWTALHFAQNGDESSSTRLLERKNASVNEVDEGRTP 540
DB 481 RRVGVVELLLARKISVNAKDEDMWTALHFAQNGDESSSTRLLERKNASVNEVDEGRTP 540
QY 541 RRVGVVELLLARKISVNAKDEDMWTALHFAQNGDESSSTRLLERKNASVNEVDEGRTP 540
DB 541 RRVGVVELLLARKISVNAKDEDMWTALHFAQNGDESSSTRLLERKNASVNEVDEGRTP 540
QY 541 MHVACQHQGENTVRLILRRGVDSLQGDWMLPLHYAAMQGHLPVKKLAKQPGVSAVNAQ 600
DB 541 MHVACQHQGENTVRLILRRGVDSLQGDWMLPLHYAAMQGHLPVKKLAKQPGVSAVNAQ 600
QY 601 TLDGTPPLHMAQORGHYVARILIDLCSDVNVCSSILAQPLHVAEFTGHTSTARILLHRG 660
DB 601 TLDGTPPLHMAQORGHYVARILIDLCSDVNVCSSILAQPLHVAEFTGHTSTARILLHRG 660
QY 661 AGKEAVTSQGYTALHAAANGHLATVKKLVEEKADVLARGPNQOTLHAAAHGSEVVE 720
DB 661 AGKEAVTSQGYTALHAAANGHLATVKKLVEEKADVLARGPNQOTLHAAAHGSEVVE 720
QY 721 ELVSAADVIDLFDQEGISALHHLAAQGRHQAQVETTLRHGHANIMQSLKTCQGHGPAATLLR 780
DB 721 ELVSAADVIDLFDQEGISALHHLAAQGRHQAQVETTLRHGHANIMQSLKTCQGHGPAATLLR 780

QY 781 RSKT 784
DB 781 RSKT 784
RESULT 6
ID ABB53291 standard; protein; 784 AA.
XX ABB53291;
AC ABB53291;
DT 12-FEB-2002 (first entry)
XX
DE Human polypeptide #31.
XX
KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
KW neuroleptic; tranquilizer; antiarrhythmic; cardiant; antiaesthetic;
KW antiinflammatory; antihypertensive; hepatotropic; vitamin; antidiabetic;
KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
KW cardiovascular disease; respiratory disease; liver disease;
KW renal disease; skeletal muscle disease; gastrointestinal disease;
KW placental disease; testicular cancer; male fertility; pancreatic disease.
XX Homo sapiens.
XX WO200181363-A1.
XX 01-NOV-2001.
XX 26-APR-2001; 2001WO-US013360.
XX 27-APR-2000; 2000US-0199963P.
XX 11-MAY-2000; 2000US-0203336P.
XX 25-MAY-2000; 2000US-0207087P.
XX 26-MAY-2000; 2000US-0207546P.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
PA (SMK) SMITHKLINE BEECHAM PLC.
PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS,
PI Lai Y, Xie Q;
XX WPI: 2002-041392/05.
XX N-PSDB; ABA90356.
XX
PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
PT and treating diseases associated the polypeptide, e.g. Alzheimer's
PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
XX
PS Claim 1; Page 101-103; 116pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
XX 844, 782, 652, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases and anticodises against the polypeptides including
XX Alzheimer's, paraneuronal nuclear palsy, Huntington's disease, myotonic
XX dystrophy, anorexia and depression; cardiovascular diseases including
XX congestive heart failure, Hodgkin's disease and myocardial infarction;
XX respiratory diseases including asthma, chronic obstructive pulmonary
XX disease, cystic fibrosis and adult respiratory distress syndrome; liver
XX diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
XX hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
XX renal disease including renal failure, acute tubular necrosis and
XX glomerulonephritis; skeletal muscle diseases including Bulenburg's
XX disease, hypoglycaemia and obesity; gastrointestinal diseases including
XX myotonia congenita and intestinal obstruction; lymph diseases including
XX lymphoglycemia; diseases of placenta including choriochorionoma; diseases
XX of testes including testicular cancer, male reproductive diseases
XX including low testosterone and male infertility; and disease of pancreas

including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence is a polypeptide of the invention

Sequence 784 AA;

Query Match 97.5%; Score 3977; DB 5; Length 784;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

QY 1 MEGDGTPTMALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMTWLAIKCPSLIHYDD 60
DB 1 MEGDGTPTMALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMTWLAIKCPSLIHYDD 60
QY 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGIVMEYMETGSLKTLASEPLPMDLRR 120
DB 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGIVMEYMETGSLKTLASEPLPMDLRR 120
QY 121 ITHETAVGNPLHCMAPLHLHLDLKXPANILLDAHYVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 ITHETAVGNPLHCMAPLHLHLDLKXPANILLDAHYVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAVLPERRIRKSRILFTDKHDVSPAIIVGWLTQKPEADKKNILHIMVKKVKGH 240
DB 181 LFGTIAVLPERRIRKSRILFTDKHDVSPAIIVGWLTQKPEADKKNILHIMVKKVKGH 240
QY 241 REELPVCARAPRACSHLIRLMQRCQGDPRVRFQBITSTEDLCERPDDEVKETAND 300
DB 241 REELPVCARAPRACSHLIRLMQRCQGDPRVRFQBITSTEDLCERPDDEVKETAND 300
QY 301 LQVSPPEERSEVRVRLKRSAPTPDNYSLSSELLSGLDSGVSQAVEGPEELSSSSSS 360
DB 301 LQVSPPEERSEVRVRLKRSAPTPDNYSLSSELLSGLDSGVSQAVEGPEELSSSSSS 360
QY 361 KLPSGSGGRSLSGVSSVDASAFSSRGSLSLSPEREPTSDLGTTREBEACGCHRYDTS 420
DB 361 KLPSGSGGRSLSGVSSVDASAFSSRGSLSLSPEREPTSDLGTTREBEACGCHRYDTS 420
QY 421 KLMKTIQPODDVLDLDSGASLHLAVAGQEBACAKMLNNANPNISNRGSTPLHMAVE 480
DB 421 KLMKTIQPODDVLDLDSGASLHLAVAGQEBACAKMLNNANPNISNRGSTPLHMAVE 480
QY 481 RRRRGVVELLARKISVNAKDEDMQWALHPAONGESSRLLLEKNAVNEVDFEGRTP 540
DB 481 RRRRGVVELLARKISVNAKDEDMQWALHPAONGESSRLLLEKNAVNEVDFEGRTP 540
QY 541 MHVACQHGENTVIRILRRGVDSIQKXAMLPPLHYAANQSHLPYKLLAKQPGVSVNAQ 600
DB 541 MHVACQHGENTVIRILRRGVDSIQKXAMLPPLHYAANQSHLPYKLLAKQPGVSVNAQ 600
QY 601 TLDRGTPLHLAQRGHYVARIIIDICSDVNVCSLLAQTPPLHVAETGHTSTARLLHNG 660
DB 601 TLDRGTPLHLAQRGHYVARIIIDICSDVNVCSLLAQTPPLHVAETGHTSTARLLHNG 660
QY 661 AGREANTSQGYTHLHAARNGHLATYKLVBEKADVLAQPLNQTALHAAAHGSEVVE 720
DB 661 AGREANTSQGYTHLHAARNGHLATYKLVBEKADVLAQPLNQTALHAAAHGSEVVE 720
QY 721 ELVSADVILDFDEQGSALHLAQAQRAQVETLHRGHAINQLSKFGQGHAPATLLR 780
DB 721 ELVSADVILDFDEQGSALHLAQAQRAQVETLHRGHAINQLSKFGQGHAPATLLR 780
QY 781 RSKT 784
DB 781 RSKT 784

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RESULT 7
ABP58150 standard; protein; 784 AA.

DT 18-MAR-2003 (first entry)

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XX DE Human death associated kinase containing ankyrin repeats (DAKAR).
XX KW Death associated kinase containing ankyrin repeats; DAKAR; human;
XX KW protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;
XX KW antipsoriatic; cytostatic.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT Domain
XX FT 22..302
XX FT /note= "catalytic or kinase domain"
XX FT Region
XX FT 142..148
XX FT /note= "serine/threonine catalytic loop motif"
XX FT Region
XX FT 160..162
XX FT /note= "serine/threonine catalytic loop motif"
XX FT Cleavage-site
XX FT 433..437
XX FT /note= "casease cleavage site"
XX FT Region
XX FT 469..482
XX FT /note= "putative nuclear localisation site"
XX PN WO200298894-A1.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002MO-US018039.
XX PR 04-JUN-2001; 2001US-0295959P.
XX PR 29-NOV-2001; 2001US-0334362P.
XX PA (IMMUNEX CORP.
XX PI Bird TA, Holland PM, Peschon JJ, Virca GD;
XX DR WPI; 2003-148648/14.
XX DR N-PSDB; ABZ24424.
XX PT New isolated human death associated kinase containing ankyrin repeats
XX PT polypeptide and polynucleotide, useful for treating psoriasis, melanoma
XX PT or squamous cell carcinoma.
XX PS Claim 1; Page 148-151; 154pp; English.
XX CC The present sequence is the protein sequence of human death associated
XX CC kinase containing ankyrin repeats (DAKAR), a novel member of the
XX CC serine/threonine protein kinase family. DAKAR is a mediator of apoptosis
XX CC and putative modulator of cellular differentiation, proliferation, cell
XX CC cycle and/or senescence. Human DAKAR includes a catalytic domain has
XX CC similarity to the receptor interaction protein (RIP) family of apoptosis-
XX CC inducing kinases, and contains 9 ankyrin repeats in its C-terminal
XX CC regulatory domain. It also includes a number of putative protein kinase C
XX CC phosphorylation sites. The invention provides DAKAR nucleic acids and
XX CC polypeptides, as well as recombinant vectors, transfected host cells and
XX CC methods of producing DAKAR polypeptides. The polypeptides are used in a
XX CC claimed method of identifying candidate compounds that modulate DAKAR
XX CC activity. DAKAR agonists can be used to treat psoriasis, melanoma and
XX CC squamous cell carcinoma (claimed). Naturally-occurring variants of DAKAR
XX CC (see ABP58154-57) have been identified
XX SQ Sequence 784 AA;

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Query Match 97.5%; Score 3977; DB 6; Length 784;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

QY 1 MEGDGTPTMALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMTWLAIKCPSLIHYDD 60
DB 1 MEGDGTPTMALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMTWLAIKCPSLIHYDD 60
QY 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGIVMEYMETGSLKTLASEPLPMDLRR 120
DB 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGIVMEYMETGSLKTLASEPLPMDLRR 120

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Qy	121	11HETAVGMNPLHCHMAPPLH1HD,KPAN1LLDHAHYVK1SDGLACNGLSHSHDLSMG	180
Db	121	11HETAVGMNPLHCHMAPPLH1DL,KPAN1LLDHAHYVK1SDGLACNGLSHSHDLSMG	180
Qy	181	1LFGTAYL,PPER1REKSRSLFDTKHVYSPAIYIWGLTOKKPEPADEKNI1H1MVKVKG	240
Db	181	1LFGTAYL,PPER1REKSRSLFDTKHVYSPAIYIWGLTOKKPEPADEKNI1H1MVKVKG	240
Qy	241	RPELPVPCRARARACSHL1RLMORCMQGBPRARPTFOETTSFEDI,CEKRPDDEVKETAHD	300
Db	241	RPELPVPCRARARACSHL1RLMORCMQGBPRARPTFOETTSFEDI,CEKRPDDEVKETAHD	300
Qy	301	LDVKSPPERSEVSEVBARLKRASAPTEFDNYSLSSELLSQLDSGVSCAQAVEGEBELSRSSSES	360
Db	301	LDVKSPPERSEVSEVBARLKRASAPTEFDNYSLSSELLSQLDSGVSCAQAVEGEBELSRSSSES	360
Qy	361	KLPSGSGSGKRLSGVSSVDSAFSSRSGSLSPFEREPSTSLGTTTRPEBEACGCHRYDTS	420
Db	361	KLPSGSGSGKRLSGVSSVDSAFSSRSGSLSPFEREPSTSLGTTDVOKKLVDAIVSGDTS	420
Qy	421	KLMLK1LOPODVLDALDSGASLLHL1VEACQOBECAKML1NNANPN1SNRGSTPLHMAVE	480
Db	421	KLMLK1LOPODVLDALDSGASLLHL1VEACQOBECAKML1NNANPN1SNRGSTPLHMAVE	480
Qy	481	RRVRGVVELL1ARK1SVNAKDESDWTALHPAANGDESSSTRLLLEKNASVEVDPEGRT	540
Db	481	RRVRGVVELL1ARK1SVNAKDESDWTALHPAANGDESSSTRLLLEKNASVEVDPEGRT	540
Qy	541	MHVAOCHGEMENVR1LLRRGVDSVLSQGXOAM1PLHYAANOCH1PYKLLAKOGVSVNQ	600
Db	541	MHVAOCHGEMENVR1LLRRGVDSVLSQGXOAM1PLHYAANOCH1PYKLLAKOGVSVNQ	600
Qy	601	TLDGRTPLHLAAORGHYVAR1LLID,CSDVNVCSSLLAQOTPLHYAAETGHTSTARLLHRG	660
Db	601	TLDGRTPLHLAAORGHYVAR1LLID,CSDVNVCSSLLAQOTPLHYAAETGHTSTARLLHRG	660
Qy	661	AGKEAVTSGCYALH1AAANGHLATYKLLVEEKADVLAAGPLNQTALH1AAAGHSVEVE	720
Db	661	AGKEAVTSGCYALH1AAANGHLATYKLLVEEKADVLAAGPLNQTALH1AAAGHSVEVE	720
Qy	721	BLVSAADV1DLFDEBQGLSALHLAAOGRHAOTVETILNRGHAIN1QSLKFGGCHGPAAATLLR	780
Db	721	BLVSAADV1DLFDEBQGLSALHLAAOGRHAOTVETILNRGHAIN1QSLKFGGCHGPAAATLLR	780
Qy	781	RSKT 784	
Db	781	RSKT 784	

XX	RESULT 8
XX	ADL61229
ID	ADL61229 standard; protein; 784 AA.
XX	
XX	ADL61229;
AC	
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Human protein tyrosine kinase biomarker ankyrin repeat domain 3 protein.
XX	
KW	predictor set; protein tyrosine kinase; cytosolic; antiangiogenic;
KW	vasoconstrictor; vulnary; pharmacogenomic; drug sensitivity; breast cancer;
KW	hypervascular disease; angiogenesis; wound healing scar; human;
KW	biomarker; ankyrin repeat domain 3.
XX	
OS	Homo sapiens.
XX	
XX	
PN	WO2004020583-A2.
XX	
PD	11-MAR-2004.
XX	
PF	26-AUG-2003; 2003WO-US026491.
XX	
PR	27-AUG-2002; 2002US-0406385P.
XX	

XX (BRM) BRISTOL-MYERS SQUIBB CO.
PA
XX
XX Huang F, Han X, Reeves KA, Amler L, Fairchild CR, Lee FY,
PI Shaw P;
XX
XX WPI, 2004-239171/22.
DR N-PSDB; ADL61092.
XX
XX
PT New predictor sets with a plurality of polynucleotides and/or
PT polypeptides whose expression pattern predicts cell response to a
PT compound that modulates protein tyrosine kinase activity, useful in
PT treating breast cancer.
XX
XX
PS Claim 9; SEQ ID NO 153; 649pp; English.
XX
XX
CC The invention relates to a novel predictor set comprising a plurality of
CC polynucleotides and/or polypeptides whose expression pattern is
CC predictive of the response of cells to treatment with a compound that
CC modulates protein tyrosine kinase activity or members of the protein
CC tyrosine kinase pathway. The molecules of the invention demonstrate
CC cystostic, antiangiogenic, vasotropic and vulnary activities and may
CC be useful in the field of pharmacogenomics, in particular for determining
CC drug sensitivity and in treating breast cancer, hypervascular diseases,
CC angiogenesis and scars in wound healing. The current sequence is that of
CC a human protein tyrosine kinase biomarker protein of the invention.
XX
XX Sequence 784 AA;

Query Match	Similarity	97.5%	Score 3976;	DB 8;	Length 784;
Best Local	Similarity	98.1%	Pred. No. 0;		
Matches	769;	Conservative	4;	Mismatches	11; Indels 0; Gaps 0;
QY	1	MEGDGDTWALALARTPDAGEFTGMEKSGSGAGVGVYKVRHVHMKWTALAKCPSLHVD	60		
Db	1	MEGDGDTWALALARTPDAGEFTGMEKSGSGAGVGVYKVRHVHMKWTALAKCPSLHVD	60		
QY	61	RERMELEBAKAKMEAKFRYLLPYGTGREVEGLVMEFMESGLEKLASRPLPMDLFR	120		
Db	61	RERMELEBAKAKMEAKFRYLLPYGTGREVEGLVMEFMESGLEKLASRPLPMDLFR	120		
QY	121	IIHETAVGAMNLFHCMAAPLHLHDLPANII,LDAAHVYISDFGLAKCNGLSHSHDLSMDG	180		
Db	121	IIHETAVGAMNLFHCMAAPLHLHDLPANII,LDAAHVYISDFGLAKCNGLSHSHDLSMDG	180		
QY	181	LFGTIAYLPPERIREKSR,LPDTHDVYSFAIVIGVLTQKKPFADEKNI,LIHMYKVGKH	240		
Db	181	LFGTIAYLPPERIREKSR,LPDTHDVYSFAIVIGVLTQKKPFADEKNI,LIHMYKVGKH	240		
QY	241	RPELPVVCARAPRACSH,IRLMQRCWQDPRVPRPFQGITSTETBLCEKPPDVEYETLHD	300		
Db	241	RPELPVVCARAPRACSH,IRLMQRCWQDPRVPRPFQGITSTETBLCEKPPDVEYETLHD	300		
QY	301	LDVKSPPPRBSVVPAR,IKRASAPFPDNDYS,ISELISQLDGSVQSAVGPBELSRSSSES	360		
Db	301	LDVKSPPPRBSVVPAR,IKRASAPFPDNDYS,ISELISQLDGSVQSAVGPBELSRSSSES	360		
QY	361	KLPSGSGSKRLSGVSSVDASFSSRGSLSLSPEREBSYDLGTTRRPEEBAOCGRVDTS	420		
Db	361	KLPSGSGSKRLSGVSSVDASFSSRGSLSLSPEREBSYDLGTTDDKLDVAIVSGDTS	420		
QY	421	KLMKTLIQODVLDLADSGASLI,LIHVAEGOEBCAMILLNNANPMLSRKSTPLHMAVE	480		
Db	421	KLMKTLIQODVLDLADSGASLI,LIHVAEGOEBCAMILLNNANPMLSRKSTPLHMAVE	480		
QY	481	RRRGGVVELLAKRISVNAKEDQWTALHFAAONDEBSSTRLLLEKNAVNEVDFEGRTP	540		
Db	481	RRRGGVVELLAKRISVNAKEDQWTALHFAAONDEBSSTRLLLEKNAVNEVDFEGRTP	540		
QY	541	MHVAQCHQGEINTVRIILRRGVDSIQGDAWMLPHYAAMOGHLPIVKLAKQPGVSVAAQ	600		
Db	541	MHVAQCHQGEINTVRIILRRGVDSIQGDAWMLPHYAAMOGHLPIVKLAKQPGVSVAAQ	600		

QY 601 TLDERPPLHAAQRGHYVARILLIDCSGVNVCSSLAQTPPLVAAEHTGTSARLLHRG 660
DB 601 TLDERPPLHAAQRGHYVARILLIDCSGVNVCSSLAQTPPLVAAEHTGTSARLLHRG 660
QY 661 AGKEAVTSQGYTALHAAARNGHATVKKLVEEKADVLARGPANTALHAAAHGSEVE 720
DB 661 AGKEAVTSQGYTALHAAARNGHATVKKLVEEKADVLARGPANTALHAAAHGSEVE 720
QY 721 ELVSADVIDLPEDEGSLALHAAQGRHAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
DB 721 ELVSADVIDLPEDEGSLALHAAQGRHAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
QY 781 RSKT 784
DB 781 RSKT 784
RESULT 9
AAB94037
ID AAB94037 standard; protein; 784 AA.
XX AAB94037;
AC
XX
XX 26-JUN-2001 (first entry)
DT
XX Human protein sequence SEQ ID NO:14189.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
XX 27-AUG-1999; 99JP-00300253.
XX 11-JAN-2000; 2000JP-00118776.
XX 02-MAY-2000; 2000JP-00183767.
XX 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX MPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
PS Claim 8; SEQ ID NO 14189; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification; where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AA03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13632 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 784 AA:
Query Match 97.1%; Score 3959; DB 4; Length 784;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 767; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 1 MEGDGGTWMALALRTDAGFTGMEKVGSGGFGQVYKVRHVHMKMTALIKCSPLHYDD 60
DB 1 MEGDGGTWMALALRTDAGFTGMEKVGSGGFGQVYKVRHVHMKMTALIKCSPLHYDD 60
QY 61 RERMELEBAKQEMAKERYILPYGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
DB 61 RERMELEBAKQEMAKERYILPYGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
QY 121 ITHETAVGMNPLHGMAPPPLHLDLKPANILLADAHYHVKISDFGLACKNGLSHSHDLSDMG 180
DB 121 ITHETAVGMNPLHGMAPPPLHLDLKPANILLADAHYHVKISDFGLACKNGLSHSHDLSDMG 180
QY 181 LFGTAYLPERIRKESLPTDKHDVYSFAIVIVGVLTQKKPAPDEKNIILHMYKVYK 240
DB 181 LFGTAYLPERIRKESLPTDKHDVYSFAIVIVGVLTQKKPAPDEKNIILHMYKVYK 240
QY 241 RPELPVPCARAPRACSHLIRIMORCMQDPVPRPTFOETSETEDLCEKPDDEVETAMD 300
DB 241 RPELPVPCARAPRACSHLIRIMORCMQDPVPRPTFOETSETEDLCEKPDDEVETAMD 300
QY 301 LDVSPPEPRSEVVPARLKRAAPTFDNDYLSLSLQDLSGVQAVGPEELSRSSSES 360
DB 301 LDVSPPEPRSEVVPARLKRAAPTFDNDYLSLSLQDLSGVQAVGPEELSRSSSES 360
QY 361 KLPSGSGKRLSGVSVUSAFSSRGSLSLSEPRBSTDLGTRRPEBACGCHVRVTS 420
DB 361 KLPSGSGKRLSGVSVUSAFSSRGSLSLSEPRBSTDLGTRRPEBACGCHVRVTS 420
QY 421 KLPSGSGKRLSGVSVUSAFSSRGSLSLSEPRBSTDLGTRRPEBACGCHVRVTS 420
DB 421 KLPSGSGKRLSGVSVUSAFSSRGSLSLSEPRBSTDLGTRRPEBACGCHVRVTS 420
QY 481 KLMKLIQPOVDLALDSGASLLHLAVEAGQECAMKMLNNANPNLSNRSGSTPLHMAVE 480
DB 481 KLMKLIQPOVDLALDSGASLLHLAVEAGQECAMKMLNNANPNLSNRSGSTPLHMAVE 480
QY 541 RRVGVEVLELARKISVANAKEDQWTALHPAQNDESSSTRLLLEKNASVNEVDPEGTLP 540
DB 541 RRVGVEVLELARKISVANAKEDQWTALHPAQNDESSSTRLLLEKNASVNEVDPEGTLP 540
QY 541 MEVACQHQENIVRLLRGVDVSLQKQDANLPLHYAAMQCHLPVKKLAAQGVSVNAQ 600
DB 541 MEVACQHQENIVRLLRGVDVSLQKQDANLPLHYAAMQCHLPVKKLAAQGVSVNAQ 600
QY 601 TLDERPPLHAAQRGHYVARILLIDCSGVNVCSSLAQTPPLVAAEHTGTSARLLHRG 660
DB 601 TLDERPPLHAAQRGHYVARILLIDCSGVNVCSSLAQTPPLVAAEHTGTSARLLHRG 660
QY 661 AGKEAVTSQGYTALHAAARNGHATVKKLVEEKADVLARGPANTALHAAAHGSEVE 720
DB 661 AGKEAVTSQGYTALHAAARNGHATVKKLVEEKADVLARGPANTALHAAAHGSEVE 720
QY 721 ELVSADVIDLPEDEGSLALHAAQGRHAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
DB 721 ELVSADVIDLPEDEGSLALHAAQGRHAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
QY 781 RSKT 784
DB 781 RSKT 784
RESULT 10
AAU03539
ID AAU03539 standard; protein; 832 AA.

XX AC AAU03539;
 XX 12-SEP-2001 (first entry)
 XX DE Human protein kinase #39.
 XX KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder.
 XX OS Homo sapiens.
 XX PN W0200138503-A2.
 XX PD 31-MAY-2001.
 XX PF 22-NOV-2000; 2000WO-US032085.
 XX PR 24-NOV-1999; 99US-0167482P.
 XX PA (SUGEN-) SUGEN INC.
 XX PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX WP1; 2001-343950/36.
 XX DR N-PSDB; AAS06739.
 XX PT Nucleic acid encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX PS Claim 7; Fig 2; 433pp; English.
 XX CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 XX SQ Sequence 832 AA;
 QY Query Match 96.8%; Score 3946; DB 4; Length 832;
 DB Best Local Similarity 92.5%; Pred. No. 0;
 DB Matches 770; Conservative 3; Mismatches 11; Indels 48; Gaps 1;
 QY 1 MEGDGGTTPALALATTPAGSEPTGMEKYGSGGFGVVYKRVHMYKMTWLAIKSPSLAYDD 60
 DB 1 MEGDGGTTPALALATTPAGSEPTGMEKYGSGGFGVVYKRVHMYKMTWLAIKSPSLAYDD 60
 QY 61 RERMELTBKAKMENAKFRYILPVYGIQREPVGLVMEYMETSTLEKLASEBPLPMDLRF 120
 DB 61 RERMELTBKAKMENAKFRYILPVYGIQREPVGLVMEYMETSTLEKLASEBPLPMDLRF 120
 QY 121 ITHETAVGNNFLHCAAPPLILHDLKPANILLDAHNVKISDGLAKCNGLSHSHLSMDG 180
 DB 121 ITHETAVGNNFLHCAAPPLILHDLKPANILLDAHNVKISDGLAKCNGLSHSHLSMDG 180
 QY 181 LEFTIAYLPPERIRKRSRLFDTKHGVSPAIYIWGVLTQKKRPFADKNNILHIMVAVVGH 240

DB 181 LEFTIAYLPPERIRKRSRLFDTKHGVSPAIYIWGVLTQKKRPFADKNNILHIMVAVVGH 240
 QY 241 RPELPPVCGARRPACSHLIRLMORCWQSGPPRRPT----- 276
 DB 241 RPELPPVCGARRPACSHLIRLMORCWQSGPPRRPT----- 276
 QY 277 -----ORITSETEDLCRKPDEVEKETAHDLVKSPPPRSE 312
 DB 301 RSPGEGFRLESEYIIRVTCPLSSPQITTSRTBELCRKPDEVEKETAHDLVKSPPPRSE 360
 QY 313 VVPARLKRAAPTFDNDYLSLELLSQLDSGVSAVEGPEELRSSSESKLPSSGSGKRUS 372
 DB 361 VVPARLKRAAPTFDNDYLSLELLSQLDSGVSAVEGPEELRSSSESKLPSSGSGKRUS 420
 QY 373 GVSSVDSAPSSRGSLSLSPEREPTSDLGTRRPEEACGCHRVRTSKMLKILQPOVDV 432
 DB 421 GVSSVDSAPSSRGSLSLSPEREPTSDLGTRRPEEACGCHRVRTSKMLKILQPOVDV 480
 QY 433 IALDSGASLHLAVEAGQEECAKMLLNANPNLSNRSGSTPLHMAVERRVGVVELLLA 492
 DB 481 IALDSGASLHLAVEAGQEECAKMLLNANPNLSNRSGSTPLHMAVERRVGVVELLLA 540
 QY 493 RKISVNAKDEDQWTALHFAAQNGDESSTRLLLEKNSVNEVDEGRTPMHVAQHQENI 552
 DB 541 RKISVNAKDEDQWTALHFAAQNGDESSTRLLLEKNSVNEVDEGRTPMHVAQHQENI 600
 QY 553 VRILIRRGVDVSLQGDAMPLPHYAMQGHLPVTKLLAQGVSVNAQTLDSGTPHLAA 612
 DB 601 VRILIRRGVDVSLQGDAMPLPHYAMQGHLPVTKLLAQGVSVNAQTLDSGTPHLAA 660
 QY 613 ORGHYVARILIDLCSPDVNCSLLAQTPLHVALETGHTSTARLLHRGAKKAVTSDGYT 672
 DB 661 ORGHYVARILIDLCSPDVNCSLLAQTPLHVALETGHTSTARLLHRGAKKAVTSDGYT 720
 QY 673 ALHLAARNGLATVKKLVBEKADVLARGPLNQTALHLAAHGSSEVEELVSAVDYDLFD 732
 DB 721 ALHLAARNGLATVKKLVBEKADVLARGPLNQTALHLAAHGSSEVEELVSAVDYDLFD 780
 QY 733 EOGISALHLAAOGRHQAQTVETLLRHGHNTLQSLKPGCGHPAATLLRBSKT 784
 DB 781 EOGISALHLAAOGRHQAQTVETLLRHGHNTLQSLKPGCGHPAATLLRBSKT 832
 DB RESULT 11
 DB ID ABB69806 standard; protein; 832 AA.
 DB XX ABB69806;
 DB DE 20-JAN-2003 (first entry)
 DB XX Human polypeptide SEQ ID NO 1853.
 DB XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; nocotropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic.
 OS Homo sapiens.
 XX PN W0200270539-A2.
 XX PD 12-SEP-2002.
 XX PF 05-MAR-2002; 2002WO-US005095.
 XX PR 05-MAR-2001; 2001US-00799451.

(HYSE-) HYSEQ INC.

PA Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Dimaac RT;
 XX
 DR MPI; 2002-759812/82.
 DR N-PSDB; ABZ12023.

PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.

XX
 PS Claim 9; SEQ ID NO 1853; 1012pp + Sequence Listing; English.

XX
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ1119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_poc_sequences

XX
 SQ Sequence 832 AA;

Query Match 96.8%; Score 3946; DB 5; Length 832;

Best Local Similarity 92.5%; Pred. No. 0;

Matches 770; Conservative 3; Mismatches 11; Indels 48; Gaps 1;

QY 1 MEGDGGTMMALALRTFDAGEPTGWEKVGSGFGQYKVVHVMKMTWAIKCSPLHVD 60
 DB 1 MEGDGGTMMALALRTFDAGEPTGWEKVGSGFGQYKVVHVMKMTWAIKCSPLHVD 60

QY 61 REMMELLEBAKKEMAKFRITLVYGI CKEPVGLVMEYMETSGLEKILASBPPLRLRR 120
 DB 61 REMMELLEBAKKEMAKFRITLVYGI CKEPVGLVMEYMETSGLEKILASBPPLRLRR 120

QY 121 IIRHTAVGNMFLHGMAPLILHLDLKPNANITLDAHYVKISDFGLAKNGLSHSDLSMDG 180
 DB 121 IIRHTAVGNMFLHGMAPLILHLDLKPNANITLDAHYVKISDFGLAKNGLSHSDLSMDG 180

QY 181 LFGTIAVLPPERIRKSRRLFDTRGDVYSFAIVIGVLTOKKPPADEKNILHIMVKVKGH 240
 DB 181 LFGTIAVLPPERIRKSRRLFDTRGDVYSFAIVIGVLTOKKPPADEKNILHIMVKVKGH 240

QY 241 REPILPVCARAPRACSHLIRLMORCMQGDPRVPTF----- 276
 DB 241 REPILPVCARAPRACSHLIRLMORCMQGDPRVPTF----- 276

QY 277 -----OITSETDLCKEPDDEVKETAHLDVKSPPRSE 312
 DB 277 -----OITSETDLCKEPDDEVKETAHLDVKSPPRSE 312

QY 301 RSTGEGFRLESSEVIRVTCPLSPQETSTEDLCEKPDSEKETAHLDVKSPPRSE 360
 DB 301 RSTGEGFRLESSEVIRVTCPLSPQETSTEDLCEKPDSEKETAHLDVKSPPRSE 360

QY 313 VVPARLKRASAPTFDNDYLSSELLSGLDSGVSQAVBEPBELSRSSSESKLPSSGSGKRLS 372
 DB 313 VVPARLKRASAPTFDNDYLSSELLSGLDSGVSQAVBEPBELSRSSSESKLPSSGSGKRLS 372

QY 361 VVPARLKRASAPTFDNDYLSSELLSGLDSGVSQAVBEPBELSRSSSESKLPSSGSGKRLS 420
 DB 361 VVPARLKRASAPTFDNDYLSSELLSGLDSGVSQAVBEPBELSRSSSESKLPSSGSGKRLS 420

QY 373 GVSSVDSARSSRSGLSISFRERPESTSLGTTTRPBEZACCHVRDTSKMLKLOQDDV 432
 DB 373 GVSSVDSARSSRSGLSISFRERPESTSLGTTTRPBEZACCHVRDTSKMLKLOQDDV 432

QY 421 GVSSVDSARSSRSGLSISFRERPESTSLGTTTQDKKLDVAIVSGTSSKMLKLOQDDV 480
 DB 421 GVSSVDSARSSRSGLSISFRERPESTSLGTTTQDKKLDVAIVSGTSSKMLKLOQDDV 480

QY 433 LALDSGASLHLAVEAGQEBECAKMLLLNNANPNLSNRGSTPLHMAVERRVGVVELLLA 492
 DB 433 LALDSGASLHLAVEAGQEBECAKMLLLNNANPNLSNRGSTPLHMAVERRVGVVELLLA 492

DB 481 LALDSGASLHLAVEAGQEBECAKMLLLNNANPNLSNRGSTPLHMAVERRVGVVELLLA 540

QY 493 KRISYNADQEDQWTLAHPAQNQDESSSTRLLLEKRAASVNEVDPEKRTPMHVAQCHQENI 552
 DB 541 KRISYNADQEDQWTLAHPAQNQDESSSTRLLLEKRAASVNEVDPEKRTPMHVAQCHQENI 600

QY 553 VRIILRRGVDSLQKQDAMLPLHYAAMQGHPIYVLAKQPGVSVAQAOTLDGRTPLHLAA 612
 DB 601 VRIILRRGVDSLQKQDAMLPLHYAAMQGHPIYVLAKQPGVSVAQAOTLDGRTPLHLAA 660

QY 613 QRGHYRVARILIDCSQVNVCSLAAQTPHVAEFTGHTSTARLLHRAQKKAATSDGYT 672
 DB 661 QRGHYRVARILIDCSQVNVCSLAAQTPHVAEFTGHTSTARLLHRAQKKAATSDGYT 720

QY 673 ALHLAARNGHATVYGLVBEKADVLRGPINOTAAHLAAAHGSHSVSEELVSADYIDLFD 732
 DB 721 ALHLAARNGHATVYGLVBEKADVLRGPINOTAAHLAAAHGSHSVSEELVSADYIDLFD 780

QY 733 EGGLSALHLAAQGRHAQVETLLRHGAHINLOSLKFGQGHGPAATLRRSKT 784
 DB 781 EGGLSALHLAAQGRHAQVETLLRHGAHINLOSLKFGQGHGPAATLRRSKT 832

RESULT 12
 ID ABP58155 standard; protein; 759 AA.
 XX
 AC ABP58155;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE Death associated kinase containing ankyrin repeats (DAKAR) variant.
 XX
 KW Death associated kinase containing ankyrin repeats; DAKAR; human;
 KW protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;
 XX antipsoriatic; cyostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200298894-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 04-JUN-2002; 2002WO-US018039.
 XX
 PR 04-JUN-2001; 2001US-0295959P.
 XX
 PR 29-NOV-2001; 2001US-0334362P.
 XX
 PA (IMMV) IMMUNE CORP.
 XX
 PI Bird TA, Holland PM, Peschon JJ, Virca GP;
 XX
 DR MPI; 2003-148648/14.
 XX
 PT New isolated human death associated kinase containing ankyrin repeats
 PT polypeptide and polynucleotide, useful for treating psoriasis, melanoma
 PT or squamous cell carcinoma.
 XX
 PS Example 1; Page: 154pp; English.

XX
 CC The present sequence is the protein sequence of a naturally occurring
 CC variant of human death associated kinase containing ankyrin repeats
 CC (DAKAR). The variant comprises amino acids 26-784 of the DAKAR sequence
 CC given in ABP58155. DAKAR is a novel member of the serine/threonine
 CC protein kinase family. It is a mediator of apoptosis and putative
 CC modulator of cellular differentiation, proliferation, cell cycle and/or
 CC senescence. The invention provides DAKAR nucleic acids and polypeptides,
 CC as well as recombinant vectors, transfected host cells and methods of
 CC producing DAKAR polypeptides. The polypeptides are used in a claimed
 CC method of identifying candidate compounds that modulate DAKAR activity.
 CC DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell
 CC carcinoma (claimed). Note: The present sequence is not shown in the
 CC specification but is derived from the human DAKAR sequence given in the

CC Sequence Listing (see ABP58150)
XX SQ Sequence 759 AA;
Query Match 94.0%; Score 3835; DB 6; Length 759;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 744; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 26 EKVGSGGQYVYKVRHVHMKWTMLAIKGPSLHVDDREMELEBAKKEMAKFRYLTVY 85
DB 1 EKVGSGGQYVYKVRHVHMKWTMLAIKGPSLHVDDREMELEBAKKEMAKFRYLTVY 60
QY 86 GICRPPVGLVMEYMTGSLSEKLLASEPLPMDLRPRITHEITAVGMNPLHOMAPRLHLPLK 145
DB 61 GICRPPVGLVMEYMTGSLSEKLLASEPLPMDLRPRITHEITAVGMNPLHOMAPRLHLPLK 120
QY 146 PANILLDAHVKISDFGLAKCNGLSHSHDLSMDGLFGTIAVLPERRIREKSRLLPDTKHD 205
DB 121 PANILLDAHVKISDFGLAKCNGLSHSHDLSMDGLFGTIAVLPERRIREKSRLLPDTKHD 180
QY 206 VYSFAIVWGVLTQKKPFADEKNIHIMVKYVKGRRPELPVYCARPRACSHLILMLQRC 265
DB 181 VYSFAIVWGVLTQKKPFADEKNIHIMVKYVKGRRPELPVYCARPRACSHLILMLQRC 240
QY 266 WQGDPRVAPTFQETSETEDLCEKPDDEYKETAHDLVYKSPPEPSSEVVPARLKASAP 325
DB 241 WQGDPRVAPTFQETSETEDLCEKPDDEYKETAHDLVYKSPPEPSSEVVPARLKASAP 300
QY 326 FDNVYSLSBELSQLDLSGVAQAVEGPEELSRSSSESKLPSSGSGKRLSGVSVDSAFSSRG 385
DB 301 FDNVYSLSBELSQLDLSGVAQAVEGPEELSRSSSESKLPSSGSGKRLSGVSVDSAFSSRG 360
QY 386 SLSLSFEREPSTSDIGTTRPREBEACGCHRVADTSTKMLIOPQVVDLALDSGASLHLHA 445
DB 361 SLSLSFEREPSTSDIGTTRPREBEACGCHRVADTSTKMLIOPQVVDLALDSGASLHLHA 420
QY 446 VEAQGEBCAKMLLNANPNLSNRGSTPLHMAVRRVGVVELLARKISVNADEPDQW 505
DB 421 VEAQGEBCAKMLLNANPNLSNRGSTPLHMAVRRVGVVELLARKISVNADEPDQW 480
QY 506 TALAHPAONGDESSSTRLLLEKNAVNEVDPEGRTPMHYACQHQENIVRIILRGVDVSL 565
DB 481 TALAHPAONGDESSSTRLLLEKNAVNEVDPEGRTPMHYACQHQENIVRIILRGVDVSL 540
QY 566 QCKDAMLPHYAAMGCHLPYVGLAKQGVSNAGTLDGRTPHLHAAGRHVRAARIID 625
DB 541 QCKDAMLPHYAAMGCHLPYVGLAKQGVSNAGTLDGRTPHLHAAGRHVRAARIID 600
QY 626 LCSDNVNCSLAQTPHYAAGTHTSTARLLHARGAGKEAVTSDGYTALHLAARGHLAT 685
DB 601 LCSDNVNCSLAQTPHYAAGTHTSTARLLHARGAGKEAVTSDGYTALHLAARGHLAT 660
QY 686 VGLVLEEKADVLARPLNQTALHLAAGHSEVEELVSADVIDLFDGQSLALHLAAQG 745
DB 661 VGLVLEEKADVLARPLNQTALHLAAGHSEVEELVSADVIDLFDGQSLALHLAAQG 720
QY 746 RHAQTVETLIRGHAINLOSLKPOGSGHAPAAATLLARSKT 784
DB 721 RHAQTVETLIRGHAINLOSLKPOGSGHAPAAATLLARSKT 759

RESULT 13
ABP58156
ID ABP58156 standard; protein; 750 AA.
XX
XX ABP58156;
AC
DT 18-MAR-2003 (first entry)
XX
XX
DE Death associated kinase containing ankyrin repeats (DAKAR) variant.
KW Death associated kinase containing ankyrin repeats; DAKAR; human;
KW protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;

KW antiapoptotic; cytostatic.
XX
XX OS Homo sapiens.
XX MO200298894-A1.
XX
XX PD 12-DEC-2002.
XX
XX PF 04-JUN-2002; 2002WO-US018039.
XX PR 04-JUN-2001; 2001US-0295959P.
XX PR 29-NOV-2001; 2001US-0334362P.
XX
XX PA (IMMUNEX CORP.
XX
XX PL Bird TA, Holland PM, Peschon JJ, Virca GD;
XX WPI; 2003-148648/14.
XX
XX PT New isolated human death associated kinase containing ankyrin repeats
XX or squamous cell carcinoma.
XX
XX PS Example 1; Page; 154pp; English.
XX
XX CC The present sequence is the protein sequence of a naturally occurring
XX variant of human death associated kinase containing ankyrin repeats
XX (DAKAR). The variant comprises amino acids 1-750 of the DAKAR sequence
XX given in ABP58150. DAKAR is a novel member of the serine/threonine
XX protein kinase family. It is a mediator of apoptosis and putative
XX modulator of cellular differentiation, proliferation, cell cycle and/or
XX senescence. The invention provides DAKAR nucleic acids and polypeptides,
XX as well as recombinant vectors, transfected host cells and methods of
XX producing DAKAR polypeptides. The polypeptides are used in a claimed
XX method of identifying candidate compounds that modulate DAKAR activity.
XX DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell
XX carcinoma (claimed). Note: The present sequence is not shown in the
XX CC specification but is derived from the human DAKAR sequence given in the
XX Sequence Listing (see ABP58150)
XX
XX SQ Sequence 750 AA;
Query Match 93.3%; Score 3803; DB 6; Length 750;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 735; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEGDGGTFPMALALRTFDAGEFTGMEKVGSGGFGQYVYKVRHVHMKWTMLAIKGPSLHVDD 60
DB 1 MEGDGGTFPMALALRTFDAGEFTGMEKVGSGGFGQYVYKVRHVHMKWTMLAIKGPSLHVDD 60
QY 61 RERRELLLEBAKKEMAKFRYLTVYGTICREPVGLVMEYMTGSLSEKLLASEPLPMDLRFR 120
DB 61 RERRELLLEBAKKEMAKFRYLTVYGTICREPVGLVMEYMTGSLSEKLLASEPLPMDLRFR 120
QY 121 IHHETAAGMNFHOMAPRLHLDLKPANILLDAHVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 IHHETAAGMNFHOMAPRLHLDLKPANILLDAHVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAVLPERRIREKSRLLPDTKHDVYSFAIVWGVLTQKKPFADEKNIHIMVKYVKG 240
DB 181 LFGTIAVLPERRIREKSRLLPDTKHDVYSFAIVWGVLTQKKPFADEKNIHIMVKYVKG 240
QY 241 RPELPVYCARPRACSHLILMLQRCWQGDPRVAPTFQETSETEDLCEKPDDEYKETAH 300
DB 241 RPELPVYCARPRACSHLILMLQRCWQGDPRVAPTFQETSETEDLCEKPDDEYKETAH 300
QY 301 LDVKSPEPSSEVVPARLKASAPTFDNVYSLSBELSQLDLSGVAQAVEGPEELSRSSSES 360
DB 301 LDVKSPEPSSEVVPARLKASAPTFDNVYSLSBELSQLDLSGVAQAVEGPEELSRSSSES 360
QY 361 KLPSGSGKRLSGVSVDSAFSSSGSLSPFEREPSTSDIGTTRPREBEACGCHRVADTS 420
DB 361 KLPSGSGKRLSGVSVDSAFSSSGSLSPFEREPSTSDIGTTRPREBEACGCHRVADTS 420

QY	421	KLMKILPOPDVDLALDSCASLIHLAVEAQOECAKMLLNANPNPISNRGSPPLHMAVE	480
Db	421	KLMKILQEPQVDLALDSCASLIHLAVEAQOECAKMLLNANPNPISNRGSPPLHMAVE	480
QY	421	RRRVGVVELLIARKEISVNAKDEDMWTFHPAONGESTRLLLEGNASVNEVDPEGRTP	540
Db	421	RRRVGVVELLIARKEISVNAKDEDMWTFHPAONGESTRLLLEGNASVNEVDPEGRTP	540
QY	541	MHVACOHGQENIVRIILIRGVDVSLQGXDAWLPPLHYAAQGHLPYVKLLAKOPGVSVNAQ	600
Db	541	MHVACOHGQENIVRIILIRGVDVSLQGXDAWLPPLHYAAQGHLPYVKLLAKOPGVSVNAQ	600
QY	601	TLDGRTPLHLAAQGRYVARILLIDCSQNVNCSLLIAQTPLHYAAFTGHTSTARLLIHRG	660
Db	601	TLDGRTPLHLAAQGRYVARILLIDCSQNVNCSLLIAQTPLHYAAFTGHTSTARLLIHRG	660
QY	661	AGKEAVTSDGYTALHLAAANGHILATYKLLVEEKADVTLAAGPLNQTLHLAAAGHSEVVE	720
Db	661	AGKEAMTSGYTALHLAAANGHILATYKLLVEEKADVTLAAGPLNQTLHLAAAGHSEVVE	720
QY	721	ELVSADVIDLFDQEGLSALHLAAQGRHAQT	750
Db	721	ELVSADVIDLFDQEGLSALHLAAQGRHAQT	750

CC DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell
CC carcinoma (claimed). Note: The present sequence is not shown in the
CC specification but is derived from the human DAKAR sequence given in the
CC Sequence Listing (see ABP58150)
CC
SQ Sequence 725 AA;
XX

Db 241 GGCAGATTTCGCTACATCTGCTGCTGTGATGCGATCTGCGCGAACCCTGTCGCGCTGAT 300
Qy 301 CATGAGATACATGAGAGAGGGCTCCCTGGAAAAAGCTGCTGGGTTGGAGCCATTGGCCATG 360
Db 301 CATGAGATACATGAGAGAGGGCTCCCTGGAAAAAGCTGCTGGGTTGGAGCCATTGGCCATG 360
Qy 361 GGATCTCGGGTTCCGATCATCAAGAGAGCGCGGTGGGACATGAATCTTCTGCACTGACAT 420
Db 361 GGATCTCGGGTTCCGATCATCAAGAGAGCGCGGTGGGACATGAATCTTCTGCACTGACAT 420
Qy 421 GGCCTCGGCACTCTGCACTTGGACCTTGAACCGCGCGCAACATCTGCTGGATGCCCCTA 480
Db 421 GGCCTCGGCACTCTGCACTTGGACCTTGAACCGCGCGCAACATCTGCTGGATGCCCCTA 480
Qy 481 CCACTTCAAGATTTTGTGATTTTGTCTGCTGCGCAAGTGGCAACGGGCTGTCCCATCTGCCATGA 540
Db 481 CCACTTCAAGATTTTGTGATTTTGTCTGCTGCGCAAGTGGCAACGGGCTGTCCCATCTGCCATGA 540
Qy 541 CCTCAGCATGATGAGCTGTTTGGACATCGCTACCTCCCTCCAGAGCGCATGAGGGA 600
Db 541 CCTCAGCATGATGAGCTGTTTGGACATCGCTACCTCCCTCCAGAGCGCATGAGGGA 600
Qy 601 GAAGAGCGGCTCTTTCGACACCAAGCACGATGTATACAGCTTTGGGATGTCATCTGAGG 660
Db 601 GAAGAGCGGCTCTTTCGACACCAAGCACGATGTATACAGCTTTGGGATGTCATCTGAGG 660
Qy 661 CGTGTCAACAGAGAGCGGTTTGGATGAGAGAACATCCCTGCACTCATATGATGA 720
Db 661 CGTGTCAACAGAGAGCGGTTTGGATGAGAGAACATCCCTGCACTCATATGATGA 720
Qy 721 GGTGTGAGAGGCGCACCGCCCGAGCTGCGCCGCTGTGACAGAGCCGCGCGCGCTG 780
Db 721 GGTGTGAGAGGCGCACCGCCCGAGCTGCGCCGCTGTGACAGAGCCGCGCGCGCTG 780
Qy 781 CAGCCACTGATACGCTTCATGACAGCGGTGCTGCGAGGGGATCCGCAATTAAGCCAC 840
Db 781 CAGCCACTGATACGCTTCATGACAGCGGTGCTGCGAGGGGATCCGCAATTAAGCCAC 840
Qy 841 CTTCGAAGAAATTAATTTCTGGAACCGAGGACCTGTGTGAAAGCTGTATGAGAAATGA 900
Db 841 CTTCGAAGAAATTAATTTCTGGAACCGAGGACCTGTGTGAAAGCTGTATGAGAAATGA 900
Qy 901 AGAAATCTGCTGATCTGAGCTGAGAGTGAAGAAAAAGCCCCGAGGCCAGAGAGAGTGTGCC 960
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (sites)
Shimizu, N., Kudoh, J. and Shibuya, K.
Homo sapiens mRNA for ANKRD3, complete cds
Published Only in Database (2001)
2 (bases 1 to 3882)
Shimizu, N., Kudoh, J. and Shibuya, K.
Direct Submission
Submitted (25-AUG-2000) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
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ORIGIN

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Query Match	98.8%;	Score 3815.2;	DB 9;	Length 3882;
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 REFERENCE
 1 Bharti, Rohwer, A., Stempka, L., Rincke, G., Marks, F. and Geschwendt, M.
 Dik, a novel protein kinase that interacts with protein kinase
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 J. Biol. Chem. 275 (46), 36350-36357 (2000)
 MEDLINE 20549657
 PUBMED 10948194
 REFERENCE 2 (bases 1 to 3879)
 AUTHORS Geschwendt, M.
 TITLE Direct Submission

JOURNAL Submitted (18-MAY-2000) Gechwendt M., Biochemistry of
Tissue-specific Regulation, German Cancer Research Center, Im
Neuenheimer Feld 280, D-69151 Heidelberg, GERMANY

FEATURES

SOURCE

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ORIGIN

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VERSION BD157754.1
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REFERENCE 1 (bases 1 to 3876)
Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Salto,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Makamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof.
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PF 28-JUL-2000 JP 2000280990
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PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
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Primer for synthesizing full-length cDNA and use thereof FH Key
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Db 1256 CAGGATGCGGTTCCCAAGAGCTCAGAGAGAGAGAGCTTGTGATGCGATGCGTTC- 1314
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LOCUS AX879283
DEFINITION Sequence 14188 from Patent Ep1074617.
ACCESSION AX879283
VERSION AX879283.1 GI:40034019
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS Ota, T., Iwagai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 14188 07-FEB-2001;
Research Association for Biotechnology (JP)
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source location/Qualifiers
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/organism="Homo sapiens"
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Qy	3606	CGTGCMAACATGTACCGTGGCGCTGTATATGATATAGAGATTGATATTAATGATACCATGTAT	3665
Db	3655	CGTGCMAACATGTACCGTGGCGCTGTATATGATATAGAGATTGATATTAATGATACCATGTAT	3714
Qy	3666	GTTAATGTGAATCTGTGGCGAGGAATCTTTTTCATGCGACGAGAAATATCCAGCTGTGAA	3725
Db	3715	GTTAATGTGAATCTGTGGCGAGGAATCTTTTTCATGCGACGAGAAATATCCAGCTGTGAA	3774
Qy	3726	ACTGGCTATGTTTAAATATAGCTCATTTGGCTTACTGTTGTGTGACCTGGGTAGGGA	3785
Db	3775	ACTGGCTATGTTTAAATATAGCTCATTTGGCTTACTGTTGTGTGACCTGGGTAGGGA	3833
Qy	3786	CAGAAGTTCATTTGATGATCATATTAAGCAAGTACTTGGCC	3826
Db	3835	CAGAAGTTCATTTGATGATCATATTAAGCAAGTACTTGGCC	3875
RESULT 6			
AK027424			
LOCUS	AK027424	3876 bp	mRNA linear PRI 30-JAN-2004
DEFINITION	Homio sapiens cDNA FLJ14518 fls, clone NT2BM1000850, weakly similar to ANKRRIN R.		
ACCESSION	AK027424		
VERSION	AK027424.1	GI:14042089	
KEYWORDS	oligo capping, fls (full insert sequence).		
SOURCE	Homio sapiens (human)		
ORGANISM	Homio sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Oobayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahara,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,K., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishihashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hirooka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Hosoda,M., Houchuta,T., Kusano,Y., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yunki,H., Oshima,A., Saeki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Kung'uama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Irahara,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hiroo,M., Omori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,K., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togaishi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Tanaka,Y., Yamashita,K., Nagase,T., Nomura,N., Kikuchi,H., Maehino,Y., Yamashita,R.,		

TITLE	Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
JOURNAL	Complete sequencing and characterization of 21,243 full-length
PUBMED	human cDNAs
REFERENCE	Nat. Genet. 36 (1), 40-45 (2004)
AUTHORS	1 2
TITLE	Isogai,T., Oca,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Mishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Maesho,Y., Nimomiya,K. and Iwayanagi,T. NEO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 3876)
AUTHORS	Isogai,T. and Otsuki,T.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomice@hi.co.jp; Tel:81-438-52-1975, Fax:81-438-52-3986) NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
COMMENT	Location/Organism: 1..3876 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="NT2RM1000850" /cell_line="NT2" /cell_type="teratocarcinoma" /clone_id="NT2RM1" /note="Cloning vector: pUC19FL3-mRNA from uninduced NT2 neutonal precursor cells." 66..2420 /note="unnamed protein product" /codon_start=1 /protein_id="BAB55102.1" /db_xref="gi:14042090" /translation="MEEDGGTFPMALRLTRPDAGEFTGMEKVGSGFGQVYVRHNH KTWLAIKSPSLIHVDREMRMLEERAKMEMAKERYILLPVGIICBPGLVWNETHT SLEKLASEPLPMDLRPRRIIHETAVGNMFICMAPLLHLDEKPANILLDAYHVHI DPEKLACNGLSHSNDLSDMGLEGTAIVAPPERIRKSRLSDPKHDVYSFAIYWVLG CKRPPADEKRNLIHWVKYGRPELPVCARPAAGSHLILMORCMGDPRVPT OBTSEPTDLCEKPPDVYKTHAHIDLVCSPEPSRVPARIKRASAPFPNDYSLS LISQDSGVSAVBGPBELSRSSSSSKIPSSSGRLSGSVYSDAIFSRGSLISLF REPSTSDIGTDDVQRKKLVDAIVSGDTSRKMTLOPQVDLALDSGAALHAIVEAG EECKAMLLNNANPNLSNRGSTPLDMAVERKRVNERLARKI SVANKKDIDOWTA HPAAONGDESSTRLLIEKNASVEVDPGFLPFMHAKCGQENIYAIVILRRGDVSL GKDAMLPIHYAMAOGHLPIVKLAPOGSVAOCTLDGRTPHLAORGHYVARIL DLCSVNVCSIALOTPELVAAETGTSTARRILLHRGAGKEATVSQGYTLHLAARG LAYVALVEEKADVLAERPPLANOTLARHLAAHGHSVVEBVSADVIDLDFEGSLSL LAAQGRHQVETYLIRGHAHINLOSILKTFQGSGHPATYILRSKTY"
FEATURES	CDS
SOURCE	Query_Match 98.1%; Score 3787.4; DB 9; Length 3876; Best Local Similarity 99.8%; Pred. No. 0; Matches 3813; Conservative 0; Mismatches 6; Indels 2; Gaps 2
ORIGIN	7 GTCCGCCGCAGATGAGAGGCGACGCGGCGGACCACCATGGGCGCTTCGGCGCACTT 66 Db GACTGCGCCGATGAGAGGCGGACGCGGCGGACCCCACATGGGCGCTTCGGCGCACTT 115 Qy CGACGCGGCGGCGATTACGCGGCGCTGGGAGAGAGTGTTGGGCGCTTCGGCGCAGGTGTA 126 Db CGAATGCGGCGGCGATTACGCGGCGCTGGGAGAGAGTGTTGGGCGCTTCGGCGCAGGTGTA 175 Qy CAAGTGGCGCATGTTCATGAGAACAACATCGGCTGGCGCATCAAGTGTCTGCCGCCGCACTGCA 186

Db	176	CAAGGTGGCCATGTCACCTGGAAGACCTGGCTGCGCATCAAGTGTGCGCCAGCTGCA	235
Qy	187	CGTCGACGACGAGGAGCGCATGAGACTTTTGGAAAGAACCAAGAAAGATGAGATGGCCAA	246
Db	236	CGTCGACGACGAGGAGCGCATGAGACTTTTGGAAAGAACCAAGAAAGATGAGATGGCCAA	295
Qy	247	GTTCGCTACATCCCTGCTGTGTATGCGATCTGCGCGCAACTGTGCGCTGTGATGGA	306
Db	296	GTTCGCTACATCCCTGCTGTGTATGCGATCTGCGCGCAACTGTGCGCTGTGATGGA	355
Qy	307	GTACATGGAAGCGGCTCTCTGGAAAAGCTGTGCTTCCGAGCCATTGCCATGGGATCT	366
Db	356	GTACATGGAAGCGGCTCTCTGGAAAAGCTGTGCTTCCGAGCCATTGCCATGGGATCT	415
Qy	367	CCGGTCCGAAATCATCCAGAGACGGGCGGTGGGCAATGAATTCCTGCACTGACGGCCCC	426
Db	416	CCGGTCCGAAATCATCCAGAGACGGGCGGTGGGCAATGAATTCCTGCACTGACGGCCCC	475
Qy	427	GCCAATCCGTAACCTGACCTCAAGCCCGCAACATCTGTGTGATGCGCCACTACAGCT	486
Db	476	GCCAATCCGTAACCTGACCTCAAGCCCGCAACATCTGTGTGATGCGCCACTACAGCT	535
Qy	487	CAAGATTTCTGAATTTTGTGTGTGCGCAATGCAACGGGCTGTGCCACTGTGCACTACAG	546
Db	536	CAAGATTTCTGAATTTTGTGTGTGCGCAATGCAACGGGCTGTGCCACTGTGCACTACAG	595
Qy	547	CATGATATGGCCGTGTTGGCAACATGCGCTACCTCCCTCACAAGGCAATCAGGGAAGAG	606
Db	596	CATGATATGGCCGTGTTGGCAACATGCGCTACCTCCCTCACAAGGCAATCAGGGAAGAG	655
Qy	607	CCGGCTCTTCGACACCAAGCAAGATGTATACGCTTTGCGATCTGATCTTGCGGCGTGTCT	666
Db	656	CCGGCTCTTCGACACCAAGCAAGATGTATACGCTTTGCGATCTGATCTTGCGGCGTGTCT	715
Qy	667	CACACAGAAAGGCCGTTTGCAATGAGAGAAACATCTCTGCAATCATGTGGAAGGTGTCT	726
Db	716	CACACAGAAAGGCCGTTTGCAATGAGAGAAACATCTCTGCAATCATGTGGAAGGTGTCT	775
Qy	727	GAAAGGCCACCGCCCCCGAGCTGCGCCCGGTGTGCAAGACCCGGCCCGCGCGCTGAGCCA	786
Db	776	GAAAGGCCACCGCCCCCGAGCTGCGCCCGGTGTGCAAGACCCGGCCCGCGCGCTGAGCCA	835
Qy	787	CTGTATACGCTCATGCAAGCGGTGTGTGCAAGGGAGATCCGAGATGTAGGCCCACTTCCA	846
Db	836	CTGTATACGCTCATGCAAGCGGTGTGTGCAAGGGAGATCCGAGATGTAGGCCCACTTCCA	895
Qy	847	AGAAATTAATCTTGAAACCGAGACCTGTGTGAAAAGCTGATGACGAAGTGAAGAAAC	906
Db	896	AGAAATTAATCTTGAAACCGAGACCTGTGTGAAAAGCTGATGACGAAGTGAAGAAAC	955
Qy	907	TGCTCATGATCTGGAACGTGAAAAGCCCCCGAGAGCCGAGAGCGAGAGGTGTGCTGCGAG	966
Db	956	TGCTCATGATCTGGAACGTGAAAAGCCCCCGAGAGCCGAGAGCGAGAGGTGTGCTGCGAG	1015
Qy	967	GCTCAAGCGGAGCTGTGCCCCCACCCTTGATGATACGACTACAGCTCTCCGAGTCTCTC	1026
Db	1016	GCTCAAGCGGAGCTGTGCCCCCACCCTTGATGATACGACTACAGCTCTCTCCGAGTCTCTC	1075
Qy	1027	ACAGCTGGAATCTGGAATTTCCAGAGCTGTGAGGGGCCCCGAGAGGCTCAAGCCGACGCTC	1086
Db	1076	ACAGCTGGAATCTGGAATTTCCAGAGCTGTGAGGGGCCCCGAGAGGCTCAAGCCGACGCTC	1135
Qy	1087	CTCTGAGTCCAGAGCTGCCATCTCTCCGAGATGGGAAGAGGCTCTGCGGGGTGTCTCTCGGT	1146
Db	1136	CTCTGAGTCCAGAGCTGCCATCTCTCCGAGATGGGAAGAGGCTCTGCGGGGTGTCTCTCGGT	1199
Qy	1147	GGACTCCGCGCTCTCTTCAGAGAGATCACTGTGCTGTCTTTGAGCGGGAACTTTCAAC	1206
Db	1196	GGACTCCGCGCTCTCTTCAGAGAGATCACTGTGCTGTCTTTGAGCGGGAACTTTCAAC	1255
Qy	1207	CAGCAATCTGGGTACCAAGACGTTCAGAGAAAGACTTGTGATGTCATCGTGTCC	1265

Db	1256	CAGCGATCTGGGTATCAC - AGACGTCCAGAAAGAAAGCTTTGGATATGCATCGTGC	1314
Qy	1266	GGGACACCAAGCAAACTGATGAAAGTCTTCGACGCTCGCAGACGTGGACCTTGGACCTTGGACA	1325
Db	1315	GGGACACCAAGCAAACTGATGAAAGTCTTCGACGCTCGCAGACGTGGACCTTGGACCTTGGACA	1374
Qy	1336	GCGGTGCGACGCTGCTGCACTCGCGGGTGGAGGCGCGGGCAAGAGAGTGGCCAAATGGGC	1385
Db	1375	GCGGTGCGACGCTGCTGCACTCGCGGGTGGAGGCGCGGGCAAGAGAGTGGCCAAATGGGC	1434
Qy	1386	TGCTGTCAAAATGACCAACCCCAACCTGAGCAACGTTAGGGGCTCCACCCCGTTGGACA	1445
Db	1435	TGCTGTCAAAATGACCAACCCCAACCTGAGCAACGTTAGGGGCTCCACCCCGTTGGACA	1494
Qy	1446	TGGCGGTGAGAGAGAGGTGCGGGGTGTCTGAGACTCTGTGGCAACGAAATCAAGT	1505
Db	1495	TGGCGGTGAGAGAGAGGTGCGGGGTGTCTGAGAGCCTGTGGCAACGAAATCAAGT	1554
Qy	1506	TCAATGCCAAGATGAGAGACAAATGAGACAGCCCTCCACTTTGACGCCAAGACGGGGATG	1565
Db	1555	TCAATGCCAAGATGAGAGACAAATGAGACAGCCCTCCACTTTGACGCCAAGACGGGGATG	1614
Qy	1566	AGCTAGACACGAGCTGCTGTTTGGAGAAAGACGCTCGATCAAGAGGTGACCTTTGAGG	1625
Db	1615	AGCTAGACACGAGCTGCTGTTTGGAGAAAGACGCTCGATCAAGAGGTGACCTTTGAGG	1674
Qy	1626	GCCGACGCCCATGACGATGACGATGACCTGACGACACGAGGAGAAATATGTCGATCTTGC	1685
Db	1675	GCTTGAAGCCCATGACGATGACGATGACCTGACGACACGAGGAGAAATATGTCGATCTTGC	1734
Qy	1686	TGCGCCGAGGCGTGGACGTGAGCCTGACAGGACCAAGATGCTTGGCTGCACTTGAATAAG	1745
Db	1735	TGCGCCGAGGCGTGGACGTGAGCCTGACAGGACCAAGATGCTTGGCTGCACTTGAATAAG	1794
Qy	1746	CTGCTGGACAGGAGCCACCTGCCCATCTGCAAGCTGTGGACCAAGCGCGGGGTGAGTG	1805
Db	1795	CTGCTGGACAGGAGCCACCTGCCCATCTGCAAGCTGTGGACCAAGCGCGGGGTGAGTG	1854
Qy	1806	TGAACGCCACAGACGCTGATGAGAGAGACGCAATTTGACCTTGGCGCACAGCGCGGACCT	1865
Db	1855	TGAACGCCACAGACGCTGATGAGAGAGACGCAATTTGACCTTGGCGCACAGCGCGGACCT	1914
Qy	1866	ACCAGGTGGCCCGCATCTCTCATCGACCTGTGCTCGAAGTCAAGTCTGACAGCCCTGCGG	1925
Db	1915	ACCAGGTGGCCCGCATCTCTCATCGACCTGTGCTCGAAGTCAAGTCTGACAGCCCTGCGG	1974
Qy	1926	CACACACACCCCTGACGTTGGCCGCGGAGAGAGGGGACACAGAGACCTGACAGGCTTGC	1985
Db	1975	CACACACACCCCTGACGTTGGCCGCGGAGAGAGGGGACACAGAGACCTGACAGGCTTGC	2033
Qy	1986	TGCATTCGAGGCGCTGGCAAGAGAGCCCTGACCTCGACGAGCTTGCACCTGACCTGG	2045
Db	2035	TGCATTCGAGGCGCTGGCAAGAGAGCCCTGACCTCGACGAGCTTGCACCTGACCTGG	2094
Qy	2046	CTGCCCGCAACGACACCTTGGCACTGTGCAAGCTGTGTTGAGAGAGAAAGCCCATTTGC	2105
Db	2095	CTGCCCGCAACGACACCTTGGCACTGTGCAAGCTGTGTTGAGAGAGAAAGCCCATTTGC	2155
Qy	2106	TGGCCCCGGGAGACCCCTGAAACAGAGAGGGGCTGACCTGAGCTGCGGCCACAGGGACCTGG	2165
Db	2155	TGGCCCCGGGAGACCCCTGAAACAGAGAGGGGCTGACCTGAGCTGCGGCCACAGGGACCTGG	2214
Qy	2166	AGGTGATGAGAGATTTGGTTCAGCGCCGATGTCTATTGACCTGTTTCAGACGAGGGCTCA	2225
Db	2215	AGGTGATGAGAGATTTGGTTCAGCGCCGATGTCTATTGACCTGTTTCAGACGAGGGCTCA	2274
Qy	2226	GCGCGCTGACCTGGCCGCGCCAGGGCCGACGACACAGACGATGAGACTCTGTCTAAGGC	2285
Db	2275	GCGCGCTGACCTGGCCGCGCCAGGGCCGACGACACAGACGATGAGACTCTGTCTAAGGC	2333
Qy	2286	ATGGGGGCCCAATCAACCTGACAGACCTCAAGTTTCAGGGGGGACATGGCCCGCGGCA	2345
Db	2335	ATGGGGGCCCAATCAACCTGACAGACCTCAAGTTTCAGGGGGGACATGGCCCGCGGCA	2394

QY	1634	CCCATGCACTGAGCTTGCCAGACCGGGCAGAGAAATATCTGTCGATCTCTGTCGCCGA	1633
Db	1620	CCCAAGCACTGAGCTTGCCAGACCGGGCAGAGAAATATCTGTCGATCTCTGTCGCCGA	1679
QY	1694	GAGCTGAGACGTAGAGCTGACAGGGCAGAGATGCTGGCTGCGCACTGACATGCTGCTGG	1753
Db	1680	GAGCTGAGACGTAGAGCTGACAGGGCAGAGATGCTGGCTGCGCACTGACATGCTGCTGG	1739
QY	1754	CAGGGCCACTGCCCCATGCTGACAGCTGCGCTTGGCCAGACAGCCGGGGGTGAGTGTGAAGCC	1813
Db	1740	CAGGGCCACTGCCCCATGCTGACAGCTGCGCGCCAGACAGCCGGGGGTGAGTGTGAAGCC	1799
QY	1814	CAGAGGCTGAGATGGAGAGACGCATTTGACCTGGCCGACAGCCGGGGCCATTCACCGGCTG	1873
Db	1800	CAGAGGCTGAGATGGAGAGACGCATTTGACCTGGCCGACAGCCGGGGCCATTCACCGGCTG	1859
QY	1874	GCCCCCATCTTCATGACCTGTGCTCCAGCGTCAACGTCTGCAGCTTGCTGGCACAACA	1933
Db	1860	GCCCCCATCTTCATGACCTGTGCTCCAGCGTCAACGTCTGCAGCTTGCTGGCACAACA	1919
QY	1934	CCCCCTGCACTGAGCCCGCGAGACCGGGGCACACAGACATGGCAGGCTGCTCTGCAATGG	1993
Db	1920	CCCCCTGCACTGAGCCCGCGAGACCGGGGCACACAGACATGGCAGGCTGCTCTGCAATGG	1979
QY	1994	GAGCTGAGCAAGAGAGGCGGTGACCTCAGACGGCTACACCGCTCTTGCACCTTGCTGCCGC	2053
Db	1980	GAGCTGAGCAAGAGAGGCGGTGACCTCAGACGGCTACACCGCTCTTGCACCTTGCTGCCGC	2039
QY	2054	AAAGGACACTGGGCCACTGTCAAGCTGCTTGTGAGAGAAAGCCGATGTGCTGCCCGG	2113
Db	2040	AAAGGACACTGGGCCACTGTCAAGCTGCTTGTGAGAGAAAGCCGATGTGCTGCCCGG	2099
QY	2114	GGAACCCCTGAAACACAGCGGCGCTGACCTGGCTGCGGCCACAGGGCACTCGAGGGTGGT	2173
Db	2100	GGAACCCCTGAAACACAGCGGCGCTGACCTGGCTGCGGCCACAGGGCACTCGAGGGTGGT	2159
QY	2174	GAGAGTTGTCAGCGCCGATGTCAATTGACTTGTTCAGACAGAGGGGCTCAGCGCGCTG	2233
Db	2160	GAGAGTTGTCAGCGCCGATGTCAATTGACTTGTTCAGACAGAGGGGCTCAGCGCGCTG	2219
QY	2234	CACCTGGCCGCCCAAGGGCCGGACGACACAGACGGTGGAGACTCTGCTCAGGCAATGGGCC	2293
Db	2220	CACCTGGCCGCCCAAGGGCCGGACGACACAGAGGTGGAGACTCTGCTCAGGCAATGGGCC	2279
QY	2294	CACATCAACTTGCAGAGCCTCAAGTTCAGAGGCGGCGCAATGGCCCGCCGACACTCTGT	2353
Db	2280	CACATCAACTTGCAGAGCCTCAAGTTCAGAGGCGGCGCAATGGCCCGCCGACACTCTGT	2339
QY	2354	CGGCGAAGACAGACTTAGTGTGCTGCTGCGGAGACCGGGGTCCAGGTGGGGCTTTGT	2413
Db	2340	CGGCGAAGACAGACTTAGTGTGCTGCTGCGGAGACCGGGGTCCAGGTGGGGCTTTGT	2399
QY	2414	CGTGTCTGTGTTCCCTCGGGGGAGTGAACGATCTCGGTGGGGGCCCGTGTGGGCTTAC	2473
Db	2400	CGTGTCTGTGTTCCCTCGGTGGGGAGTGAACGATCTCGGTGGGGGCCCGTGTGGGCTTAC	2458
QY	2474	CTTAAATGTTTAAACAAGACAGAGGTGACATGTGTCATCAGAGAGCGGCTGTCTTGAACCG	2533
Db	2459	CTTAAATGTTTAAACAAGACAGAGGTGACATGTGTCATCAGAGAGCGGCTGTCTTGAACCG	2518
QY	2534	ACTGTCCCTCCAGGTTGAAGCTGGCTCAGGTGCAATGCGCGCTCACAATCGAATCTAGG	2593
Db	2519	ACTGTCCCTCCAGGTTGAAGCTGGCTCAGGTGCAATGCGCGCTCACAATCGAATCTAGG	2578
QY	2594	CACCTGCTGTCTGAAGAGGACCGTGGGTGAGATCAATTCGTTGTGCTCTTATGGTGGC	2653
Db	2579	CACCTGCTGTCTGAAGAGGACCGTGGGTGAGATCAATTCGTTGTGCTCTTATGGTGGC	2638
QY	2654	TGAGGCTGTCTCTCAGTATGATGAAGCCCAAGCGTGGAAAGATCCACTCTCTCTGAGGC	2713
Db	2639	TGAGGCTGTCTCTCAGTATGATGAAGCCCAAGCGCGTGGAAAGATCCACTCTCTCTGAGGC	2698

QY	2714	GAGCCACCTTGGGTTGCTGGAGCTCACCAAGCTCTTGAGGAGGTGCAGAGGAAACTGTGTT	2773
Db	2699	GAGCCACCTTGGGTTGCTGGAGCTCACCAAGCTCTTGAGGAGGTGCAGAGGAAACTGTGTT	2758
QY	2774	TTTATCTCTCAATCATGACGGTGGGGCAGAGAGCCCTGTCTTAAAGTTTCCATGAAATTGT	2833
Db	2759	TTTATCTCTTCAATCATGACGGTGGGGCAGAGAGCCCTGTCTTAAAGTTTCCATGAAATTGT	2818
QY	2834	TTTATAAAAATATCTTAAAGAGATGAAATACCTTATCAGCTGTTCCTTGAACCTGTTAAAA	2893
Db	2819	TTTATAAAAATATCTTAAAGAGATGAAATACCTTATCAGCTGTTCCTTGAACCTGTTAAAA	2878
QY	2894	TGTTCAATPAACATTTGGATATGTCATGCTCTTAAATGATGCGCTAAGTATGAGGTGGCTTGG	2953
Db	2879	TGTTCAATPAACATTTGGATATGTCATGCTCTTAAATGATGCTAAGTATGAGGTGGCTTGG	2938
QY	2954	AAAACAATGTTTATATGCAACAAAGGAAGAAATGATGAGACAGCTTTGCGGGGCGTATGT	3013
Db	2939	AAAACAATGTTTATATGCAACAAAGGAAGAAATGATGAGACAGCTTTGCGGGGCGTATGT	2998
QY	3014	GTGGCCAGCTCTTAAACCAATTCAGTCTTATTACTTGGGTGAGTCCCTTGTGACACACAC	3073
Db	2999	GTGGCCAGCTCTTAAACCAATTCAGTCTTATTACTTGGGTGAGTCCCTTGTGACACACAC	3058
QY	3074	AACAGTCCCAACATGATATAGTCTGAGTCCGCTGCTTCTGCTTGCTTAAGATGTTTGGCAA	3133
Db	3059	AACAGTCCCAACATGATATAGTCTGAGTCCGCTGCTTCTGCTTGCTTAAGATGTTTGGCAA	3118
QY	3134	CTCTAGAGCCACAGGCGCTAAGAGTCATTTAAAAAATTCCTCCCTTGTAAACCTCAGTGCCTG	3193
Db	3119	CTCTAGAGCCACAGGCGCTA - AGTCATTTAAAAAATTCCTCCCTTGTAAACCTCAGTGCCTG	3176
QY	3194	GGACTGAGGCGAGGCCCTCAGGTCGCTGAGTGCACACAGTCTTGGGGAAGAAGGTGCAGG	3253
Db	3177	GGACTGAGGCGAGGCCCTCAGGTCGCTGAGTGCACACAGTCTTGGGGAAGAAGGTGCAGG	3236
QY	3254	AGAAAGCTGTGTTTTTATCTTCCACACGCAAGTATGAAATGATAATTAATTAATTAATTAATTA	3313
Db	3237	AGAAAGCTGTGTTTTTATCTTCCACACGCAAGTATGAAATGATAATTAATTAATTAATTAATTA	3296
QY	3314	GACATPAGCACTATTAACCTAGTATGATGAGCACTGTCACCTGCAACCTTCCAGGCTTCAT	3373
Db	3297	GACATPAGCACTATTAACCTAGTATGATGAGCACTGTCACCTGCAACCTTCCAGGCTTCAT	3356
QY	3374	TTTTGTATGATGATTTGGGATAGGGAATATGTTTTGGGGTATGGGGGAGTGTTCGCAC	3433
Db	3357	TTTTGTATGATGATTTGGGATAGGGAATATGTTTTGGGGTATGGGGGAGTGTTCGCAC	3416
QY	3434	CTGCTTTGCAGACGTGCTCTCCGCACTTCAGCAAGTTTGGGAGTGTGGCCCAAGGGCGGTTCT	3493
Db	3417	CTGCTTTGCAGACGTGCTCTCCGCACTTCAGCAAGTTTGGGAGTGTGGCCCAAGGGCGGTTCT	3476
QY	3494	TGATATPAAAGATATGCGGCAATCTAGCTCGTAACCTTCACTGTCACCTGTGTCCATAGG	3553
Db	3477	TGATATPAAAGATATGCGGCAATCTAGCTCGTAACCTTCACTGTCACCTGTGTCCATAGG	3536
QY	3554	GTGCGCTTCTGAATCTGTATTTAGAAATATGTTTGGCAGAACCTGCACCTCGCTGCAAA	3613
Db	3537	GTGCGCTTCTGAATCTGTATTTAGAAATATGTTTGGCAGAACCTGCACCTCGCTGCAAA	3596
QY	3614	CATGTACCGTGGCGCTGTATATGATATGAGATTTGATATTAATGATCAATGATGTTAATGT	3673
Db	3597	CATGTACCGTGGCGCTGTATATGATATGAGATTTGATATTAATGATCAATGATGTTAATGT	3656
QY	3674	GAATCTGTGGCAGAGATATCTTTTTCATGCGCAGAAATATCCAACTGTGTGAAACTTGCTTA	3733
Db	3657	GAATCTGTGGCAGAGATATCTTTTTCATGCGCAGAAATATCCAACTGTGTGAAACTTGCTTA	3716
QY	3734	TGTTTAAATATAGCCCATATGTCCTTATATGTCGTGATGAGCATGCGTGAAGGGAACAAGAT	3793
Db	3717	TGTTTAAATATAGCCCATATGTCCTTATATGTCGTGATGAGCATGCGTGAAGGGAACAAGAT	3776
QY	3794	TCCATTTGATGTCATATTAAGCAAAATCTTGCTCACTTTTGTGAACTGAAAAAATAA	3853

|||||
Db 3777 TCCATTGATGATCAATAGCAAGTACTTGCCTACTTTTGGAAAAA 3836
|||
QY 3854 AAAA 3858
|||
Db 3837 AAAA 3841
|||
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LOCUS Homo sapiens genomic DNA, chromosome 21, clone:KB57H6, MX1-D21S171
DEFINITION
ACCESSION AP001615 GI:7670569
VERSION AP001615.1
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 124516)
TITLES Shimizu,N., Kudoh,J. and Shibuya,K.
JOURNAL Homo sapiens genomic DNA, chromosome 21, clone:KB57H6, MX1-D21S171
region
Published Only in DataBase (2000)
2 (bases 1 to 124516)
REFERENCE
AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
TITLES Direct Submission
JOURNAL Submitted (04-APR-2000) Nobuyoshi Shimizu, Keio University, School
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Location/Qualifiers
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Best Local Similarity 99.5%; Pred. No. 0;
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RESULT 9
AP001743/c

LOCUS 219256 bp DNA linear PRI 21-MAY-2003

DEFINITION Homo sapiens genomic DNA, chromosome 21q, section 87/105.

ACCESSION AP001743 AL163288 BA000005

VERSION AP001743.1 GI:7768735

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS

1 Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Pak,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
Aasaka,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyma,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordleik,G.,
Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloecher,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Rieselmann,L., Dgand,E., Wehrmeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaepo,M.L.

TITLE The DNA sequence of human chromosome 21

JOURNAL Nature 405 (6784), 311-319 (2000)

MEDLINE 20289799

PUBMED 10830953

AUTHORS

2 (bases 1 to 219256)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Pak,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
Aasaka,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyma,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordleik,G.,
Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloecher,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Rieselmann,L., Dgand,E., Wehrmeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaepo,M.L.

TITLE Direct Subcloning

JOURNAL Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GIB, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)

COMMENT On May 30, 2000 this sequence version replaced gi:7717391. The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagami-hara 228-8535, Japan, * e.mail: hattori@gsc.riken.go.jp and * URL: <http://hgp.gsc.riken.go.jp/> and * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: <http://genome.imb-jena.de/> and * Keio University School of Medicine, Molecular Biology, * Tokyo 160-8582, Japan, * e.mail: nshimizu@mb.med.keio.ac.jp * URL: <http://www.dmb.med.keio.ac.jp/> and

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Db	153481	TCATTTTTGTAGTGAATTTGGGATAGGATATGTGTTTTGGGGTATGGGGGAGTGTTC	153422
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 LOCUS Pan troglodytes chromosome 22 clone:CH251-010A09, map 22, complete
 DEFINITION
 sequences
 ACCESSION BS000130 BA000046
 VERSION BS000130.1 GI:37537397
 KEYWORDS HTG.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 REFERENCE
 AUTHORS 1
 TITLE The International Chimpanzee Chromosome 22 Consortium.
 JOURNAL DNA sequence and comparative analysis of chimpanzee chromosome 22
 REFERENCE Nature 429, 382-388 (2004)
 AUTHORS 2 (bases 1 to 201997)
 Hattori,M., Toyoda,A., Watanabe,H., Taylor,T.D., Kuroki,Y.,
 Fujiyama,A. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAY-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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 Tel:81-45-503-9111, Fax:81-45-503-9170)
 *The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
 *Chinese National Human Genome Center at Shanghai, Shanghai, China;
 *GDF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
 of Molecular Biotechnology, Jena, Germany; *KIRB Genome Research
 Center, Daejeon, Korea;
 *Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
 *National Institute of Genetics, Mishima, Japan;
 *National Yang Ming University Genome Research Center, Taipei,
 Taiwan;
 *RIKEN Genomic Sciences Center, Yokohama, Japan.
 COMMENT
 ----- Genomic Sciences Center
 Center: RIKEN Genomic Sciences Center
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center Project name:The Chimpanzee Chromosome 22 Sequencing Project
 Center clone name: CH251-010A09
 ----- Summary Statistics
 Sequencing vector: pUC18, pUC13, pTZ19R; 100% of reads Chemistry:
 Dye-terminator Big Dye and ET; 100% of reads Assembly program:
 Phrap; version 0.990339
 Consensus quality: 201,997 bases at least Q40

Consensus quality: 0 bases at least Q30
 Consensus quality: 0 bases at least Q20

 This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by at one
 plasmid or more than one M13 subclone;
 and the assembly was confirmed by restriction digest.

 Source information:
 The RORI-43 chimpanzee BAC library was prepared from DNA isolated
 from the blood of a single male chimpanzee using published
 protocols (Osogawa,K. et al. Genomics 52:1-8). The DNA from the
 chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
 Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
 Kazutoyo Osogawa, Evan Richler & Pieter J de Jong. The library
 characteristics are described at
 http://www.chori.org/bacpac/mchimp43.htm.
 The clone may be obtained from Pieter J. de Jong and coworkers
 (http://www.chori.org/bacpac).
 VECTOR: pBACe3.6
 The CHORI-251 chimpanzee BAC library was prepared from DNA isolated
 from the blood of a single male chimpanzee using published
 protocols (Osogawa,K. et al. Genomics 52:1-8). The DNA from the
 chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
 Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
 Kazutoyo Osogawa, Evan Richler & Pieter J de Jong. The library
 characteristics are described at
 http://www.chori.org/bacpac/chimpanzee251.htm.
 The clone may be obtained from Pieter J. de Jong and coworkers
 (http://www.chori.org/bacpac).
 VECTOR: pTARBAC2.1
 The PTB1 chimpanzee BAC library was prepared from DNA isolated from
 cultured cells established from the blood of a single male
 chimpanzee.
 Clones may be obtained from Aaao Fujiyama and co-workers
 (http://www.gsc.riken.go.jp).
 VECTOR: pKS145
 The PTR22 chimpanzee Fosmid library was prepared from DNA isolated
 from cultured cells established from the blood of a single male
 chimpanzee.
 Clones may be obtained from Aaao Fujiyama and co-workers
 (http://www.gsc.riken.go.jp).
 VECTOR: pKS143

 Sequence Quality Assessment:
 This entry has been annotated with sequence
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than 1 error in
 10,000 bp.

 Neighboring clones:
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 /chromosome="22"
 /clone="CH251-010A09"
 /clone_lib="CHORI-251 chimpanzee BAC"
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 Query Match 64.3%; Score 2482.4; DB 9; Length 201997;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 2563; Conservative 0; Mismatches 37; Indels 29; Gaps 5;
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Db	155084	CACCAAGCAAACTGATGATGATCTTGACGCAACAGACGTGACCTTGACACGGCG	155025
Qy	1330	TGCGACCTCTGCTGACACTTGCCGTGAGAGCGCGGCAAGAGATGGCCAACTGGCTGT	1389
Db	155024	TGCCAGCTCTGCTGACCTTGCCGTGAGAGCGCGGCAAGAGATGGCTCAAGTGGCTGT	154965
Qy	1390	GCTCAACAAATGCAACCCCAACCTTGACCAACGTAGAGGGCTCCACCCTGTGACATGGC	1449
Db	154964	GCTTGAACAAATGCCAACCCCAACCTTGACCAACGTAGAGGGCTCCACCCTGTGACATGGC	154905
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Db	154664	CCGAGGCGTGAAGCTGAGCCTGACAGGCAAGATGCTTGCTGCACCTGACCTAACGCTGC	154605
Qy	1750	CTGGCAAGGGCCCACTCTGCCATTCGTCAAGCTGTGCGCAACCAACCGGGGTTGAGTGGAA	1809
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Qy	1990	TGCGGGCGCTGGCAAGAGGCGGTGACCTTCAACCGGCTAACCGGCTTGCACCTTGAGCTGC	2049
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QY	2590	TAGGCACTGTGTCTGTAAGGAGCCGTGGGTGAGATCATTTGTTGTGCTCTTAATGAG	2649
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Db	153344	CGTATGTGGGCACACTCTTAACCAATCCAGCTCTGTTACTTTGGTGAAGTCTTGTGACAC	153285
QY	3067	ACCAACACACGTGCCACATGTATCTAGCTGCGGTTGTTTCTCGTTGCTGAATGTT	3126
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QY	3187	GTCGTGGGAGCTGAGCGGAGCCCTCAGGTGCTGAGATGACACAGTCTTGGGGAAG	3246
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QY	3247	GTCGAGAGAAAGCTGTGTTTTTATCTCCACACGCAAGTATGAAATTAATTAATGATG	3306
Db	153104	GTCGAGAGAAAGCTGTGTTTTTATCTCCACACACGATGAAATTAATTAATTAATGATG	153045
QY	3307	TTACTTAGACATAGACAGATTAATCTAGGTAGATGACATGCTCACCTTGACCTTCCAG	3366
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QY	3727	CTGGCGATGTGTTTAAATATGCTCATTTGTGCTT-----TACGTGTGTGGGA	3773
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DEFINITION	Sequence 3 from patent US 6630335.				
ACCESSION	AR406004				
VERSION	AR406004.1	GI:40155104			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2355)				
TITLE	Kapeller-Libermann, R.				
JOURNAL	1471 protein kinase, a novel human protein kinase and uses thereof				
FEATURES	Patent: US 6630335-A 3 07-OCT-2003;				
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QY	197	AGGAGCGCATGAGCTTTTGGAGAAGAGCAAGAGATGAGATGGCCAAAGTTTCGTCAC	256		
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QY	317	AAGGCTCTCCGGAAGAAAGCTGTGGCTTCGAGGCATTTGCATGGAGATCTCCGTTCCGA	376
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QY	377	ATCATCCACGAGACGGCGGTGGGACATGAACTTCTGCACTGCAATGGCCCGCACTCTCG	436
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1937 CTGCAAGTGGCGCGGAGAGCGGAGCAACAGAGCATGCGAGCTGTCTCTGATGGAGC 1996
1921 CTGCAAGTGGCGCGGAGAGCGGAGCAACAGAGCATGCGAGCTGTCTCTGATGGAGC 1980
1997 GGTGGAGAGAGGCGGTGACCTTCAAGCGGCTACACCGGCTGCACTGAGCTGCGCGAC 2056
1981 GGTGGAGAGAGGCGGTGACCTTCAAGCGGCTACACCGGCTGCACTGAGCTGCGCGAC 2040
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2117 CCCCTGAGCAAGCGGCGCTGCACTGTGCTGCGCGCAAGGAGCTCGAGAGTGTGAG 2176
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COJ31804
LOCUS COJ31804 2499 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 17738 from Patent WO02068579.
ACCESSION COJ31804
VERSION COJ31804.1 GI:42309361
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Ventner,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 17738 06-SEP-2002;
PE Corporation (NY) (US)
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61 GAGTTACCGGCTGAGAGAGAGTGGGCTTCGGGCGGCTTCGGGCGAGTGTACAGGATGGC 120
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 VERSION AX166548.1 GI:14546893
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Plozman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
 Flanagan,P. and Clardy,D.S.
 TITLE Novel human protein kinases and protein kinase-like enzymes
 JOURNAL Patent: WO 0138503-A 39 31-MAY-2001;
 Sugen, Inc. (US)
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 ACCESSION AF302127.3 GI:18087895
 VERSION AF302127.3
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 SOURCE Mus musculus (house mouse)
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 1 (bases 1 to 3559)
 Chen, L., Haider, K., Ponda, M., Cariappa, A., Rowitch, D. and Pillai, S.
 Protein kinase C-associated, ankyrin repeat-containing protein kinase
 J. Biol. Chem. 276 (24), 21737-21744 (2001)
 JOURNAL 21293027
 MEDLINE 11278382
 PUBMED 2 (bases 1 to 3559)
 REFERENCE 2 (bases 1 to 3559)
 AUTHORS Chen, L., Haider, K., Cariappa, A. and Pillai, S.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-2000) Cancer Center, Massachusetts General
 Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
 3 (bases 1 to 3559)
 Chen, L., Haider, K., Cariappa, A. and Pillai, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2002) Cancer Center, Massachusetts General
 Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
 REMARK 4 (bases 1 to 3559)
 REFERENCE Sequence update by submitter
 AUTHORS Chen, L., Haider, K., Cariappa, A. and Pillai, S.
 TITLE Direct Submission
 JOURNAL Submitted (08-JAN-2002) Cancer Center, Massachusetts General
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 REMARK Nucleotide sequence update by submitter
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REFERENCE	1 (baaes 1 to 3558)			
AUTHORS	Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klauser,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Hsieh,F., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marinina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L., Scheet,T.E., Brownstein,M.J., Ubedin,T.B., Toshitsugu,Y.S., Carimini,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.U., Holys,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Hellton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Boutford,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Stalska,U., Smilows,D.E.,			

TITLE Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
JOURNAL Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 3558)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Lothar Henighausen Ph.D., Priscilla Furch
Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Laric, P., Legaspi, R.,
Maduro, O.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantipop, S., Thomas, P.J., Touchman, J.W.,
Tougeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINT at: <http://image.lnl.gov>
Series: IRK Plate: 123 Row: k Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 2445774.
Location/Qualifiers

FEATURES

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CDS

ORIGIN

Query Match 45.7%; Score 1765.8; DB 10; Length 3558;
Best Local Similarity 83.7%; Pred. No. 2.7e-285;
Matches 2049; Conservative 0; Mismatches 387; Indels 11; Gaps 4;

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Search completed: September 16, 2005, 01:18:20
Job time : 15989.8 secs

PS Claim 1; SEQ ID NO 1; 62bp; English.

XX The invention provides novel human 14171 protein kinase polypeptides and
CC polymucleotides. The methods and compositions of the present invention
CC are useful for the diagnosis and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of a 14171 protein kinase
CC such as cancer, immunological disorder, inflammation, heart failure,
CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.
CC The invention can also be used in chromosome mapping, tissue typing,
CC predictive medicine, forensic biology and prognostic assays. The present
CC sequence is human 14171 protein kinase cDNA.

XX Sequence 3860 BP; 810 A; 1066 C; 1167 G; 816 T; 0 U; 1 Other;

Query Match 100.0%; Score 3859; DB 12; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0;
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KM		prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;
XV		protein 14171.
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OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
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XX	07-Aug-2003.	
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PR	16-APR-2002; 2002US-0372984P.	
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PR	24-MAY-2002; 2002US-0382995P.	
PR	31-MAY-2002; 2002US-0385023P.	
PR	14-JUN-2002; 2002US-0388853P.	
PR	17-JUN-2002; 2002US-0389395P.	
PR	25-JUN-2002; 2002US-0391324P.	
PR	15-JUL-2002; 2002US-0395944P.	
PR	22-JUL-2002; 2002US-0397726P.	
PR	13-AUG-2002; 2002US-0403046P.	
PR	22-AUG-2002; 2002US-0405155P.	
PR	27-AUG-2002; 2002US-0406361P.	
PR	25-OCT-2002; 2002US-0421195P.	
PR	12-NOV-2002; 2002US-0425456P.	
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PR	10-DEC-2002; 2002US-0432122P.	
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PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Hunter JI, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES,	
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DR	WPI, 2003-646176/61.	
XX	P-PDB: ADS38377.	
PT	Treating subject having tumorigenic disorder or angiogenic disorder	
PT	caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic	
PT	acid, by administering a modulator.	
XX		
PS	Disclosure; SEQ ID NO 37; 454bp; English.	
XX		
CC	This invention relates to a novel method of treating a human subject	
CC	having a tumorigenic disorder or angiogenic disorder, caused by aberrant	
CC	gene expression or activity of an isolated protein, by administering a	
CC	modulator. The modulator may have cytostatic, antihypoid, antidiabetic	
CC	or ophthalmological activity. The method is useful for treating a subject	
CC	having a tumorigenic or angiogenic disorder, in particular for treating	
CC	cancer (for example breast cancer, colon cancer, lung cancer or prostatic	
CC	cancer) and, for example, Grave's disease and diabetic retinopathy. The	
CC	present sequence is a DNA sequence which encodes the novel isolated human	
CC	protein 14171 of the invention.	
XX		
SQ	Sequence 3860 BP; 809 A; 1066 C; 1169 G; 816 T; 0 U; 0 Other;	
Query Match	99.4%; Score 3836; DB 10; Length 3860;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 3858; Conservative	0; Mismatches 1; Indels 2; Gaps 2	
OY	1 CCACGCGTCCGGCGCATGAGGCGCACGCCGCGAACCACATGAGCCTTGCGCTGTGCG 60	
Dd	1 CCACGCGTCCGGCGCATGAGGCGCACGCCGCGAACCACATGAGCCTTGCGCTGTGCG 60	
OY	61 CACCTTCGACGCGGCGCAATTACGGGCTGGGAGAAAGTGGGCTCGGCGCGGCTTCGAGCA 120	

Db	61	CACCTTGAGCGCGGCGAGTTCAACGGGCTGGAGAAAGTGGGCTCGGGCGGCTTTCGGGCA	120
QY	121	GGTGTACAAGTGTGGCCATGTCCATCTGGAGAACCTGGCTGGCCATCAAGTGTCCGCCAG	180
Db	121	GGTGTACAAGGTGGCCATGTCTCCATGGAAAGACTGGCTGGCCATCAAGTGTCCGCCAG	180
QY	181	CTTCGACGTGACGACAGAGGAGCGCATGGAAGCTTTTGGAAAGAGCCAAAGAAATGAGAT	240
Db	181	CTTCGACGTGACGACAGGAGAGCGCATGGAAGCTTTTGGAAAGAGCCAAAGAAATGAGAT	240
QY	241	GGCCAAAGTTTCGTACATCTCTGCTGTGTATGTGCATCTGCCGCGAACCCTGTCCGCTGGT	300
Db	241	GGCCAAAGTTTCGTACATCTCTGCTGTGTATGTGCATCTGCCGCGAACCCTGTCCGCTGGT	300
QY	301	CATGAGATACATGAGAACGGGCTCCCTGGAAAAAGCTGTGGCTTCGGAGGCATTGGCATG	360
Db	301	CATGAGATACATGAGAACGGGCTCCCTGGAAAAAGCTGTGGCTTCGGAGGCATTGGCATG	360
QY	361	GGATCTCCGGTTCGGAATCATCCACAGAGACGGCGGTGGGATGAACTTCTCGCACTCAT	420
Db	361	GGATCTCCGGTTCGGAATCATCCACAGAGACGGCGGTGGGATGAACTTCTCGCACTCAT	420
QY	421	GGCCCGCGCACTCTCGCACTCGAACCCTCAAGCCCGCAACATCTGCTGATGTCCTCA	480
Db	421	GGCCCGCGCACTCTCGCACTCGAACCCTCAAGCCCGCAACATCTGCTGATGTCCTCA	480
QY	481	CCACGTCAAGATTTCTGATTTTGGTCTGGCCAAATGCAAGGGCTGTCCACTCGGCATGA	540
Db	481	CCACGTCAAGATTTCTGATTTTGGTCTGGCCAAATGCAAGGGCTGTGTCCACTCGGCATGA	540
QY	541	CCTGAGCATGGAATGGCCGTTTGGCAATCGCTACCTCCCTCAAGACGCATCAAGGGA	600
Db	541	CCTGAGCATGGAATGGCCGTTTGGCAATCGCTACCTCCCTCAAGACGCATCAAGGGA	600
QY	601	GAAAGCGCGGCTCTTTCGACACCAAGCAAGATGTATACAGTTTTCGATCGTCAATCTGGG	660
Db	601	GAAAGCGCGGCTCTTTCGACACCAAGCAAGATGTATACAGTTTTCGATCGTCAATCTGGG	660
QY	661	CGTGTCTCACAGAAAGAACCGGTTTGCAGATGAAAGAACATCTGTGCAATCATATGTGAA	720
Db	661	CGTGTCTCACAGAAAGAACCGGTTTGCAGATGAAAGAACATCTGTGCAATCATATGTGAA	720
QY	721	GGTGTGAAGGGCCACCGGCCCGGAGCTGGCCGCGTGTGCAGAGCCCGGCGCGGCTGTG	780
Db	721	GGTGTGAAGGGCCACCGGCCCGGAGCTGGCCGCGTGTGTGCAGAGCCCGGCGCGGCTGTG	780
QY	781	CAGCCACTGTGATGAGCTCATGACAGCGGTGTGCAAGGGGAGTCCGAGATTGAGCCAC	840
Db	781	CAGCCACTGTGATGAGCTCATGACAGCGGTGTGCAAGGGGAGTCCGAGATTGAGCCAC	840
QY	841	CTTCCAGAAATTAATTCTGAAACCGAGGACTGTGTGAAAAAGCTGTATGACGAATGAA	900
Db	841	CTTCCAGAAATTAATTCTGAAACCGAGGACTGTGTGAAAAAGCTGTATGACGAATGAA	900
QY	901	AGAAATGCTCTATATCTGGAAGTGAAGAAAGCCCCCGGAGCCCAAGAGCGAGTGTGCC	960
Db	901	AGAAATGCTCTATATCTGGAAGTGAAGAAAGCCCCCGGAGCCCAAGAGCGAGTGTGCC	960
QY	961	TGCGAGGCTCAAGCGGCGCTCTGCCCCCACTTGATATACATACAGCTCTCCGAGCT	1020
Db	961	TGCGAGGCTCAAGCGGCGCTCTGCCCCCACTTGATATACATACAGCTCTCCGAGCT	1020
QY	1021	TCTCTCAAGCTGGAATCTGTGAAGTTTCCAGGCTGTGAGGGCCCCGAGAGCTCAGCCG	1080
Db	1021	TCTCTCAAGCTGGAATCTGTGAAGTTTCCAGGCTGTGAGGGCCCCGAGAGCTCAGCCG	1080
QY	1081	CAGCTCTCTGTAGTTCGAAGCTGTCATCTGTCCGCGATGTGGAAAGAGGCTCTCGGGGGTTC	1140
Db	1081	CAGCTCTCTGTAGTTCGAAGCTGTCATCTGTCCGCGATGTGGAAAGAGGCTCTCGGGGGTTC	1140
QY	1141	CTCGGTGAGACTCGGCTTCTCTTCCAGAGGATCACTGTCCGTGTCTTGAAGCGGGAACC	1200
Db	1141	CTCGGTGAGACTCGGCTTCTCTTCCAGAGGATCACTGTCCGTGTCTTGAAGCGGGAACC	1200

Db	1141	CTCGGTGAGCTTCGCGCTTCTCTTCCAGAGATCACTGCTGCTGCTTTGAGCGGGAAACC	1200
QY	1201	TTCAACACGACATCTGGGTACCAAGACGTCACGAAGAAGACTGTGATGCCATCG	1260
Db	1201	TTCAACACGACATCTGGGTACCAACAGCGTCCAGGAAGAAGACTGTGATGCCATCG	1259
QY	1261	TGTCC-GGGACACAGCAAACTGATGAAGATCTTGCAGCCGCGAGACGTGACCTGGCAC	1319
Db	1260	TGTCGGGGAGACACAGCAAACTGATGAAGATCTTGCAGCCGCGAGAGGTGACCTGGCAC	1319
QY	1320	TGGAACAGGGGTGCCAGCGCTGTCGACCTCGGGGGTGAAGGAGCGGGCAAGAGATGCGCCA	1379
Db	1320	TGGAACAGGGGTGCCAGCGCTGTCGACCTCGGGGGTGAAGGAGCGGGCAAGAGATGCGCCA	1379
QY	1380	AGTGGCTCTCTCTCAACAATGCCAACCCCAACTGAGCAACTGAGGGGCTCCACCCCGT	1439
Db	1380	AGTGGCTCTCTCTCAACAATGCCAACCCCAACTGAGCAACTGAGGGGCTCCACCCCGT	1439
QY	1440	TGCACATGACCGTGGAGAGAGGGGTGTCGTGAGACTCTCTGTCGACCGAAGA	1499
Db	1440	TGCACATGACCGTGGAGAGAGGGGTGTCGTGAGACTCTCTGTCGACCGAAGA	1499
QY	1500	TCACTGTCAAGCCCAAGATGAGAACCACTGTGACAGCCCTCCACTTTGACGCCAAGACG	1559
Db	1500	TCACTGTCAAGCCCAAGATGAGAACCACTGTGACAGCCCTCCACTTTGACGCCAAGACG	1559
QY	1560	GGGATGAGTCTAGCAACAGGCGCTGTTGAGAGAAAGCCTCGGTCAACAGAGGTGACT	1619
Db	1560	GGGATGAGTCTAGCAACAGGCGCTGTTGAGAGAAAGCCTCGGTCAACAGAGGTGACT	1619
QY	1620	TTGAGAGGCGGAGACGCCCAATGACGCTGACGACGAGCGGACAGAGAAATATCTGTCGA	1679
Db	1620	TTGAGAGGCGGAGACGCCCAATGACGCTGACGACGAGCGGACAGAGAAATATCTGTCGA	1679
QY	1680	TCTCTCTGCGCGAAGGCGTGGACCTGACCGTGCAGAGGCGCAAGAGTCTGTCGACTGCG	1739
Db	1680	TCTCTCTGCGCGAAGGCGTGGACCTGACCGTGCAGAGGCGCAAGAGTCTGTCGACTGCG	1739
QY	1740	ACTAGCGCTGCGTGGAGGAGCAACCTGSCCATCTGTCAAGTCTTGGCCAAAGCGCGGGG	1799
Db	1740	ACTAGCGCTGCGTGGAGGAGCAACCTGSCCATCTGTCAAGTCTTGGCCAAAGCGCGGGG	1799
QY	1800	TGAGTGTGAACGCCCAAGACGCTGATGAGGAGAGCGCCATTGACCTTGGCGGCAACGCGG	1859
Db	1800	TGAGTGTGAACGCCCAAGACGCTGATGAGGAGAGCGCCATTGACCTTGGCGGCAACGCGG	1859
QY	1860	GGCAGCTAACCGCGTGGCCGCTCATGACCTGTGCTCCGAGGTCAACTCTTGCAGACC	1919
Db	1860	GGCAGCTAACCGCGTGGCCGCTCATGACCTGTGCTCCGAGGTCAACTCTTGCAGACC	1919
QY	1920	TGCTGGGACAGACACCCCTGACCGTGGCGCGGAGACGGGGCAACAGAGCACTGCCAAGC	1979
Db	1920	TGCTGGGACAGACACCCCTGACCGTGGCGCGGAGACGGGGCAACAGAGCACTGCCAAGC	1979
QY	1980	TGCTCTGTGATGGGGCGCTGGCAAGAGCCGTGACCTCAACGAGCTAACCGCTCTGC	2039
Db	1980	TGCTCTGTGATGGGGCGCTGGCAAGAGCCGTGACCTCAACGAGCTAACCGCTCTGC	2039
QY	2040	ACCTGGCTGCGCGGCAACGAGCACTTGGCCACTGTCAAGCTGTTGTCAAGAGAAAGCTCG	2099
Db	2040	ACCTGGCTGCGCGGCAACGAGCACTTGGCCACTGTCAAGCTGTTGTCAAGAGAAAGCTCG	2099
QY	2100	ATGTGCTGGCGCGGGAGCCCTGAAACAGACGGGCGCTGACCTGGCTGCGCGCCACGGGCG	2159
Db	2100	ATGTGCTGGCGCGGGAGCCCTGAAACAGACGGGCGCTGACCTGGCTGCGCGCGCCACGGGCG	2159
QY	2160	ACTCGAGGTGTGAGAGAGTGTCAAGCGCGATGTCAATTGACCTGTTTCAGAGCAGG	2219
Db	2160	ACTCGAGGTGTGAGAGAGTGTGTCAAGCGCGATGTCAATTGACCTGTTTCAGAGCAGG	2219
QY	2220	GGCTCAGCGCGCTGCACCTGGCGCGCCAGAGGCGGGCAAGACAGCGGTGAGACTCTGC	2279
Db	2220	GGCTCAGCGCGCTGCACCTGGCGCGCCAGAGGCGGGCAAGACAGCGGTGAGACTCTGC	2279

QY	2280	TCAGGCATGGGGCCCAATCACTCGAGAGCCTCAAGTTCCAGGGGGGCAATGAGCCCG	2339
DB	2280	TCAGGCATGGGGCCCAATCACTCGAGAGCCTCAAGTTCCAGGGGGGCAATGAGCCCG	2339
QY	2340	CCGCACAATCTGAGGGGGAAGGAAGACCTTAGCTGGCTGCTCGAGGACAACGGAGGAGTCCA	2399
DB	2340	CCGCACAATCTGAGGGGGAAGGAAGACCTTAGCTGGCTGCTCGAGGACAACGGAGGAGTCCA	2399
QY	2400	CGTGGGGCTCTTGTCTCGTCCCTGTGTCTCTGAGGGAGTGAACGATCTGCGTGGGACC	2459
DB	2400	CGTGGGGCTCTTGTCTCGTCCCTGTGTCTCTGAGGGAGTGAACGATCTGCGTGGGACC	2459
QY	2460	CCGTTTGGGCTTACCTTAATGTTAACCAAGACAAGGTGACATGTGTCCATCAGAGGCCG	2519
DB	2460	CCGTTTGGGCTTACCTTAATGTTAACCAAGACAAGGTGACATGTGTCCATCAGAGGCCG	2519
QY	2520	CTGCTGCTGACCCGGAAGTGTCCCTCCAGAGTGAAGCTGGCTCAAGTGTACATGACCCGCTCC	2579
DB	2520	CTGCTGCTGACCCGGAAGTGTCCCTCCAGAGTGAAGCTGGCTCAAGTGTACATGACCCGCTCC	2579
QY	2580	ATCATGCATCAGGACACCTGCTGTCTGAAGGGAACCGTGGCTCAAGATCATTTGCTGTGAC	2639
DB	2580	ATCATGCATCAGGACACCTGCTGTCTGAAGGGAACCGTGGCTCAAGATCATTTGCTGTGAC	2639
QY	2640	TCTTAATGGGTGCGCTGAGGCTGTGCTCTCAGATGATGAAGCCCAAGCGTGAAGCATCCA	2699
DB	2640	TCTTAATGGGTGCGCTGAGGCTGTGCTCTCAGATGATGAAGCCCAAGCGTGAAGCATCCA	2699
QY	2700	CTCTCTCCTGAGGCGAGCCACCTTGGGTTGTGGAAGCTCACCAAGCTTTGAGGGAAGTGA	2759
DB	2700	CTCTCTCCTGAGGCGAGCCACCTTGGGTTGTGGAAGCTCACCAAGCTTTGAGGGAAGTGA	2759
QY	2760	GGGGAAACGTAGTTTTTATCTTATCATACATGACGATGGGAGAGAGGACCTGTCTTAAAGT	2819
DB	2760	GGGGAAACGTAGTTTTTATCTTATCATACATGACGATGGGAGAGAGGACCTGTCTTAAAGT	2819
QY	2820	TTCCATGGAATGTTTATTAATAAATATCTTAAGAGATGAATACCTTATCAAGCTGTGCTTG	2879
DB	2820	TTCCATGGAATGTTTATTAATAAATATCTTAAGAGATGAATACCTTATCAAGCTGTGCTTG	2879
QY	2880	AAACCTGTTAAAAATGTTCAATACATTTGGATAGTCTCTTAATGATGGCTTAAGTAG	2939
DB	2880	AAACCTGTTAAAAATGTTCAATACATTTGGATAGTCTCTTAATGATGGCTTAAGTAG	2939
QY	2940	TGGGTTGGCTTTGAAAAAATAGTTTTTATGCAACAAGGAAGAAATGTGACGACAGCTT	2999
DB	2940	TGGGTTGGCTTTGAAAAAATAGTTTTTATGCAACAAGGAAGAAATGTGACGACAGCTT	2999
QY	3000	TGCGGGGGGTATGATGTGCGCAGCTCTTAACCAATTCAGTCAATTAATTGGGTGAGTCTT	3059
DB	3000	TGCGGGGGGTATGATGTGCGCAGCTCTTAACCAATTCAGTCAATTAATTGGGTGAGTCTT	3059
QY	3060	GTGACAAACAACAACGATGCCACATGTACTAGCTGCGGTTGCTTCTCGTTGCCCTA	3119
DB	3060	GTGACAAACAACAACGATGCCACATGTACTAGCTGCGGTTGCTTCTCGTTGCCCTA	3119
QY	3120	AGATGTTTGGCACTCTAGAGCCAACAGGCTTAAGAGTCAATTAATAAAATTCCTCCCTTGT	3179
DB	3120	AGATGTTTGGCACTCTAGAGCCAACAGGCTTAAGAGTCAATTAATAAAATTCCTCCCTTGT	3179
QY	3180	AACTCAGTGTGGGGACAAGAGGGAGGAGCCCTCAGAGCTGTGAGAGTGCACAGTCTTGG	3239
DB	3180	AACTCAGTGTGGGGACAAGAGGGAGGAGCCCTCAGAGCTGTGAGAGTGCACAGTCTTGG	3239
QY	3240	GGAAAGGTGACGAGGAAGTGTGTTTTTATCTCCACAACGCAATATGAAGATTAATAATTA	3299
DB	3240	GGAAAGGTGACGAGGAAGTGTGTTTTTATCTCCACAACGCAATATGAAGATTAATAATTA	3299
QY	3300	CATAGTATTAATCTTAACAATAGACAGATTAATCTAGATGATGACATGCTGCACCTGCACCC	3359
DB	3300	CATAGTATTAATCTTAACAATAGACAGATTAATCTAGATGATGACATGCTGCACCTGCACCC	3359

QY	3360	TTCCAGCTCTCATATTTTGTTAAGTGATGATTTGGAGATAGGGATAGCTTTTGGGGTATAGGGG	3419
Db	3360	TTCCAGCTCTCATATTTTGTTAAGTGATGATTTGGAGATAGGGATAGCTTTTGGGGTATAGGGG	3419
QY	3420	GGAGTGTTCTGACCTGCTTTGACACGNGCCTCCGACCTCAGCAGTTTGGGGTGAGC	3479
Db	3420	GGAGTGTTCTGACCTGCTTTGACACGNGCCTCCGACCTCAGCAGTTTGGGGTGAGC	3479
QY	3480	CCGAGGGGGGTTCTTGAGTGTAAAGATGTGGCCATCTAGCTCTGTAATTCACCTGTAC	3539
Db	3480	CCGAGGGGGGTTCTTGAGTGTAAAGATGTGGCCATCTAGCTCTGTAATTCACCTGTAC	3539
QY	3540	CTGTGTCCATPAGGGTGCCCTCTGAAATCTGTATTTAGAAATAGTTTGTGCAGAACGTG	3599
Db	3540	CTGTGTCCATPAGGGTGCCCTCTGAAATCTGTATTTAGAAATAGTTTGTGCAGAACGTG	3599
QY	3600	ACCTGCGTGCAACATGTACCGTGGGCTGTATATGATATGATTAATATGTAAC	3659
Db	3600	ACCTGCGTGCAACATGTACCGTGGGCTGTATATGATATGATTAATATGTAAC	3659
QY	3660	ATGTAATGTAATGTGATCTGTGGGCGACGATATCTTTCATGCGCAGGAATATATCCAACT	3719
Db	3660	ATGTAATGTAATGTGATCTGTGGGCGACGATATCTTTCATGCGCAGGAATATATCCAACT	3719
QY	3720	GTTGAACTGGCTATGTTTAAATATATGCTCATGTGCTTTACCTGTTGTGGACTGCGT	3779
Db	3720	GTTGAACTGGCTATGTTTAAATATATGCTCATGTGCTTTACCTGTTGTGGACTGCGT	3779
QY	3780	GAGGGACAAAGAGTCCATTTGATGTCATAATAAGAAAGTACTGGCCATCTTTTGGAN	3839
Db	3780	GAGGGACAAAGAGTCCATTTGATGTCATAATAAGAAAGTACTGGCCATCTTTTGGAN	3839
QY	3840	CTGAAAAAATAAAAAAGG	3860
Db	3840	CTGAAAAAATAAAAAAGG	3860

RESULT 3

ADL61092
ID ADL61092 standard; DNA; 3879 BP.

AC ADL61092;

DT 03-JUN-2004 (first entry)

DE Human protein tyrosine kinase ankyrin repeat domain 3 DNA.

KW predictor set; protein tyrosine kinase; cytostatic; antiangiogenic;

KW hypervascular disease; angiogenesis; wound healing scar; human;

[illegible]

XX 3

XX

XX 3

XX :

XX

XX

[illegible]

DR WPI; 2004-239171/22.

XXX

PT polypeptides whose

PT		treating breast cancer.
XX		
PS		
Claim 2; SEQ ID NO 16; 649pp; English.		
XX		
CC	The invention relates to a novel predictor set comprising a plurality of polynucleotides and/or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. The molecules of the invention demonstrate cytostatic, antiangiogenic, vasotropic and vulnereary activities and may be useful in the field of pharmacogenomics, in particular for determining drug sensitivity and in treating breast cancer. Hypervascular diseases, such as angio genesis and scars in wound healing. The current sequence is that of a human protein tyrosine kinase biomarker DNA of the invention.	
CC		
XX		
SQ	Sequence 3879 BP; 807 A; 1074 C; 1178 G; 820 T; 0 U; 0 Other;	
Query Match	98.6%; Score 3804.2; DB 12; Length 3879;	
Best Local Similarity	99.7%; Pred.No. 0;	
Matches 3831; Conservative	0; Mismatches 9; Indels 2; Gaps 2	

Query Match	98.6%	Score 3804.2	DB 12	Length 3879
Best Local Similarity	99.7%	Pred. No. 0		
Matches 3831	Conservative 0	Indels 9	Gaps 2	
QY	7	GTCCGCGCGCATGAGGGCGA	CGGGGGAGCCCATG	GGGCGCTGTGCGCACTT 66
Db	39	GACGTGCGGATGAGGGCGA	CGCGGGAGCCCATG	GGGCGCTGTGCGCACTT 98
QY	67	CGACGCGGGCGAGTT	CACGGGCTGGGAGAAGGTGGGCT	CGGGCGCTTCGGGCAAGTGA 126
Db	99	CGACGCGGGCGAGTT	CACGGGCTGGGAGAAAGTGGGCT	CGGGCGGCTTCGGGCAAGTGA 158
QY	127	CAAGGTGGCCATGTGCCA	CTGTGCACTGGAACCTGTGCTGCGCAT	CAAGTGTGCGCCAGCTTGA 186
Db	159	CAAGGTGGCCATGTGCCA	CTGTGCACTGGAACCTGTGCTGCGCAT	CAAGTGTGCGCCAGCTTGA 218
QY	187	CGTCGACGACAGGGAGCG	CATGAGCTTTTGGAGAAAGCCAA	GAAAGATGGAATGGAGCCAA 246
Db	219	CGTCGACGACAGGGAGCG	CATGAGCTTTTGGAGAAAGCCAA	GAAAGATGGAATGGAGCCAA 278
QY	247	GTTTGCGCTACATCTG	CGCTGTGTATGGCATCTGCGCGCA	CTGTGTGCGGCTGTGTATGGA 306
Db	279	GTTTGCGCTACATCTG	CGCTGTGTATGGCATCTGCGCGCA	CTGTGTGCGGCTGTGTATGGA 338
QY	307	GTACATGAGAGAGGGGCT	CCGTGGAAAGCTGTGCTTC	CGAGCCATTGTGCCATGGGATCT 366
Db	339	GTACATGAGAGAGGGGCT	CCGTGGAAAGCTGTGCTTC	CGAGCCATTGTGCCATGGGATCT 398
QY	367	CGGGTTCGGAATCATCA	CGAGACGGCGGTGGGCA	TGAATCTTCGCACTGCGATGGCCCC 426
Db	399	CGGGTTCGGAATCATCA	CGAGACGGCGGTGGGCA	TGAATCTTCGCACTGCGATGGCCCC 458
QY	427	GCCACTCTCGACCTT	GGAACCTCGCGAAACAT	CTGTCTGTGATGTGCCACTATACAGT 486
Db	459	GCCACTCTCGACCTT	GGAACCTCGCGAAACAT	CTGTCTGTGATGTGCCACTATACAGT 518
QY	487	CAAGATTTCTGATTTT	TGGCTGGGCGAAGTGCA	CGGGCTGTGCCACTCGCATGACCTCAG 546
Db	519	CAAGATTTCTGATTTT	TGGCTGGGCGAAGTGCA	CGGGCTGTGCCACTCGCATGACCTCAG 578
QY	547	CATGATGGCTGTTTG	CAATCGCTA	CTCTCCCTCAAGCGGCATCAAGGAGAGAG 606
Db	579	CATGATGGCTGTTTG	CAATCGCTA	CTCTCCCTCAAGCGGCATCAAGGAGAGAG 638
QY	607	CGGCTCTTTCACAC	CAAGACAGATGTATAC	GGCTTTCGATTCGATCTGTGGGGGTGCT 666
Db	639	CGGCTCTTTCACAC	CAAGACAGATGTATAC	GGCTTTCGATTCGATCTGTGGGGGTGCT 698
QY	667	CACACAGAAAGCGGTT	TGCATGAGAAAGACAT	CTGCAATCATGTGTGAAGTGGT 726
Db	699	CACACAGAAAGCGGTT	TGCATGAGAAAGACAT	CTGCAATCATGTGTGAAGTGGT 758
QY	727	GAAAGGCCACCGGCT	CGAGCTGCGGCTGTG	CAGAGCCGGGCGCGGCGCTGTGACCA 786
Db	759	GAAAGGCCACCGGCT	CGAGCTGCGGCTGTG	CAGAGCCGGGCGCGGCGCTGTGACCA 818

QY 787 CCTGATACGCTCATGACGCGTGTGCGACGCGGGATCCGCGAAGTTAGACCCACCTTCCA 846
DB 819 CCGATACGCTCATGACGCGTGTGCGACGCGGGATCCGCGAAGTTAGACCCACCTTCCA 878
QY 847 AGAATTTACTTCTGTAACCGAGAGCCTGTGTGTAAGAAAGCCTGATGACGAAGTGAAGAAAC 906
DB 879 AGAATTTACTTCTGTAACCGAGAGCCTGTGTGTAAGAAAGCCTGATGACGAAGTGAAGAAAC 938
QY 907 TGCCTGATGATGACGTAAGAAAGCCCGGAGGCCGAGAGCGAGGTGTGCTCGAG 966
DB 939 TGCCTGATGATGACGTAAGAAAGCCCGGAGGCCGAGAGCGAGGTGTGCTCGAG 998
QY 967 GCTCAAGGCGGCTCTGCCCCCACTTGTGATTAACAATTACAGCTTCTCGAGCTTCTTC 1026
DB 999 GCTCAAGGCGGCTCTGCCCCCACTTGTGATTAACAATTACAGCTTCTCGAGCTTCTTC 1058
QY 1027 ACAGCTGACCTGTGAGTTTCCAGAGCTGTGAGGGGCCCGAGAGCTCAGCGGAGCTC 1086
DB 1059 ACAGCTGACCTGTGAGTTTCCAGAGCTGTGAGGGGCCCGAGAGCTCAGCGGAGCTC 1118
QY 1087 CTCTGAGTCCAGAGCTGACATCGTCCGACGTGGAAGAGCTCTCGGGGTGTCTCGGT 1146
DB 1119 CTCTGAGTCCAGAGCTGACATCGTCCGACGTGGAAGAGCTCTCGGGGTGTCTCGGT 1178
QY 1147 GGAATCCGCTTCTCTTCAAGAGATCACTGTGCTTCTTGTGACGGGAACTTTCAAC 1206
DB 1179 GGAATCCGCTTCTCTTCAAGAGATCACTGTGCTTCTTGTGACGGGAACTTTCAAC 1238
QY 1207 CAGCGATCGGGTACCAAGAGCTGCAAGAGAAAGAGCTTGTGATGCACTGATGTC- 1265
DB 1239 CAGCGATCGGGTACCAAGAGCTGCAAGAGAAAGAGCTTGTGATGCACTGATGTCG 1297
QY 1266 GGAACACAGCAAGATGATGATCTGTGACGCGGACGTAAGAGCTGTGACCTGACCTGAC 1325
DB 1298 GGAACACAGCAAGATGATGATCTGTGACGCGGACGTAAGAGCTGTGACCTGACCTGAC 1357
QY 1326 GCGGTGCGAGCTGCTGACCTGTGAGGTGAGAGCGGGGCAAGAGAGTGTGCAATGTGC 1385
DB 1358 GCGGTGCGAGCTGCTGACCTGTGAGGTGAGAGCGGGGCAAGAGAGTGTGCAATGTGC 1417
QY 1386 TGCCTGTCAAAGTCCCAACCCCACTGAGCAACGTAAGGGGCTCAACCCGTTGACA 1445
DB 1418 TGCCTGTCAAAGTCCCAACCCCACTGAGCAACGTAAGGGGCTCAACCCGTTGACA 1477
QY 1446 TGCCTGTCAGAGAGGTGCGGTGTGTGTGAGAGTCTGTGTGACGGAAGATCAAGT 1505
DB 1478 TGCCTGTCAGAGAGGTGCGGTGTGTGTGAGAGTCTGTGTGACGGAAGATCAAGT 1537
QY 1506 TCAACGCGCAAGATGAGACCAAGTGAACGCTTCACTTTGCAAGCCGGAATG 1565
DB 1538 TCAACGCGCAAGATGAGACCAAGTGAACGCTTCACTTTGCAAGCCGGAATG 1597
QY 1566 AATCTAGACACAGGCTGCTGTGAGAAAGAGCCCTCGTCAACAGAGTGAATTGAG 1625
DB 1598 AATCTAGACACAGGCTGCTGTGAGAAAGAGCCCTCGTCAACAGAGTGAATTGAG 1657
QY 1626 GCCGAGCGCCATGACGTAAGCTGTGACAGACGCGGAGGAATATCTGTGCGCATCTGC 1685
DB 1658 GCCGAGCGCCATGACGTAAGCTGTGACAGACGCGGAGGAATATCTGTGCGCATCTGC 1717
QY 1686 TGCCTGAGAGCTGACGTAAGCTGTGAGAGGCAAGATGCTGTGCTGCACTGACTAG 1745
DB 1718 TGCCTGAGAGCTGACGTAAGCTGTGAGAGGCAAGATGCTGTGCTGCACTGACTAG 1777
QY 1746 CTGCGTGGAGGGCACTGCGCATGTCAAGCTGTGACAGAGCGGAGGATGAGTG 1805
DB 1778 CTGCGTGGAGGGCACTGCGCATGTCAAGCTGTGACAGAGCGGAGGATGAGTG 1837
QY 1806 TGAAGCCCAAGAGCTGATGAGAGAGAGCCATTGCACTGTGCGGACAGCGCGGAGCT 1865
DB 1838 TGAAGCCCAAGAGCTGATGAGAGAGAGCCATTGCACTGTGCGGACAGCGCGGAGCT 1897
QY 1866 ACCGCTGGCCGCACTCTCATGACCTGTGCTCGACGTCGAAGCTGTGCAAGCTGTGCTG 1925

DB 1925 ACCGCTGGCCGCACTCTCATGACCTGTGCTCGACGTCGAAGCTGTGCAAGCTGTGCTG 1957
QY 1926 CACAGACCCCTGACAGTGGCCCGGAGACGCGGACACAGAGCACTGCGAGGCTGCC 1985
DB 1958 CACAGACCCCTGACAGTGGCCCGGAGACGCGGACACAGAGCACTGCGAGGCTGCC 2017
QY 1986 TGCATCGGGGCGTGGAGAGAGGCGGTGAACCTGACAGCGGTACACCGCTGTGACCTGG 2045
DB 2018 TGCATCGGGGCGTGGAGAGAGGCGGTGAACCTGACAGCGGTACACCGCTGTGACCTGG 2077
QY 2046 CTGCGCGCAACGACACCTGCGCACCTGTCAAGCTGTGTGTGAGAGAGAGCCGATGTGC 2105
DB 2078 CTGCGCGCAACGACACCTGCGCACCTGTCAAGCTGTGTGTGAGAGAGAGCCGATGTGC 2137
QY 2106 TGCCTCGGGAGACCCCTGAACAGACGCGGCTGACCTGTGCTCGGCCACGCGACCTCG 2165
DB 2138 TGCCTCGGGAGACCCCTGAACAGACGCGGCTGACCTGTGCTCGGCCACGCGACCTCG 2197
QY 2166 AGGTGTGAGAGAGTGTGACGCGCGATGTCACTTGAACCTGTGACAGAGAGGGGCTCA 2225
DB 2198 AGGTGTGAGAGAGTGTGACGCGCGATGTCACTTGAACCTGTGACAGAGAGGGGCTCA 2257
QY 2226 GCGCGCTGCACTGCGCGCCGAGGGCGGACACGACAGACGCTGTGACAGGC 2285
DB 2258 GCGCGCTGCACTGCGCGCCGAGGGCGGACACGACAGAGCTGTGACAGGC 2317
QY 2286 ATGCGGCCCATCATACCTGACAGAGCTCAAGTTCCAGAGGCTGTGCCCCCGGCA 2345
DB 2318 ATGCGGCCCATCATACCTGACAGAGCTCAAGTTCCAGAGGCTGTGCCCCCGGCA 2377
QY 2346 CACTTCCGCGCGAGAGAGAGCTGAGCTGTGCTGCGAGAGACGCGGGGCTCAAGTGG 2405
DB 2378 CACTTCCGCGCGAGAGAGAGCTGAGCTGTGCTGCGAGAGACGCGGGGCTCAAGTGG 2437
QY 2406 GCTCTTGTCTGTCTGTGTCTCTGAGGAGTGAAGCATCTGTGCGGGCCCGTGG 2465
DB 2438 GCTCTTGTCTGTCTGTGTCTCTGAGGAGTGAAGCATCTGTGCGGGCCCGTGG 2497
QY 2466 TGCCTTACCTAATGTTAACAGAGAGGTGACATGTGTGCAATCAAGAGCGCTGTG 2525
DB 2498 TGCCTTACCTAATGTTAACAGAGAGGTGACATGTGTGCAATCAAGAGCGCGTGTG 2557
QY 2526 CTGACCGGAGGTGCTCCCTCCAGGTGAAGCTGCTCAGGTGACAGTCCGCTCATATC 2585
DB 2558 CTGACCGGAGGTGCTCCCTCCAGGTGAAGCTGCTCAGGTGACAGTCCGCTCATATC 2617
QY 2586 GATCTAGGACCTGCTGTGAGAGGACCGTGGGTCAAGATCAATTCGTTGTGCTTAA 2645
DB 2618 GATCTAGGACCTGCTGTGAGAGGACCGTGGGTCAAGATCAATTCGTTGTGCTTAA 2677
QY 2646 TGGGTCTGAGAGCTGTCTCTCAGTATGAAGCCCGAGCGGTGAGACATCTCTCT 2705
DB 2678 TGGGTCTGAGAGCTGTCTCTCAGTATGAAGCCCGAGCGGTGAGACATCTCTCT 2737
QY 2706 CTTGAGGAGACCACTTGGGTGTGTGAGCTCAACAGCTTTGAGGAGGTGCGGGGAA 2765
DB 2738 CTTGAGGAGACCACTTGGGTGTGTGAGCTCAACAGCTTTGAGGAGGTGCGGGGAA 2797
QY 2766 ACTGTGTTTTTATCTTCAATGACGAGTGGGAGAGGCGCTGTCTTAAAGTTCCAT 2825
DB 2798 ACTGTGTTTTTATCTTCAATGACGAGTGGGAGAGGCGCTGTCTTAAAGTTCCAT 2857
QY 2826 GGAATTTGTTTAAATAATATCTTAAAGATGAATCTTATCAAGCTGTGCTTGAACCT 2885
DB 2858 GGAATTTGTTTAAATAATATCTTAAAGATGAATCTTATCAAGCTGTGCTTGAACCT 2917
QY 2886 GTTAAATTTGTTCAATTAATGATGATGCTGTCTTAAAGATGAGTGGGAGT 2945
DB 2918 GTTAAATTTGTTCAATTAATGATGATGCTGTCTTAAAGATGAGTGGGAGT 2977
QY 2946 TGCCTTGAATAATGTTTATGCAACAGAAAGATGTGAGAGCAGCTTGTGCGGG 3005

DB 2978 TGGCTTGAACAAATGTTTATGCAACAGGAAGCATGTGTAGCAGCCAGCTTTGGCGG 3037
QY 3006 GCGTATGTGTGGCCAGCTCTTAACCATTCAGTCTATTACTTTGGTGAGTCTTGTGGAC 3065
DB 3038 GCGTATGTGTGGCCAGCTCTTAACCATTCAGTCTATTACTTTGGTGAGTCTTGTGGAC 3097
QY 3066 AACCAACACACGTCGCCACATGGTACTAGTGGCCGTTGTTTCGTTGCTCTAGATGT 3125
DB 3098 AACCAACACACGTCGCCACATGGTACTAGTGGCCGTTGTTTCGTTGCTCTAGATGT 3157
QY 3126 TTTGGCACTCTAGAGCCACAGCCCTTAAGATGATCAATTAATAAATTCCTCTTTGTAACCTC 3185
DB 3158 TTTGGCACTCTAGAGCCACAGCCCTTAAGATGATCAATTAATAAATTCCTCTTTGTAACCTC 3217
QY 3186 AGTGTGGGGACGTAGGGGAGCCCTCAAGTGTGTGGAGTGCACCACTTTGGGGAAAGA 3245
DB 3218 AGTGTGGGGACGTAGGGGAGCCCTCAAGTGTGTGGAGTGCACCACTTTGGGGAAAGA 3277
QY 3246 GGTGAGAGAGAGCTGTGTTTATCTCCACAGCAGATGAGATAAATAATTAATCATAGT 3305
DB 3278 GGTGAGAGAGAGCTGTGTTTATCTCCACAGCAGATGAGATAAATAATTAATCATAGT 3337
QY 3306 ATTAACCTAGACATAGACAGATTAACCTAGATGATGACATGCTCACTGCAACCTTCCCA 3365
DB 3338 ATTAACCTAGACATAGACAGATTAACCTAGATGATGACATGCTCACTGCAACCTTCCCA 3397
QY 3366 GCTCTCATTTTGTAGTGTATTTGGGATAGGGATAGTGTGTTGGGGTATGGGGGAGTGT 3425
DB 3398 GCTCTCATTTTGTAGTGTATTTGGGATAGGGATAGTGTGTTGGGGTATGGGGGAGTGT 3457
QY 3426 TTTTCGACCTGCTTTGAGAGAGTGTGCTCGACACCTCAGACAGTTTGGGGTGTGGCCGACG 3485
DB 3458 TTTTCGACCTGCTTTGAGAGAGTGTGCTCGACACCTCAGACAGTTTGGGGTGTGGCCGACG 3517
QY 3486 GCGGTTCTTGTAGATTAAGATGTGGCCATCTAGCCTGTAACTTCACTGTCACTGTGT 3545
DB 3518 GCGGTTCTTGTAGATTAAGATGTGGCCATCTAGCCTGTAACTTCACTGTCACTGTGT 3577
QY 3546 CCCATAGGCTGCTTCTGAATCTGTATTTAGAAATAGTTTGTTCAGAGCTGACCTTG 3605
DB 3578 CCCATAGGCTGCTTCTGAATCTGTATTTAGAAATAGTTTGTTCAGAGCTGACCTTG 3637
QY 3606 CGTGCAAAATGTATCCGTGGCCCTGTATATGATAGATTGATTAATTAATTAATTAATTAAT 3665
DB 3638 CGTGCAAAATGTATCCGTGGCCCTGTATATGATAGATTGATTAATTAATTAATTAATTAAT 3697
QY 3666 GTTAATGTAAATCTGTGGGCAAGATCTTTTCCATGAGCAAGAAATATCCAAAGCTGTGAA 3725
DB 3698 GTTAATGTAAATCTGTGGGCAAGATCTTTTCCATGAGCAAGAAATATCCAAAGCTGTGAA 3757
QY 3726 ACTGCTATGTTTAAATATGCTCATTTGTGCTTTACTGTGTGTGTGACTGTGTAGAGGA 3785
DB 3758 ACTGCTATGTTTAAATATGCTCATTTGTGCTTTACTGTGTGTGTGACTGTGTAGAGGA 3817
QY 3786 CAAGAAGTTCATTTGATGTCAATTAAGCAAAAGTCTTGCTACTTTTGTGAATCTGAAA 3845
DB 3818 CAAGAAGTTCATTTGATGTCAATTAAGCAAAAGTCTTGCTACTTTTGTGAATCTGAAA 3877
QY 3846 AA 3847
DB 3878 AA 3879

RESULT 4
ID ADR25979 standard; DNA; 3879 BP.
XX ADR25979;
AC
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1840.
XX

KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN MO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PE 15-JAN-2004; 2004MO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.
XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
PS Disclosure; SEQ ID NO 1840; 226bp; English.
XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
SQ Sequence 3879 BP; 807 A; 1074 C; 1178 G; 820 T; 0 U; 0 Other;
QY
Best Match 98.6%; Score 3804.2; DB 13; Length 3879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 7 GTCCGCGCGATGAGGAGGCGACGCGGGAACCCCATGAGGACCTGCTGCGCACCTT 66
DB 39 GACGTGGCCATGAGAGGCGACGCGGGAACCCCATGAGGACCTGCTGCGCACCTT 98
QY 67 CGACGCGGCGAGTTCA CGGCTGTGGAGAAAGTGGGCTCGGCGGCTTGGGCAAGTGTGA 126
DB 99 CGACGCGGCGAGTTCA CGGCTGTGGAGAAAGTGGGCTCGGCGGCTTGGGCAAGTGTGA 158
QY 127 CAAAGTGGCCATTTCCATGGAAGACCTGTGCGCATCAAGTGTGCGCCAGCTGCA 186
DB 159 CAAAGTGGCCATTTCCATGGAAGACCTGTGCGCATCAAGTGTGCGCCAGCTGCA 218
QY 187 CGTGAAGACAGGAGCGCATGTAGAGCTTTTGAAGAAAGCCAAAGATGAGATGSCAA 246
DB 219 CGTGAAGACAGGAGCGCATGTAGAGCTTTTGAAGAAAGCCAAAGATGAGATGSCAA 278
QY 247 GTTTCGTACTATCTGCTGTGTATGTCATCTGCGGAACTGTGCGGCTGTGTATGGA 306
DB 279 GTTTCGTACTATCTGCTGTGTATGTCATCTGCGGAACTGTGCGGCTGTGTATGGA 338
QY 307 GTACATGGAAGACGGGCTCCCTGGAAGCTGTGGCTTTCGAGCATTTGGCATGGATCT 366
DB 339 GTACATGGAAGACGGGCTCCCTGGAAGCTGTGGCTTTCGAGCATTTGGCATGGATCT 398
QY 367 CCGGTTCCGAATCATTCACAGAGACGGCGGTGGCATGAATCTTCTGCACTGCAATGSCCC 426
DB 399 CCGGTTCCGAATCATTCACAGAGACGGCGGTGGCATGAATCTTCTGCACTGCAATGSCCC 458
QY 427 GCCACTCTGTGCACTGCACTCAAGCCCGGCAACATCTGTGTGATGCGCCATCAACGT 486
DB 459 GCCACTCTGTGCACTGCACTCAAGCCCGGCAACATCTGTGTGATGCGCCATCAACGT 518

QY 487 CAAAGATTCTGATTTTGGTGTGGCCCAAGTGCACCGGGCTGTGCCACTGCGATGACCTCAG 546
 DB |||||
 DB 519 CAAAGATTCTGATTTTGGTGTGGCCCAAGTGCACCGGGCTGTGCCACTGCGATGACCTCAG 578
 QY 547 CANTGATGGCCGTGTTGGCACAATGGCCATCCCTCCAGAGCGCATCAGGGAGAAG 606
 DB |||||
 DB 579 CANTGATGGCCGTGTTGGCACAATGGCCATCCCTCCAGAGCGCATCAGGGAGAAG 638
 QY 607 CCGGCTCTTCGACACCAAGCAGATGTATACGCTTTGGCATCTGTGATCTGGGGGTGTCT 666
 DB |||||
 DB 639 CCGGCTCTTCGACACCAAGCAGATGTATACGCTTTGGCATCTGTGATCTGGGGGTGTCT 698
 QY 667 CACACAGAAAGAACCGGTTTGCAGATGAGAAACAATCTTCGACATCATGTGTGAAGTGT 726
 DB |||||
 DB 699 CACACAGAAAGAACCGTITTCAGATGAGAAACAATCTTCGACATCATGTGTGAAGTGT 758
 QY 727 GAAGGGCCACCGCCCGAGCTGCGCGGTGTGCAGAGCCGGCGCGCGCTTCGACCA 786
 DB |||||
 DB 759 GAAGGGCCACCGCCCGAGCTGCGCGGTGTGCAGAGCCGGCGCGCGCTTCGACCA 818
 QY 787 CCTGATACGCTCATGTCAGCGGTGTGCAGAGGGGATCCGCGATTTAGGCCCACTTCCA 846
 DB |||||
 DB 819 CCTGATACGCTCATGTCAGCGGTGTGCAGAGGGGATCCGCGATTTAGGCCCACTTCCA 878
 QY 847 AGAATATTCTTCTGAAACCGAGGACCTGTGTGAAAACCTGATGACGAAGTGAAGAAC 906
 DB |||||
 DB 879 AGAATATTCTTCTGAAACCGAGGACCTGTGTGAAAACCTGATGACGAAGTGAAGAAC 938
 QY 907 TECTCATGATCTGGAAGTGAAGAACCCCGGAGCCCAAGAGCGAGGTGTCTGCGAG 966
 DB |||||
 DB 939 TECTCATGATCTGGAAGTGAAGAACCCCGGAGCCCAAGAGCGAGGTGTCTGCGAG 998
 QY 967 GCTCAAGCGGGCTCTGCCCCCACTTCGATTAACGACTACAGCTTCTCGAGCTTCTCTC 1026
 DB |||||
 DB 999 GCTCAAGCGGGCTCTGCCCCCACTTCGATTAACGACTACAGCTTCTCGAGCTTCTCTC 1058
 QY 1027 ACAGCTGGACTGTGAGTTTCCAGGCTGTCCAGGGCCCCGAGAGCTCAGCCGAGCTTC 1086
 DB |||||
 DB 1059 ACAGCTGGACTGTGAGTTTCCAGGCTGTCCAGGGCCCCGAGAGCTCAGCCGAGCTTC 1118
 QY 1087 CTCTGAGTCCAAAGCTGCCATCTGTCGGGCAGTGGGAAGAGCTCTCGGGGGTGTCCCGGT 1146
 DB |||||
 DB 1119 CTCTGAGTCCAAAGCTGCCATCTGTCGGGCAGTGGGAAGAGCTCTCGGGGGTGTCCCGGT 1178
 QY 1147 GGACTCCGCTTCTCTTCCAGAGGATCACTGTGCTGTCTTTCGAGCGGAAACCTTCAAC 1206
 DB |||||
 DB 1179 GGACTCCGCTTCTCTTCCAGAGGATCACTGTGCTGTCTTTCGAGCGGAAACCTTCAAC 1238
 QY 1207 CAGCGATCTGGGTACCAAGAGCGTCCAGAAAGAAAGCTTGTGATGTCATGTGTCC- 1265
 DB |||||
 DB 1239 CAGCGATCTGGGTACCAAGAGCGTCCAGAAAGAAAGCTTGTGATGTCATGTGTCCG 1297
 QY 1266 GGGACACGAGCAAACTGATGAAATCTCTGACGCCGAGAGCTGTGACCTGTGACCTGGA 1325
 DB |||||
 DB 1298 GGGACACGAGCAAACTGATGAAATCTCTGACGCCGAGAGCTGTGACCTGTGACCTGGA 1357
 QY 1326 GGGGTGACGAGCTGTGACCTGTGAGAGGCGGGGCAAGAGAGTGTGCGCAATGTGAC 1385
 DB |||||
 DB 1358 GGGGTGACGAGCTGTGACCTGTGAGAGGCGGGGCAAGAGAGTGTGCGCAATGTGAC 1417
 QY 1386 TGTGTCTCAACAAATGCAACCCCAACCTGAGCAACCTGAGGGCTCACCCGTTGCACA 1445
 DB |||||
 DB 1418 TGTGTCTCAACAAATGCAACCCCAACCTGAGCAACCTGAGGGCTCACCCGTTGCACA 1477
 QY 1446 TGGCGTGTGAGAGAGGTGTGGGTGTGTGTGAGCTCTCTGCTGTGAGACGGAAGATGAG 1505
 DB |||||
 DB 1478 TGGCGTGTGAGAGAGGTGTGGGTGTGTGTGAGCTCTCTGCTGTGAGACGGAAGATGAG 1537
 QY 1506 TCAACGCCAAGAGTGAAGACCAATGACAGCCCTTCCACTTTTGCAGCCCAAGAACGGGATG 1565
 DB |||||
 DB 1538 TCAACGCCAAGAGTGAAGACCAATGACAGCCCTTCCACTTTTGCAGCCCAAGAACGGGATG 1597

QY 1566 AGTCTAGCACAGGCTGTGTTGGAGAAAGCGCTCGGTCAACGAGGTGACTTTGAG 1625
 DB |||||
 DB 1598 AGTCTAGCACAGGCTGTGTTGGAGAAAGCGCTCGGTCAACGAGGTGACTTTGAG 1657
 QY 1626 GCCGAGCGCCATGACAGTGGCTGTGACACCGGGCAGAGAGATATGTGTGCACTCTGC 1685
 DB |||||
 DB 1658 GCCGAGCGCCATGACAGTGGCTGTGACACCGGGCAGAGAGATATGTGTGCACTCTGC 1717
 QY 1686 TGGCGGAGGCTGTGAGCTGTGACAGGCGCAAGATATGCTGTGCTGCACTGACCTAG 1745
 DB |||||
 DB 1718 TGGCGGAGGCTGTGAGCTGTGACAGGCGCAAGATATGCTGTGCTGCACTGACCTAG 1777
 QY 1746 CTGCGCTGACAGGGCCACTGCGCCATCGTCAAGCTGTGAGCAGACAGCCGGGGGTGAG 1805
 DB |||||
 DB 1778 CTGCGCTGACAGGGCCACTGCGCCATCGTCAAGCTGTGAGCAGACAGCCGGGGGTGAG 1837
 QY 1806 TGAACGCCCAGACGCTGAGTGGAGAGAGCCATTGCACTTGGCCGACAGCGCGGCACT 1865
 DB |||||
 DB 1838 TGAACGCCCAGACGCTGAGTGGAGAGAGCCATTGCACTTGGCCGACAGCGCGGCACT 1897
 QY 1866 ACCGCTGGCCCGCATCTTCATGCACTGTGTCTCCAGAGTCAACGTCTGACAGCTGTGG 1925
 DB |||||
 DB 1898 ACCGCTGGCCCGCATCTTCATGCACTGTGTCTCCAGAGTCAACGTCTGACAGCTGTGG 1957
 QY 1926 CACAGACACCCCTGACGTGGCCGGAGAGACGGGGCACAAGAGCACTGCCAGGCTGTCC 1985
 DB |||||
 DB 1958 CACAGACACCCCTGACGTGGCCGGAGAGACGGGGCACAAGAGCACTGCCAGGCTGTCC 2017
 QY 1986 TGCATCGGGGCGTGGCAAGAGAGCCGTGACCTGACAGCGGTACACCGCTCTGACCTGG 2045
 DB |||||
 DB 2018 TGCATCGGGGCGTGGCAAGAGAGCCGTGACCTGACAGCGGTACACCGCTCTGACCTGG 2077
 QY 2046 CTGCGCCGACAGACACTGTGCACTGTGCAAGCTGTGTGTGAGAGAAAGCCGATGTGC 2105
 DB |||||
 DB 2078 CTGCGCCGACAGACACTGTGCACTGTGCAAGCTGTGTGTGAGAGAAAGCCGATGTGC 2137
 QY 2106 TGGCCCGGGGACCCCTGAAACAGACGGGCTGACCTGGCTGGCCGCCAGGGGCTCGG 2165
 DB |||||
 DB 2138 TGGCCCGGGGACCCCTGAAACAGACGGGCTGACCTGGCTGGCCGCCAGGGGCTCGG 2197
 QY 2166 AGGTGTGAGAGAGTTGTGACGCGCGATGTCAATTGACCTGTTGACAGACAGGGGCTCA 2225
 DB |||||
 DB 2198 AGGTGTGAGAGAGTTGTGACGCGCGATGTCAATTGACCTGTTGACAGACAGGGGCTCA 2257
 QY 2226 GCGCGCTGACCTGGCGGCCCAAGGGCCGACACAGACGCTGTGAACCTGTCTCAAGC 2285
 DB |||||
 DB 2258 GCGCGCTGACCTGGCGGCCCAAGGGCCGACACAGACGCTGTGAACCTGTCTCAAGC 2317
 QY 2286 ATGGGGCCCAATCAACCTGAGAGGCTCAAGTTCCAGGGGCGCATGAGCCCGCGCA 2345
 DB |||||
 DB 2318 ATGGGGCCCAATCAACCTGAGAGGCTCAAGTTCCAGGGGCGCATGAGCCCGCGCA 2377
 QY 2346 CACTCTGCGGGAAGCAAGCTTGTGAGCTGTGCGGAGACCGGGGGTTCACAGTGGG 2405
 DB |||||
 DB 2378 CACTCTGCGGGAAGCAAGCTTGTGAGCTGTGCGGAGACCGGGGGTTCACAGTGGG 2437
 QY 2406 GCTCTTGTCTGTCTGTGTCTCTGTGGGAGTGAACGATCTGTGCGGGGCCCGCTTG 2465
 DB |||||
 DB 2438 GCTCTTGTCTGTCTGTGTCTCTGTGGGAGTGAACGATCTGTGCGGGGCCCGCTTG 2497
 QY 2466 TGGCTTAATTAATTTAAACCAAGAGAGTGAACATGTGTCATGAGAGGCGGTGCG 2525
 DB |||||
 DB 2498 TGGCTTAATTAATTTAAACCAAGAGAGTGAACATGTGTCATGAGAGGCGGTGCG 2557
 QY 2526 CTGACCGAGTGTCCCTTCAGGTGAACCTGACCTGACAGTGCATGCCCCGTCTCATATC 2585
 DB |||||
 DB 2558 CTGACCGAGTGTCCCTTCAGGTGAACCTGACCTGACAGTGCATGCCCCGTCTCATATC 2617
 QY 2586 GATCTTAGGACCTGTGTGTGAAGGACCGTGTGTGAGATCAATTTGTTGTCTCTTAA 2645
 DB |||||
 DB 2618 GATCTTAGGACCTGTGTGTGAAGGACCGTGTGTGAGATCAATTTGTTGTCTCTTAA 2677
 QY 2646 TGGGTGCTGAGGCTGTGTCTCATGTGATGAAGCCCAAGGGGTGAGACATCTCTCT 2705

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Db      2678 TGGGTCGTGAGGCTGCTCTCTCACTGATGAAGCCCGGCGGTGAGACATCCACTCTCT 2737
Qy      2706 CCTGAGGCGAGCCACTTGGGTGCTGAGAGCTCACCACTTTGAGAGAGTGCAGGAGAA 2765
Db      2738 CCTGAGCGAGCCACTTGGGTGCTGAGAGCTCACCACTTTGAGAGAGTGCAGGAGAA 2797
Qy      2766 ACTGCTTTTATTTATCTGATACATGACGTGGGCGAGAGAGGCTGTCTTAAAGTTCCAT 2825
Db      2798 ACTGCTTTTATTTATCTGATACATGACGTGGGCGAGAGAGGCTGTCTTAAAGTTCCAT 2857
Qy      2826 GGAATTTGTTTATATAATATCTTAAGAGATGAATCTTATCAGCTGTGTGTTGAAACCT 2885
Db      2858 GGAATTTGTTTATATAATATCTTAAGAGATGAATCTTATCAGCTGTGTGTTGAAACCT 2917
Qy      2886 GTTAAAAATGTTCAATACATTTGAGATGCTGCTCTTAATGATGAGCTTAAGTGGGCT 2945
Db      2918 GTTAAAAATGTTCAATACATTTGAGATGCTGCTCTTAATGATGAGCTTAAGTGGGCT 2977
Qy      2946 TGGCTTTGAAAAATGTTTATATGACAGAGAGAGATGATGAGCAGCTTTGGCGGG 3005
Db      2978 TGGCTTTGAAAAATGTTTATATGACAGAGAGAGATGATGAGCAGCTTTGGCGGG 3037
Qy      3006 GCGTATGCTGGGCGAGCTCTTAACCATTTCACTATTACTTGGTGAAGCTTGTGAGC 3065
Db      3038 GCGTATGCTGGGCGAGCTCTTAACCATTTCACTATTACTTGGTGAAGCTTGTGAGC 3097
Qy      3066 AACCAACAACAACGTCGCCACATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 3125
Db      3098 AACCAACAACAACGTCGCCACATGATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCT 3157
Qy      3126 TTTGGCACTCTAGAGCCACAGGCGCTAAGAGTCATTTAAAAATTTCCCTTTGTAACCTC 3185
Db      3158 TTTGGCACTCTAGAGCCACAGGCGCTAAGAGTCATTTAAAAATTTCCCTTTGTAACCTC 3217
Qy      3186 AGTGTGGGAGACTGAGGCGAGGCCCCCTCAGAGTGTGCTGAGTGCACAGCTTGTGGGAGAA 3245
Db      3218 AGTGTGGGAGACTGAGGCGAGGCCCCCTCAGAGTGTGCTGAGTGCACAGCTTGTGGGAGAA 3277
Qy      3246 GGTGACGAGAAAGCTGTGTTTATTTCTCAGACGCGATGATGAATGAATTAATCAATAGT 3305
Db      3278 GGTGACGAGAAAGCTGTGTTTATTTCTCAGACGCGATGATGAATGAATTAATCAATAGT 3337
Qy      3306 ATTACTGAGACATACAGATATTAACCTAGGTGATGACCTGCTACCTGCACTCCCTCCCA 3365
Db      3338 ATTACTGAGACATACAGATATTAACCTAGGTGATGACCTGCTACCTGCACTCCCTCCCA 3397
Qy      3366 GCTCTCATTTTGTAGGTGATTTGGAGATGAGTGTGTTGGGAGTATGGGGGAGAGTG 3425
Db      3398 GCTCTCATTTTGTAGGTGATTTGGAGATGAGTGTGTTGGGAGTATGGGGGAGAGTG 3457
Qy      3426 TTTCTGACCTGCTTTGACAGAGCTGCTCCGACCTCAGACGTTTGGGCTGTGCCCCAGG 3485
Db      3458 TTTCTGACCTGCTTTGACAGAGCTGCTCCGACCTCAGACGTTTGGGCTGTGCCCCAGG 3517
Qy      3486 GGGGTTCTTGAATGTAAGATGAGGCGATCAGGCTGTATCTTCACTGTCACCTGATGT 3545
Db      3518 GGGGTTCTTGAATGTAAGATGAGGCGATCAGGCTGTATCTTCACTGTCACCTGATGT 3577
Qy      3546 CCCATAGGCTGCTTCTGATATCTGTATTAAGATTAAGTTGTTGTCAGAACCTGACCTG 3605
Db      3578 CCCATAGGCTGCTTCTGATATCTGTATTAAGATTAAGTTGTTGTCAGAACCTGACCTG 3637
Qy      3606 CGTGCAGAAATGATCCGTGGCTGCTGATATGATAGATGATGATTAATGATCCATGAT 3665
Db      3638 CGTGCAGAAATGATCCGTGGCTGCTGATATGATAGATGATGATTAATGATCCATGAT 3697
Qy      3666 GTTAAATGGAATCTGTGGGCGAGATACCTTTCCATGAGGAGAAATATCCAACTGTGAA 3725
Db      3698 GTTAAATGGAATCTGTGGGCGAGATACCTTTCCATGAGGAGAAATATCCAACTGTGAA 3757
Qy      3726 ACTGCTATGTTTATATATGCTCATGTGCTTACTGTTGTGTGAGCTGCGTGAAGGGA 3785

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Db      3758 ACTGCTATGTTTATATATGCTCATTTGCTTACTGTGTGTGAGCTGCGTGAAGGA 3817
Qy      3786 CAAGAATTCATTTGATGATGCAATAAGCAAAAGACTTGCTACTTTTGAATCTGAAA 3845
Db      3818 CAAGAATTCATTTGATGATGCAATAAGCAAAAGACTTGCTACTTTTGAATCTGAAA 3877
Qy      3846 AA 3847
Db      3878 AA 3879

RESULT 5
AAH15762
ID AAH15762 standard; cDNA; 3876 BP.
XX
AC AAH15762;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14188.
XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Ito gai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14188; 2537bp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH13166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

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QY	2106	TGGCCCGGGGACCCCTGAACCAAGACGGGCTGCACACTGGCTGCGGCCCACGGGCACTGG	2165
Dp	2155	TGGCCCGGGGACCCCTGAACCAAGACGGGCTGCACACTGGCTGCGGCCCACGGGCACTGG	2214
QY	2166	AGGTGGTGAAGAGATTGGTTCAGCGCGCAATGTCATTTGACTGTGTGACAGAGAGGGGCTCA	2225
Dp	2215	AGGTGGTGAAGAGATTGGTTCAGCGCGCAATGTCATTTGACTGTGTGACAGAGAGGGGCTCA	2274
QY	2226	GCGCGCTGCACCTGGCGCGCCAGGGCGCGCACACACACACGGTGGAGACTCTGCTCAAGC	2285
Dp	2275	GCGCGCTGCACCTGGCGCGCCAGGGCGCGCACACACACGGTGGAGACTCTGCTCAAGC	2334
QY	2286	ATGGGGGCCCACTCAACCTGCGAGACCTCAAGTTCCAGGGCGGCCAATGGCCCGCGCGCA	2345
Dp	2335	ATGGGGGCCCACTCAACCTGCGAGACCTCAAGTTCCAGGGCGGCCAATGGCCCGCGCGCA	2394
QY	2346	CACCTCTGCGGGAAGCAAGACTGAGCTGCTGCGGAGACCGGGGGTTCACGTGGG	2405
Dp	2395	CACCTCTGCGGGAAGCAAGACTGAGCTGCTGCGGAGACCGGGGGTTCACGTGGG	2454
QY	2406	GCTCTTGTCTCTGCTCTGTGTTCTCTGTGGGGGATGGAAGATCTCGGCGGGGCCCGTTG	2465
Dp	2455	GCTCTTGTCTCTGCTCTGTGTTCTCTGTGGGGGATGGAAGATCTCTGCGGGGCCCGTTG	2514
QY	2466	TGGCTTAACTTAAATTTTAAACCAAGCAGAGGTGACATGTGTGCATCAGAGAGCGCTGCTG	2525
Dp	2515	TGGCTTAACTTAAATTTTAAACCAAGCAGAGGTGACATGTGTGCATCAGAGAGCGCTGCTG	2574
QY	2526	CTGACCGGAGTGTCCCCCTTCAGGTGAAGCTGGCTAGGTGCACATGCCCGCTCATATC	2585
Dp	2575	CTGACCGGAGTGTCCCCCTTCAGGTGAAGCTGGCTAGGTGCACATGCCCGCTCATATC	2634
QY	2586	GATCTAGGCACTGTCTGTCTGAAGGGGACCGTGGGTCAAGATCATTTCTGTGTCCTAA	2645
Dp	2635	GATCTAGGCACTGTCTGTCTGAAGGGGACCGTGGGTCAAGATCATTTCTGTGTCCTAA	2694
QY	2646	TGGGTGCGTAGAGCTGTGTCTCAGTGATGAAGCCCGCGGTGGAGCATTCACCTCT	2705
Dp	2695	TGGGTGCGTAGAGCTGTGTCTCAGTGATGAAGCCCGCGGTGGAGCATTCACCTCT	2754
QY	2706	CGTAGGGGAGGCACTTGGGGTGTGTGAAGCTCAACAATCTTGAAGGAGGTGCAGGGGAA	2766
Dp	2755	CGTAGGGGAGGCACTTGGGGTGTGTGAAGCTCAACAATCTTGAAGGAGGTGCAGGGGAA	2814
QY	2766	ACTGTGTTTTTATCTTCATACATGACGGTGGGCGAGAGGGCTGTCTTAAAGTTTCAT	2825
Dp	2815	ACTGTGTTTTTATCTTCATACATGACGGTGGGCGAGAGGGCTGTCTTAAAGTTTCAT	2874
QY	2826	GGAATTTGTTTATTAATAATCTTAAAGATGAATACCTTATTCAGCTGTGTGCTGAACCT	2888
Dp	2875	GGAATTTGTTTATTAATAATCTTAAAGATGAATACCTTATTCAGCTGTGTGCTGAACCT	2934
QY	2886	GTTAAAAAATGTTCAATACATTGGATGAGTCTAGTCTCTAAATGATGGCTAAAGTAGGGGT	2945
Dp	2935	GTTAAAAAATGTTCAATACATTGGATGAGTCTAGTCTCTAAATGATGGCTAAAGTAGGGGT	2994
QY	2946	TGGCTTTGAAAACAATGTTTTATGCAACAAGGACGAATGTAGACGCCACTTTGCGGG	3005
Dp	2995	TGGCTTTGAAAACAATGTTTTATGCAACAAGGACGAATGTAGACGCCACTTTGCGGG	3054
QY	3006	GCGTATGTGTGGCGAGCTTAAACAATTCAGTCTATTAATTGGGGTGAAGTCCCTGTGAC	3066
Dp	3055	GCGTATGTGTGGCGAGCTTAAACAATTCAGTCTATTAATTGGGGTGAAGTCCCTGTGAC	3114
QY	3066	AACCAACAACAGTCCCAATGATGACTAGCTGCGGTTGTTTCTCGTGTGCTTAAGATGT	3125
Dp	3115	AACCAACAACAGTCCCAATGATGACTAGCTGCGGTTGTTTCTCGTGTGCTTAAGATGT	3174
QY	3126	TTTGGCAACTCTAGAGCCAAGGCGCTAAGATCATTTAAAAAATTCCTCCCTTTGTAACCTC	3188
Dp	3175	TTTGGCAACTCTAGAGCCAAGGCGCTAAGATCATTTAAAAAATTCCTCCCTTTGTAACCTC	3234

QY	3186	AGTGTCTGGGGACATAGGCGAGACCCCCCTCAGGTGCTGTGAAGGACACAGTCTTGGGGAGA	3245
Db	3235	AGTGTGGGGACGTAGGGAGACCCCCCTCAGGTGCTGTGAAGGACACAGTCTTGGGGAGA	3294
QY	3246	GGTCAAGAGAAAGCTGTGTGTTTTTATCTCCACAGCAGTATGAAGATTAATTCATAGT	3305
Db	3255	GGTCAAGAGAAAGCTGTGTGTTTTTATCTCCACAGCAGTATGAAGATTAATTCATAGT	3354
QY	3306	ATTACCTTAGACATAGACAGTATTAACCTTAGTAGATGCACTGCTCACTGCACCTTCCCA	3365
Db	3355	ATTACCTTAGACATAGACAGTATTAACCTTAGTAGATGCACTGCTCACTGCACCTTCCCA	3414
QY	3366	GCTCTCATTTTTGTTAGGTGATTTTGGATATGGGATAGTGTGAGGATATGGGGAGGTG	3425
Db	3415	GCTCTCATTTTTGTTAGGTGATTTTGGATATGGGATAGTGTGAGGATATGGGGAGGTG	3474
QY	3426	TTTCTGACCTCTCTTGGCAGACGTGCTCCGACCTCAGCAGTTTGGGGTGTGGCCGAGG	3485
Db	3475	TTTCTGACCTCTCTTGGCAGACGTGCTCCGACCTCAGCAGTTTGGGGTGTGGCCGAGG	3534
QY	3486	GCGGTTCTTGAGTGTAAAGATGAGTGCCCATCTAGCCTTGTACTTCACTGTCACTGTGT	3545
Db	3535	GCGGTTCTTGAGTGTAAAGATGAGTGCCCATCTAGCCTTGTACTTCACTGTCACTGTGT	3594
QY	3546	CCCATAGGGGTGCTCTTGCATATCTGTATTTAGATTAAGTTGTTGGCAGAACGTGACCTG	3605
Db	3595	CCCATAGGGGTGCTCTTGCATATCTGTATTTAGATTAAGTTGTTGGCAGAACGTGACCTG	3654
QY	3606	CGTGCAAAACATGTACCGTGCCCTGTATATGATGTAGATTGATATTAATGTACCATGTAT	3655
Db	3655	CGTGCAAAACATGTACCGTGCCCTGTATATGATGTAGATTGATATTAATGTACCATGTAT	3714
QY	3666	GTTATGTGAATCTGTGGGACAGATPACTTTTCATGTGACGAGAAATATCCAAGCTGTGAA	3725
Db	3715	GTTATGTGAATCTGTGGGACAGATPACTTTTCATGTGACGAGAAATATCCAAGCTGTGAA	3774
QY	3726	ACTGGCTATGTTTAAATATGCTTCAATGTCCTTACCTTACCTGTGTGTGACCTGCGAGGGA	3785
Db	3775	ACTGGCTATGTTTAAATATGCTTCAATGTCCTTACCTTACCTGTGTGTGACCTGCGAGGGA	3834
QY	3786	CAAGAGTTTCATTTGATGTCAATTAAGCAAAAGTACTTGCC	3826
Db	3835	CAAGAGTTTCATTTGATGTCAATTAAGCAAAAGTACTTGCC	3875
RESULT 6			
ABZ12023			
ID	ABZ12023	standard; cDNA, 3981 BP.	
XX	ABZ12023;		
AC			
XX			
DT	20-JAN-2003	(first entry)	
XX			
DE	Human polynucleotide SEQ ID NO 905.		
XX			
KW	Human; genome mapping; gene therapy; food supplement; virus; fungus;		
KW	cell-proliferative disorder; neurodegenerative disease; bacterial;		
KW	Parkinson's disease; Alzheimer's disease; autoimmune disease;		
KW	multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;		
KW	arthritis; cyostatic; immunomodulator; nootropic; neuroprotective;		
KW	antiparkinsonian; antidiabetic; immunosuppressive; dermatological;		
KW	haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;		
KW	antiarthritic; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200270539-A2.		
XX			
PD	12-SEP-2002.		
XX			
PF	05-MAR-2002; 2002WO-US005095.		
XX			
PR	05-MAR-2001; 2001US-00799451.		

Db 1560 CACCCGTTTGCACTATGCGCGTGAAGAGAGGGGTGCGGGGTGTCTGTGAGACTCTCTGCTGAC 1619
QY 1492 ACGGAAGATCAAGTGTCAACGCCAAGAGATGAGGACCAAGTGGACAGCCCTTCACTTTGGCAGC 1551
Db 1620 GCGGAAGATCAAGTGTCAACGCCAAGAGATGAGGACCAAGTGGACAGCCCTTCACTTTGGCAGC 1679
QY 1552 CCAGAACCGGGGATGAGTCTAGACACAGGCTGCTGTGTGAGAAAGAACGCTCGGTCAACGA 1611
Db 1680 CCAGAACCGGGGACGAGTCTAGACACAGGCTGCTGTGTGAGAAAGAACGCTCGGTCAACGA 1739
QY 1612 GGTGACCTTTGAGGGCCGGACGCCCATGACAGTGGCCTTCCAGACAGGGCAGAGAAATAT 1671
Db 1740 GGTGACCTTTGAGGGCCGGACGCCCATGACAGTGGCCTTCCAGACAGGGCAGAGAAATAT 1799
QY 1672 CGTGGCAATCTGTGCTGCGCCGAGGCGTGGACGTGAGCTTGGCAGGGCAGAGATGCTGGCT 1731
Db 1800 CGTGGCAATCTGTGCTGCGCCGAGGCGTGGACGTGAGCTTGGCAGGGCAGAGATGCTGGCT 1859
QY 1732 GCCACTGACCTACGCTGCTGGCAGGGGCACTGGCCATCGTCAAGCTGCTGGCCAAAGCA 1791
Db 1860 GCCACTGACCTACGCTGCTGGCAGGGGCACTGGCCATCGTCAAGCTGCTGGCCAAAGCA 1919
QY 1792 GCCCGGGGTGAGTGTGAACGCCACAGCGCTGATGGAGAGACGCCATTGGCACTTGGCCGC 1851
Db 1920 GCCCGGGGTGAGTGTGAACGCCACAGCGCTGATGGAGAGACGCCATTGGCACTTGGCCGC 1979
QY 1852 ACAAGCGGGGCACTACCGGCTGGCCCGCATCTCTATCCAGCTGTGTCTCCGAGTCAAGT 1911
Db 1980 ACAAGCGGGGCACTACCGGCTGGCCCGCATCTCTATCCAGCTGTGTCTCCGAGTCAAGT 2039
QY 1912 CTGCAAGCTGTGGGACAGACACCCCTGACAGTGGCCCGGAGAGAGGGGCAACAGAGAC 1971
Db 2040 CTGCAAGCTGTGGGACAGACACCCCTGACAGTGGCCCGGAGAGAGGGGCAACAGAGAC 2099
QY 1972 TGGCAGCTGTCTCTGTGATCGGAGCGCTGGCAAGAGAGCGCTGACTTCAAGCGCTTAC 2031
Db 2100 TGGCAGCTGTCTCTGTGATCGGAGCGCTGGCAAGAGAGCGCTGACTTCAAGCGCTTAC 2159
QY 2032 CGCTGTGACCTGTGGCTGGCCCGCAAGGACACTTGGCCACTGTCAAGCTGTCTTGTGAAGA 2091
Db 2160 CGCTGTGACCTGTGGCTGGCCCGCAAGGACACTTGGCCACTGTCAAGCTGTCTTGTGAAGA 2219
QY 2092 GAAAGGCGATGTGTGCGCCCGGGGACCCCTGAACAGACAGGCGCTGCACTTGGCTGGCC 2151
Db 2220 GAAAGGCGATGTGTGCGCCCGGGGACCCCTGAACAGACAGGCGCTGCACTTGGCTGGCC 2279
QY 2152 CCACGGGCACTCGAGAGTGTGAGAGAGTGTGTCAAGCGCGATGTCTATTTGACTTGTGCA 2211
Db 2280 CCACGGGCACTCGAGAGTGTGAGAGAGTGTGTCAAGCGCGATGTCTATTTGACTTGTGCA 2339
QY 2212 CGAGCAGGGGCTCAAGCGGCTGTCACTTGGCCCGCCAGAGGGCCGGACAGCAGAGCGGTGA 2271
Db 2340 CGAGCAGGGGCTCAAGCGGCTGTCACTTGGCCCGCCAGAGGGCCGGACAGCAGAGCGGTGA 2399
QY 2272 GACTGTGCTCAGAGCATGGGGCCCACTCAACTCAGCTGAGAGCTCAAGTTTCAAGGCGGCA 2331
Db 2400 GACTGTGCTCAGAGCATGGGGCCCACTCAACTCAGCTGAGAGCTCAAGTTTCAAGGCGGCA 2459
QY 2332 TGGCCCGCGCCACACTCTTGCAGGAGAGCAAGACTTACGCTGCTGCGAGAGCCG 2391
Db 2460 TGGCCCGCGCCACACTCTTGCAGGAGAGCAAGACTTACGCTGCTGCGAGAGCCG 2519
QY 2392 GGGGTCACAGTGGGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2451
Db 2520 GGGGTCACAGTGGGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2579
QY 2452 GTGGGGCCCGGTGTGGCTTAACTAAATGTAAACCAAGCAGAGGTGACATGTGTCATCA 2511
Db 2580 GTGGGGCCCGGTGTGGCTTAACTAAATGTAAACCAAGCAGAGGTGACATGTGTCATCA 2639
QY 2512 GGAAGCGAGTGTGCTGACCGAGAGTGTCCCTTCAGGTGAAGCTGAGCTCAGGTGACATG 2571
Db 2640 GGAAGCGAGTGTGCTGACCGAGAGTGTCCCTTCAGGTGAAGCTGAGCTCAGGTGACATG 2699

QY 2572 CCGGCTCATCATCATCTAGGACCTGTGTCTGAAGGAGCCGTGGGTCAAGATCATTT 2631
Db 2700 CCGGCTCATCATCATCTAGGACCTGTGTCTGAAGGAGCCGTGGGTCAAGATCATTT 2759
QY 2632 CGTGTGCTCTTAATGGGTGCTGAGGCTGATCTCTCAGTGAATGAAGCCCGAGCGTGA 2691
Db 2760 CGTGTGCTCTTAATGGGTGCTGAGGCTGATCTCTCAGTGAATGAAGCCCGAGCGTGA 2819
QY 2692 AGCATTCATCTCTCTGAGGCGGACCTTGGGTGTGCTGAGACTCAACAGTCTTGAAG 2751
Db 2820 AGCATTCATCTCTCTGAGGCGGACCTTGGGTGTGCTGAGACTCAACAGTCTTGAAG 2879
QY 2752 GAGGTGAGGGGAAACTGTGTTTTTATCTTATACATGACGCGGGGCAAGAGCGCTGT 2811
Db 2880 GAGGTGAGGGGAAACTGTGTTTTTATCTTATACATGACGCGGGGCAAGAGCGCTGT 2939
QY 2812 CTTAAAGTTTCCATGGAATGTGTTTATTAATAATCTTAAGAGATGAATACCTTATCAGCT 2871
Db 2940 CTTAAAGTTTCCATGGAATGTGTTTATTAATAATCTTAAGAGATGAATACCTTATCAGCT 2999
QY 2872 GTTGCTTGAACCTGTGTTAAATGTTCATTAACATTTGATAGTCTTAATGATGG 2931
Db 3000 GTTGCTTGAACCTGTGTTAAATGTTCATTAACATTTGATAGTCTTAATGATGA 3059
QY 2932 CTAAGTATGGGGGTGGCTTTGAAACATGTGTTTATGCAACAGAAACGAATGTAGCA 2991
Db 3060 CTAAGTATGGGGGTGGCTTTGAAACATGTGTTTATGCAACAGAAACGAATGTAGCA 3119
QY 2992 GCCAGCTTTGGGGGCGTATGTGTGGCCAGCTCTTAAACATTCAGTCTATTAACCTTGGGT 3051
Db 3120 GCCAGCTTTGGGGGCGTATGTGTGGCCAGCTCTTAAACATTCAGTCTATTAACCTTGGGT 3179
QY 3052 GAGTCTTTGGGGAACAACAACAAGTGGCCCAATGATCTTACCTGCGCTTCTC 3111
Db 3180 GAGTCTTTGGGGAACAACAACAAGTGGCCCAATGATCTTACCTGCGCTTCTC 3239
QY 3112 GTTGCTTAAGATGTGTTTGGCAACTCTAGAGCCAGAGCCTTAAGATGATTAATAATCT 3171
Db 3240 GTTGCTTAAGATGTGTTTGGCAACTCTAGAGCCAGAGCCTTAAGATGATTAATAATCT 3239
QY 3172 CCCTTTGTAACTCAGTGTCTGGGACCTGAGCGAGCCCTCAGGTGCTGGAAGTCAAC 3231
Db 3300 CCCTTTGTAACTCAGTGTCTGGGACCTGAGCGAGCCCTCAGGTGCTGGAAGTCAAC 3359
QY 3232 AGTCTTTGGGGAAGAGTGTGAGAGAGAGTGTGTTTTTATCTTCAACGCAAGTATGAAGA 3291
Db 3360 AGTCTTTGGGGAAGAGTGTGAGAGAGAGTGTGTTTTTATCTTCAACGCAAGTATGAAGA 3419
QY 3292 TAAATTTACATAGTATTTACCTPAGACATPAGACATPAGTATGATGACAGTCTCAC 3351
Db 3420 TAAATTTACATAGTATTTACCTPAGACATPAGACATPAGTATGATGACAGTCTCAC 3479
QY 3352 CTGACCCCTTCCAGCTCTCAATTTTGTAGTATTTGGATTAAGGATATGTTTTGGG 3411
Db 3480 CTGACCCCTTCCAGCTCTCAATTTTGTAGTATTTGGATTAAGGATATGTTTTGGG 3539
QY 3412 GTATGGGGGAGTGTGTTCTGACCTGCTTGGAGAGCGGCTCCGACCTCGACAGTTTGG 3471
Db 3540 GTATGGGGGAGTGTGTTCTGACCTGCTTGGAGAGCGGCTCCGACCTCGACAGTTTGG 3599
QY 3472 GGTGTGGCCCAAGGCGGTTCTTGGATGTAAAGATGTGGCCATAGCTCCTGTAACCTC 3531
Db 3600 GGTGTGGCCCAAGGCGGTTCTTGGATGTAAAGATGTGGCCATAGCTCCTGTAACCTC 3659
QY 3532 ACTGTCACTGTGTCTTCCATAGGGTGTCTTGAATCTGTTATTTAAGATTAAGTTTGGC 3591
Db 3660 ACTGTCACTGTGTCTTCCATAGGGTGTCTTGAATCTGTTATTTAAGATTAAGTTTGGC 3719
QY 3592 AGAAGTGAACCTGTGTCGAACAACATGTACCGTGGCCGTGTATATGATGAATGATTT 3651
Db 3720 AGAAGTGAACCTGTGTCGAACAACATGTACCGTGGCCGTGTATATGATGAATGATTT 3779

Db	1081	GTGTCCTCGGAGGCTAAGGAGGCGCTTCGTGCCCCACCTTCGATACGATCAACGCTC	1140
Qy	1013	TCGAGCTTCTCTCAACAGCTGGACCTGTGAATTTCCAGGCTGTTCAGAGGCCCGGAGAG	1072
Db	1141	TCCGAGCTGTCTCAACAGCTGGACCTGTGAATTTCCAGGCTGTTCAGAGGCCCGGAGAG	1200
Qy	1073	CTCAGCCCGAGGCTCTCTTGAAGTCCAAAGCTGCCATGTCTCCGAGATGTGGAAAGGCTCTCG	1132
Db	1201	CTCAGCCCGAGGCTCTCTTGAAGTCCAAAGCTGCCATGTCTCCGAGATGTGGAAAGGCTCTCG	1260
Qy	1133	GGGGGTCTCTGGTGGAGCTCGGCTCTCTTCCAGAGGATCACTGTGCTGTCTCTTGAG	1192
Db	1261	GGGGGTCTCTGGTGGAGCTCGGCTCTCTTCCAGAGGATCACTGTGCTGTCTCTTGAG	1320
Qy	1193	CGGGAACCTTCAACCAAGGATCTGTGGTACCAACAGACGTTCAGAAAGAAAGCTTGTGGA	1252
Db	1321	CGGGAACCTTCAACCAAGGATCTGTGGGACACAC-ACACGTTCAGAAAGAAAGCTTGTGGA	1379
Qy	1253	TGCCATCTGTTC-GGAGACCAAGCAAACTGATGAAGTCTGTGACGCCGACGAGCTGTGA	1311
Db	1380	TGCCATCTGTTCGGGGGACACCAAGCAAACTGATGAAGTCTGTGACGCCGACGAGCTGTGA	1439
Qy	1312	CTTGGCACTGGACAACCGGTGCCAGGCTGTGCACTTGGCGGTGGAGGCGCGGGCAAGAGGA	1371
Db	1440	CTTGGCACTGGACAACCGGTGCCAGGCTGTGCACTTGGCGGTGGAGGCGCGGGCAAGAGGA	1499
Qy	1372	GTGCGCCAAAGTGGCTGTCTCAACAAATGSCAAACCCCAACTGAGCAACCTGAAAGGCTC	1431
Db	1500	GTGCGCCAAAGTGGCTGTCTCAACAAATGSCAAACCCCAACTGAGCAACCTGAAAGGCTC	1559
Qy	1432	CACCCCTTTGACATGCCCCGTGTGAGAGAGAGAGGATGCGGGGTGTCTGTAGACTTCCTGTGGC	1491
Db	1560	CACCCCTTTGACATGCCCCGTGTGAGAGAGAGAGGATGCGGGGTGTCTGTAGACTTCCTGTGGC	1619
Qy	1492	ACGGAAAGTCAATGTCCAAACGCCAAGATGAGAGACAGGTGTGACAGGCCCTCCACTTTGACAG	1551
Db	1620	GGGGAAGATCAATGTCCAAACGCCAAGATGAGAGACAGGTGTGACAGGCCCTCCACTTTGACAG	1679
Qy	1552	CCAGAAACGGGAGTGAATGTAGCAACACGGCTGTGTGTGGAAGAAACGCTCGGTCAACGA	1611
Db	1680	CCAGAAACGGGAGTGAATGTAGCAACACGGCTGTGTGTGGAAGAAACGCTCGGTCAACGA	1739
Qy	1612	GGTGAATTTTGAGGGCGGAGCGCCATGTGACGTGACCTGTGCAGACGSGGACAGAGATAT	1671
Db	1740	GGTGAATTTTGAGGGCGGAGCGCCATGTGACGTGACCTGTGCAGACGSGGAGGAATAT	1759
Qy	1672	CGTGGCATCTCTGTCTGTCCGCCAGAGGCTGTGACCTGTGACGGGCAAGATTCCTGGCT	1731
Db	1800	CGTGGCATCTCTGTCTGTCCGCCAGAGGCTGTGACCTGTGACGGGCAAGATTCCTGGCT	1859
Qy	1732	GGCATCTGCACTACGCTGTGGACAGGACCACTGTCCATCGTCAAGCTGTGTGACCAACGA	1791
Db	1860	GGCATCTGCACTACGCTGTGGACAGGACCACTGTCCATCGTCAAGCTGTGTGACCAACGA	1919
Qy	1792	GGCGGGGTGAATGTGGAACGCCACAGCGCTGTGATGGAGAGACGCCATTGTGACTTGTGCGC	1851
Db	1920	GGCGGGGTGAATGTGGAACGCCACAGCGCTGTGATGGAGAGACGCCATTGTGACTTGTGCGC	1979
Qy	1852	ACAGGCGGGGCACTACCGGTGTGGCGCCAGCGCTGTGATGGAGAGACGCCATTGTGACTTGTGCGC	1911
Db	1980	ACAGGCGGGGCACTACCGGTGTGGCGCCAGCTCTCATCGACCTGTGTCTCCAGCTTCAAAGT	2039
Qy	1912	CTGAGGCTGTGGGACAGACACCCCTGTGACGTGGCGCGAGGAGCGGGGACACAGAGAC	1971
Db	2040	CTGAGGCTGTGGGACAGACACCCCTGTGACGTGGCGCGAGGAGCGGGGACACAGAGAC	2099
Qy	1972	TGCACAGCTGTCTCTGTGATCGGAGGCGCTGTGGCAAGAGGCGCTGTGACTGTGACAGCGCTACAC	2031
Db	2100	TGCACAGCTGTCTCTGTGATCGGAGGCGCTGTGGCAAGAGGCGCTGTGACTGTGACAGCGCTACAC	2155
Qy	2032	CGCTCTGCACTTGTGCTCCCGCAACGAGACACTGTGCACCTGTCAAGCTGTCTGTGAGGA	2091
Db	2160	CGCTCTGCACTTGTGCTCCCGCAACGAGACACTGTGCACCTGTCAAGCTGTCTGTGAGGA	2219

QY	2092	GAAAGCCGATGTGCTGGCCCGGAGGACCCCTTGAAACCAAGCCGCTTGACACTCGCTGGCCG	2151
Db	2220	GAAAGCCGATGTGCTGGCCCGGAGGACCCCTTGAAACCAAGCCGCTTGACACTCGCTGGCCG	2279
QY	2152	CCAGCGGACCTCGAGAGGTGTGAGAGATTGGTCAGCGCCGATGTCAATTGACCTGTTGCA	2211
Db	2280	CCAACGGACCTCGAGAGGTGTGAGAGATTGGTCAGCGCCGATGTCAATTGACCTGTTGCA	2339
QY	2212	CGAGCAGGGGCTCAGCGCGCTGACACTGGCGCCGACAGGCGGAGCCGACACAGAGGTGGA	2271
Db	2340	CGAGCAGGGGCTCAGCGCGCTGACACTGGCGCCGACAGGCGGAGCCGACACAGAGGTGGA	2399
QY	2272	GACTCTGCTCAGGGATGGGGCCCACTAACCTSCAGAGCCTCAAGTITCCAGGCGGACCA	2331
Db	2400	GACTCTGCTCAGGGATGGGGCCCACTAACCTSCAGAGCCTCAAGTITCCAGGCGGACCA	2459
QY	2332	TGGCCCGCGCCACAACCTCTCTGGCGGAGACAGAACCTTACGTGGCTGCTGCGGAGACCG	2391
Db	2460	TGGCCCGCGCCACAACCTCTCTGGCGGAGACAGAACCTTACGTGGCTGCTGCGGAGACCG	2519
QY	2332	GGGGTCCACGTGGGGCTCTTGTCTCTGTCTGTGTCTCTGTGGGGAGTGGAAACGATCTCG	2451
Db	2520	GGGGTCCACGTGGGGCTCTTGTCTCTGTCTGTGTCTCTGTGGGGAGTGGAAACGATCTCG	2579
QY	2452	GTGGGGCCCCGTTGGGCTTACTCTTAATGTATTAACAAGACAGAGGTGACATGTCACATCA	2511
Db	2580	GTGGGGCCCCGTTGGGCTTACTCTTAATGTATTAACAAGACAGAGGTGACATGTCACATCA	2639
QY	2512	GAAGCGGCTGCTGTGTCAGCCGAGTGTCCCTCCAGATTGAAGCTGCTCAGGTGACATG	2571
Db	2640	GAAGCGGCTGCTGTGTCAGCCGAGTGTCCCTCCAGATTGAAGCTGCTCAGGTGACATG	2699
QY	2572	CCCGCTCATCATGATGATCTTAGGCAACCTGCTCTGGAAGGGAACCTGGGTCAGAATCATTT	2631
Db	2700	CCCGCTCATCATGATGATCTTAGGCAACCTGCTCTGGAAGGGAACCTGGGTCAGAATCATTT	2759
QY	2632	CGTTGTGCTCTTAATGGGTGCTGAGCTGGTCTCTCAGTATGAAGCCCGAGCGTGGAA	2691
Db	2760	CGTTGTGCTCTTAATGGGTGCTGAGCTGGTCTCTCAGTATGAAGCCCGAGCGTGGAA	2819
QY	2692	AGCATCCACTCTCCTCGAGGCGAGGCCACTTGGGGTTCGGAAGTCCACAGCTCTTGAGG	2751
Db	2820	AGCATCCACTCTCCTCGAGGCGAGGCCACTTGGGGTTCGGAAGTCCACAGCTCTTGAGG	2879
QY	2752	GAGGTGACGGGAAACTGTGTGTTTTTATCTTACATACATGACGGTGGCAGAGAGCCGT	2811
Db	2880	GAGGTGACGGGAAACTGTGTGTTTTTATCTTACATACATGACGGTGGCAGAGAGCCGT	2939
QY	2812	CTTAAAGTTTCCATGGAAATTGTTTTATTAATAATCTTAAGAGATGAATACCTTATCAGCT	2871
Db	2940	CTTAAAGTTTCCATGGAAATTGTTTTATTAATAATCTTAAGAGATGAATACCTTATCAGCT	2999
QY	2872	GTGTCCTTAAACCTGTTTAAATATGTTCAATCATGATGATGCTCAATTAATGATGG	2931
Db	3000	GTGTCCTTAAACCTGTTTAAATATGTTCAATCATGATGATGCTCAATTAATGATGA	3059
QY	2932	CTTAAGTAGTGGGGTGGCTTTGAAACAATGTTTTATGCAACAAGAACGAAATGGTAGCA	2991
Db	3060	CTTAAGTAGTGGGGTGGCTTTGAAACAATGTTTTATGCAACAAGAACGAAATGGTAGCA	3119
QY	2992	GCGAGCTTTGGGGGCGTATGTGTGGGCGACGCTTAAACATTTCCAGTCTAATTACTTGGGT	3051
Db	3120	GCGAGCTTTGGGGGCGTATGTGTGGGCGACGCTTAAACATTTCCAGTCTAATTACTTGGGT	3179
QY	3052	GAGTGCCTGTGGACAAACACACACACGTCGCCACATGTGATCTAGCTGCGCTTGGTTCTC	3111
Db	3180	GAGTGCCTGTGGACAAACACACACACGTCGCCACATGTGATCTAGCTGCGCTTGGTTCTC	3239
QY	3112	GTGTCCTAAGATGTTTTGGCACTCTTAGGCCACAGGCTCTAAGATCATTTAAAAATTCCT	3171
Db	3240	GTGTCCTAAGATGTTTTGGCACTCTTAGGCCACAGGCTCTAAGATCATTTAAAAATTCCT	3299

QY	3172	CCCTTTGTAACCTCAGTCTGTGGGACATGAGCGAGCCGCCCTCAGTGTGCTGGAGTGGAC	3321
Db	3300	CCCTTTGTAACCTCAGTCTGTGGGACATGAGCGAGCCGCCCTCAGTGTGCTGGAGTGGAC	3359
QY	3232	AGCTTGGGGAGAGAGGTGCAGAGAGAGCTGTGTGTTTTTATCTCCACAGCAGTATGAAGA	3291
Db	3360	AGCTTGGGGAGAGAGGTGCAGAGAGAGCTGTGTGTTTTTATCTCCACAGCAGTATGAAGA	3419
QY	3292	TAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGGTAGATGCACTGCTAC	3351
Db	3420	TAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGGTAGATGCACTGCTAC	3479
QY	3332	CTGCACACCTTCCAGCTCTCATATTTTGTAGATGATTTGGATAGAGGATAGTGTGTTGGG	3411
Db	3480	CTGCACACCTTCCAGCTCTCATATTTTGTAGATGATTTGGATAGAGGATAGTGTGTTGGG	3539
QY	3412	GTAATGGGGAGAGTGTGTTCTGACCTGCTTGGACAGTGTGCTCCGCACTCAGCAGTTGG	3471
Db	3540	GTAATGGGGAGAGTGTGTTCTGACCTGCTTGGACAGTGTGCTCCGCACTCAGCAGTTGG	3599
QY	3472	GGTGTGGCCCCAGGCGGTTCTTGGATGAAAAGATGTGGCCATCTAGCCTCGTAACCTC	3531
Db	3600	GGTGTGGCCCCAGGCGGTTCTTGGATGAAAAGATGTGGCCATCTAGCCTCGTAACCTC	3659
QY	3532	ACTGTCACTGTGTCTCCATAGGGTGCCTTCTGAAATCTGTATTAGATTAAGATTGTGTC	3591
Db	3660	ACTGTCACTGTGTCTCCATAGGGTGCCTTCTGAAATCTGTATTAGATTAAGATTGTGTC	3719
QY	3592	AGAAAGTAAACCTGTGGTGAACATATGACCGTGGCTGTGATATGATGAGATTGATAT	3651
Db	3720	AGAAAGTAAACCTGTGGTGAACATATGACCGTGGCTGTGATATGATGAGATTGATAT	3779
QY	3652	AATGTACATGTATGTATGTGAATCTGTGGGACAGATACTTTTCCATGGCAGGAATA	3711
Db	3780	AATGTACATGTATGTATGTGAATCTGTGGGACAGATACTTTTCCATGGCAGGAATA	3839
QY	3712	TCCAACTGTGTAACCTGGCTATGTGTTTAATATATGCTCTATGTGCTTTACTGTGTGTG	3771
Db	3840	TCCAACTGTGTAACCTGGCTATGTGTTTAATATATGCTCTATGTGCTTTACTGTGTGTG	3899
QY	3772	GACTGCGTGAAGGACAGAAAGTTCCATTGTGATGTCAATTAAGCAAGTACTTGCTACTT	3831
Db	3900	GACTGCGTGAAGGACAGAAAGTTCCATTGTGATGTCAATTAAGCAAGTACTTGCTACTT	3959
QY	3832	TTTTGAACTGAAAAAATAAATAA 3853	
Db	3960	TTTTGAACTGAAAAAATAAATAA 3981	
RESULT 8			
ADR24463			
ID	ADR24463	strand; DNA; 2691 BP.	
AC	ADR24463;		
XX	21-OCT-2004	(first entry)	
DT	Breast cancer prognosis marker #324.		
XX			
XX	de; breast cancer; prognosis; gene expression; diagnosis.		
KW			
OS	Homo sapiens.		
XX			
PN	WO2004065545-A2.		
PD	05-AUG-2004.		
XX			
PF	15-JAN-2004; 2004WO-US001100.		
XX			
PR	15-JAN-2003; 2003US-00342887.		
XX			
PA	(ROSE-) ROSETTA INPHARMATICS LLC.		
PA	(NECA-) NETHERLANDS CANCER INST.		

Pt	Van't Veer LJ, He Y;
Dl	wpi; 2004-593473/57.
Cd	Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
Ps	Disclosure; SEQ ID NO 324; 226pp; English.
Xx	The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
Sq	Sequence 2691 BP; 593 A; 707 C; 798 G; 593 T; 0 U; 0 Other;
Qy	Query Match 67.5%; Score 2606.4; DB 13; Length 2691; Best Local Similarity 99.5%; Pred. No. 0; Matches 2635; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
Oy	1211 GATCTGGGTACCAAGACGTCGCAGAAGAAAGACTTGTGGATGCCATCGTGCC-GGGA 1269 Db 36 GATCGGGTTACCAC-AAGCGTCCAGAAGAAAGAACCTTGTGGATTCCATCGTCCGGGA 94
Oy	1270 CACCAAGCAACTGATGAAGATCTTCAGCCGCGAGAGCTGGACTTGCACTGACAACCG 1329
Db	95 CACCAAGCAACTGATGAAGATCTTCAGCCGCGAGAGCTGGACTTGCACTGACAACCG 154
Oy	1330 TGCCAGCCTGTGCACTCGGCGGCGTAGAGGCCGCGCAAGAGAGTCGCAAGTGGCTGCT 1389
Db	155 TGCACGCTGTGTGCACTCGGCGGCGTAGAGGCCGCGCAAGAGAGTCGCAAGTGGCTGCT 214
Oy	1390 GCTCAACCATGCTCCAACCCCAACTGAGCAACCTGAGGGGCTCCAACCCGTTGCAATGAC 1449
Db	215 GCTCAACCATGCTCCAACCCCAACTGAGCAACCTGAGGGGCTCCAACCCGTTGCAATGAC 274
Oy	1450 CGTGGAGAAGAGGGTCGGGGTGTCTGTGAAGCTCTCTGTGCAAGAGATCAAGTTCAA 1509
Db	275 CGTGGAGAAGAGGGTCGGGGTGTCTGTGAAGCTCTCTGTGCAAGAGATCAAGTTCAA 334
Oy	1510 GGCCAGAATGAGGACCAAGTAGAGACAGCCCTTCACTTTGAGGCCAGAAACGGGGATGAGTC 1569
Db	335 GGCCAGAATGAGGACCAAGTAGAGACAGCCCTTCACTTTGAGGCCAGAAACGGGGATGAGTC 394
Oy	1570 TAGCACACGGCTGCTGTGAGAAGAAACGCTCGATCAACGAGGTGCACTTTGAGGGCCG 1629
Db	395 TAGCACACGGCTGCTGTGAGAAGAAACGCTCGATCAACGAGGTGCACTTTGAGGGCCG 454
Oy	1630 GACGCCCATGCACTGTGGCTTGCGCAACAAGGAGAGAAATATGTCGCGCATCTGCTTGC 1689
Db	455 GACGCCCATGCACTGTGGCTTGCGCAACAAGGAGAGAAATATGTCGCGCATCTGCTTGC 514
Oy	1690 CTGAGGGCTGGACTGTAGAGCTTCAGAGGGGAGAAAGATGCTTGGGCTGCACTGCACTTAAGCTGC 1749
Db	515 CTGAGGGCTGGACTGTAGAGCTTCAGAGGGGAGAAAGATGCTTGGGCTGCACTGCACTTAAGCTGC 574
Oy	1750 CTGGAGAGGCCAATCGGCCCATCGTCAAGCTCTGAGCAAGCAGCGCGGGGGTGAATGTAAA 1809
Db	575 CTGGAGAGGCCAATCGGCCCATCGTCAAGCTCTGAGCAAGCAGCGCGGGGGTGAATGTAAA 634
Oy	1810 CGCCCAAGACGCTGATGAGAGAGACGCCATTGCACTTGGCCGCAAGCGCGGAGCACTAACG 1869
Db	635 CGCCCAAGACGCTGATGAGAGAGACGCCATTGCACTTGGCCGCAAGCGCGGAGCACTAACG 694
Oy	1870 CGTGCCCCGACCTCTCATGACCTGTGTCCGAGGTCAACGCTTCGCAAGCTGTCTGCGACA 1929

Db 695 |CGTGCCCGGCATCTCCATCGACTGTGCTCCGACCTCAACGCTGCGACCGCTGCTGGCACA 754
Qy 1930 |GACACCCCTGCACTGTGGCCGCGGAGACGCGGCAACGAGCACTGCGAGGCTGCTCTGCA 1989
Db 755 |GACACCCCTGCACTGTGGCCGCGGAGACGCGGCAACGAGCACTGCGAGGCTGCTCTGCA 814
Qy 1990 |TCGGGGCCCTGGCAAGGAGGCGCTGACCTCGACGCGCTACACCGCTCTGCGACTGGGCGC 2049
Db 815 |TCGGGGCCCTGGCAAGGAGGCGCTGACCTCGACGCGCTACACCGCTCTGCGACTGGGCGC 874
Qy 2050 |CCGCAACGGAACACTGGCCACTGTCAAGCTGCTTCGAGAGAGAGCCGATGTCGTCGAC 2109
Db 875 |CCGCAACGGAACACTGGCCACTGTCAAGCTGCTTCGAGAGAGAGCCGATGTCGTCGAC 934
Qy 2110 |CCGGGGACCCCTGAAACGAGCGGCGCTGCACTGGCTGCGCCACGCGGCACTCGAGAGT 2169
Db 935 |CCGGGGACCCCTGAAACGAGCGGCGCTGCACTGGCTGCGCCACGCGGCACTCGAGAGT 994
Qy 2170 |GATGAGAGATTTGGTCAAGCCGAGATGTGATTCGCTGTCGACGAGAGGGGCTCAGGGC 2229
Db 995 |GATGAGAGATTTGGTCAAGCCGAGATGTGATTCGCTGTCGACGAGAGGGGCTCAGGGC 1054
Qy 2230 |GCTGCACTGGCCGCGCCAGGGCCGCGACGACAGACGCGTGAAGACTCTGCTCAGGCACTG 2289
Db 1055 |GCTGCACTGGCCGCGCCAGGGCCGCGACGACAGACGCGTGAAGACTCTGCTCAGGCACTG 1114
Qy 2290 |GGCCCAATCAAACCTGCAAGAGCTCTCAAGTTCAGGGGCGCCATGGCCCCCGCGCAACT 2349
Db 1115 |GGCCCAATCAAACCTGCAAGAGCTCTCAAGTTCAGGGGCGCCATGGCCCCCGCGCAACT 1174
Qy 2350 |CCTGGGGAGAGACCAAGACTGCTGCTGCGCGAGAGACGCGGGGCTCAGTGGGGCTC 2409
Db 1175 |CCTGGGGAGAGACCAAGACTGCTGCTGCGCGAGAGACGCGGGGCTCAGTGGGGCTC 1234
Qy 2410 |TTGTCCTGCTCTGTCTCTCGTGGGAGATGAAACGATCCTGCGTGGGGCCCCGTTGTGAC 2469
Db 1235 |TTGTCCTGCTCTGTCTCTCGTGGGAGATGAAACGATCCTGCGTGGGGCCCCGTTGTGAC 1294
Qy 2470 |TTACTTAATGTTAAACCAAGCAGAGGTGACATGTGGCATCAGAGGCGGCTGCTGCTGA 2529
Db 1295 |TTACTTAATGTTAAACCAAGCAGAGGTGACATGTGGCATCAGAGGCGGCTGCTGCTGA 1354
Qy 2530 |CCGAGATGCCCCCTCAAGGTGAAGCTGCTCAGGTGACATGCGGCTCCATCATCGATC 2589
Db 1355 |CCGAGATGCCCCCTCAAGGTGAAGCTGCTCAGGTGACATGCGGCTCCATCATCGATC 1414
Qy 2590 |TAGGCACTGCTGTCTGAAGGAGCGTGGGTCAGAATCATTTCTGTTGCTCTTAATGGG 2649
Db 1415 |TAGGCACTGCTGTCTGAAGGAGCGTGGGTCAGAATCATTTCTGTTGCTCTTAATGGG 1474
Qy 2650 |TCGCTGAGGCTGGTCTCTCAAGTGAAGACCCCAAGGCTGGAAAGCATCTCTCTCTG 2709
Db 1475 |TCGCTGAGGCTGGTCTCTCAAGTGAAGACCCCAAGGCTGGAAAGCATCTCTCTCTG 1534
Qy 2710 |AGGCAAGCACTTGGGTTGCTGAGGCTGACAGCTTGAAGGAGGTGACGGGAAACTG 2769
Db 1535 |AGGCAAGCACTTGGGTTGCTGAGGCTGACAGCTTGAAGGAGGTGACGGGAAACTG 1594
Qy 2770 |TGTGTTTATCTTCAATACATGACGCTGGGCAAGAGGCGCTGTCTTAAAGTTTCATGGA 2829
Db 1595 |TGTGTTTATCTTCAATACATGACGCTGGGCAAGAGGCGCTGTCTTAAAGTTTCATGGA 1654
Qy 2830 |TTGTTTATTAATAATCTTAAAGATGAATACCTTATCAGCTGTTGCTTGAACCTGTTA 2889
Db 1655 |TTGTTTATTAATAATCTTAAAGATGAATACCTTATCAGCTGTTGCTTGAACCTGTTA 1714
Qy 2890 |AAAAATTCATTAACATGGAATGTCTAGCTCTTAAATGAATGATGCTGAGTGGGCTGGC 2949
Db 1715 |AAAAATTCATTAACATGGAATGTCTAGCTCTTAAATGAATGATGCTGAGTGGGCTGGC 1774
Qy 2950 |TTTGAATAATGTTTATGCAACAGAAAGAAATGTGACGACGCTTTGCGGGCGCT 3009

Db 1775 |TTTGAATAATGTTTATGCAACAGAAAGAAATGTGATGACGACGACCTTTGCGGGCGCT 1834
Qy 3010 |ATGTGTGGCCAGCTCTTAACATTCAGTCTAATTAATTTGGGTGAGTCTGTGGAACCC 3069
Db 1835 |ATGTGTGGCCAGCTCTTAACATTCAGTCTAATTAATTTGGGTGAGTCTGTGGAACCC 1894
Qy 3070 |ACACACAGTGGCCACATGGAATGATGCTGCGGTTGCTGTTGCTGTTGCTGTTGTTG 3129
Db 1895 |ACACACAGTGGCCACATGGAATGATGCTGCGGTTGCTGTTGCTGTTGCTGTTGTTG 1954
Qy 3130 |GCAACTGTAGGCAACAGCCCTAAGATCAATTAATAAATTCCTCTTTGTAACCTCAGTG 3189
Db 1955 |GCAACTGTAGGCAACAGCCCTAAGATCAATTAATAAATTCCTCTTTGTAACCTCAGTG 2014
Qy 3190 |CTGGGAGCTAGAGGAGACCCCTCAGGTCGTGAGAGGACACAGTCTGGGGAAAGAGTG 3249
Db 2015 |CTGGGAGCTAGAGGAGACCCCTCAGGTCGTGAGAGGACACAGTCTGGGGAAAGAGTG 2074
Qy 3250 |CAGGAGAACTGTGTTTATCTCCACAGCAGATGAGATTAATAATTAATTAATTAATTA 3309
Db 2075 |CAGGAGAACTGTGTTTATCTCCACAGCAGATGAGATTAATAATTAATTAATTAATTA 2134
Qy 3310 |CTTAGACATAGACAGATTAATCTTAGTAGATGACCTGCTCAGCTGCACTCTCCAGCTC 3369
Db 2135 |CTTAGACATAGACAGATTAATCTTAGTAGATGACCTGCTCAGCTGCACTCTCCAGCTC 2194
Qy 3370 |TCATTTTGTGTAAGGTGATTTGGGATAGGATAGTCTTTGGGGATAGGGGGAGTGTTC 3429
Db 2195 |TCATTTTGTGTAAGGTGATTTGGGATAGGATAGTCTTTGGGGATAGGGGGAGTGTTC 2254
Qy 3430 |TGACCTGCTTGGCAGAGGTCCTCCGACCTCAGCAGTGTGGGGTGTGGCCCGAGGGCG 3489
Db 2255 |TGACCTGCTTGGCAGAGGTCCTCCGACCTCAGCAGTGTGGGGTGTGGCCCGAGGGCG 2314
Qy 3490 |TTCTTGAATGTAATAAGATGTGGCATGTAGCTTGCTGTAACCTTCACTGTCACCTGTGCCA 3549
Db 2315 |TTCTTGAATGTAATAAGATGTGGCATGTAGCTTGCTGTAACCTTCACTGTCACCTGTGCCA 2374
Qy 3550 |TAGGTCCTCTTGAATAATGTTAATTAATTAATTAATTTGGTGAAGAGTGAACCTGGGTG 3609
Db 2375 |TAGGTCCTCTTGAATAATGTTAATTAATTAATTAATTTGGTGAAGAGTGAACCTGGGTG 2434
Qy 3610 |CAAAATGATCCGTCGCTGCTGATATGATGATGATGATGATGATTAATTAATTAATTAAT 3669
Db 2435 |CAAAATGATCCGTCGCTGCTGATATGATGATGATGATGATGATTAATTAATTAATTAAT 2494
Qy 3670 |ATGTGAATCTGTGGGCAAGGATACCTTTTCATGCGACAGAAATATCCAAAGCTGTGAAC 3729
Db 2495 |ATGTGAATCTGTGGGCAAGGATACCTTTTCATGCGACAGAAATATCCAAAGCTGTGAAC 2554
Qy 3730 |GCTAATGTTTAAATATGCTCATGTCCTTAATGTTGCTGAGCTGGGAGGAGCAAG 3789
Db 2555 |GCTAATGTTTAAATATGCTCATGTCCTTAATGTTGCTGAGCTGGGAGGAGCAAG 2614
Qy 3790 |AAGTTCATTTGATGTCATTAACAAAGTACTTTTGAANCTGAANCTGAANCTGAANCT 3849
Db 2615 |AAGTTCATTTGATGTCATTAACAAAGTACTTTTGAANCTGAANCTGAANCTGAANCT 2674
Qy 3850 |AAAAAAAA 3858
Db 2675 |AAAAAAAA 2683

RESULT 9
ADE29194
ID ADE29194 standard; DNA; 2355 BP.
XX
AC ADE29194;
XX
XX 29-JAN-2004 (first entry)
DT
XX
DE Human novel protein kinase 14171 gene coding sequence Seg103.
XX

KW kinase protein 14171; cell growth; cell division; gene therapy;
KW cell differentiation; cellular metabolic pathway; cell metabolism;
KW viral infection; hepatitis B; cellular growth related disorder;
KW heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy;
KW idiopathic cardiomyopathy; angina; differentiative disorder;
KW proliferative disorder; cancer; liver cancer; melanoma cancer;
KW prostate cancer; cervical cancer; breast cancer; colon cancer; sarcoma;
KW programmed cell death; Alzheimer's disease; Parkinson's disease;
KW epilepsy; autoimmune disorder; systemic lupus erythematosus; human; gene;
de.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..2355

FT /tag= a

FT /product= "Human protein kinase"

US6630335-B1.

PD 07-OCT-2003.

XX 12-FEB-2001; 2001US-00781882.

XX 11-FEB-2000; 2000US-0182096P.

XX (MILL-) MILLENNIUM PHARM INC.

PI Kapeller-Libermann R;

DR WPI; 2003-810551/76.

XX P-PSDB; ADE29193.

XX New 14171 human protein kinase and nucleic acids encoding the protein,
PT useful for treating viral infections, cellular growth related disorders,
PT cancers, disorders related with programmed cell death, or autoimmune
PT disorders.

PT Claim 1; SEQ ID NO 3; 50pp; English.

XX This invention relates to a novel isolated nucleic acid sequence and the
XX novel kinase protein encoded by it. Protein kinases play critical roles
XX in the regulation of biochemical and morphological changes associated
XX with cellular growth and division. The sequences of the invention may be
XX useful for gene therapy. The protein kinase or the nucleic acid encoding
XX the protein is useful for modulating cellular growth, differentiation
XX and/or development, and for modulating cellular metabolic pathways,
XX particularly for regulating one or more proteins involved in growth and
XX metabolism. The invention may also be useful for development of
XX therapeutics for the treatment of viral infections (for example hepatitis
XX B), cellular growth related disorders (for example heart failure,
XX hypertension, atrial fibrillation, dilated and idiopathic cardiomyopathy
XX or angina), proliferative or differentiative disorders such as cancer
XX (for example liver, melanoma, prostate, cervical, breast, colon or
XX sarcoma), disorders related with programmed cell death (for example
XX Alzheimer's disease, Parkinson's disease or epilepsy), or autoimmune
XX disorders (for example systemic lupus erythematosus). The present
XX sequence is the novel human kinase protein 14171 gene coding sequence of
XX the invention.

SQ Sequence 2355 BP; 464 A; 738 C; 759 G; 394 T; 0 U; 0 Other;

Query Match 61.0%; Score 2355; DB 10; Length 2355;

Best local similarity 100.0%; Pred. No. 0;

Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGGCGGACGCGGACCCCATGCGCTGCTGCGCACCTTCGACGCGGCG 76
DB 1 ATGAGGCGGACGCGGACCCCATGCGCTGCTGCGCACCTTCGACGCGGCG 60
QY 77 GAGTTTCACGCGGCGGAGAGTGGGCTCGGCGCGGCTTCGCGGCGAGGTACAAGGTGCGC 136
DB 61 GAGTTTCACGCGGCGGAGAGTGGGCTCGGCGCGGCTTCGCGGCGAGGTACAAGGTGCGC 120

QY 137 CATGTCCATGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCCTGCACTGACGAC 196
DB 121 CATGTCCATGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCCTGCACTGACGAC 180
QY 197 AGGAGCGCATGAGCTTTTGAAGAAAGCCAAAGATGAGATGGCCAAAGTTGCGTAC 256
DB 181 AGGAGCGCATGAGCTTTTGAAGAAAGCCAAAGATGAGATGGCCAAAGTTGCGTAC 240
QY 257 ATCTGCTCTGTATGAGATCTGCGCGGAACCTGTCGCGCTGTGATGAGTACATGAG 316
DB 241 ATCTGCTCTGTATGAGATCTGCGCGGAACCTGTCGCGCTGTGATGAGTACATGAG 300
QY 317 ACGGCTCTCCGGAAGACCTGCTGAGCTTCGAGCATTCGATGGATCTCCGTTCCGA 376
DB 301 ACGGCTCTCCGGAAGACCTGCTGAGCTTCGAGCATTCGATGGATCTCCGTTCCGA 360
QY 377 ATCATCCAGAGACGGCGGTGGGATGAACCTTCTGCACTGCAATGCGCCCGCACTCTG 436
DB 361 ATCATCCAGAGACGGCGGTGGGATGAACCTTCTGCACTGCAATGCGCCCGCACTCTG 420
QY 437 CACTGGAACCTGAGCCCGGCAATCTGCTGATGCGCCCTACAGATGAGTTCT 496
DB 421 CACTGGAACCTGAGCCCGGCAATCTGCTGATGCGCCCTACAGATGAGTTCT 480
QY 457 GATTTTGTGTCGCGCAAGTGCACGGGCTGCCACTGCGATGACCTGAGATGAGC 556
DB 481 GATTTTGTGTCGCGCAAGTGCACGGGCTGCCACTGCGATGACCTGAGATGAGC 540
QY 557 CTGTTTGGCAACATGCTTACTCTCCCTCAGAGCGCATCAAGGAGAAAGCGGCTTTC 616
DB 541 CTGTTTGGCAACATGCTTACTCTCCCTCAGAGCGCATCAAGGAGAAAGCGGCTTTC 600
QY 617 GACACCAAGCATGATGATACGCTTTGCGATCTGATCTGGGGCTGCTCACAAGAG 676
DB 601 GACACCAAGCATGATGATACGCTTTGCGATCTGATCTGGGGCTGCTCACAAGAG 660
QY 677 AAGCGTTTGGAGAGAGAAACATCTGCAATCATGATGATGATGATGATGATGATGAT 736
DB 661 AAGCGTTTGGAGAGAGAAACATCTGCAATCATGATGATGATGATGATGATGATGAT 720
QY 737 CGCCCGGAGCTGCGCGCGGTGTCAGAGCCCGCGCGGCTGCAACCTGATATGCG 796
DB 721 CGCCCGGAGCTGCGCGCGGTGTCAGAGCCCGCGCGGCTGCAACCTGATATGCG 780
QY 797 CTCATGACGCGGTGTCGAGGGGATTCGCGATGATGAGCCCACTTCCAAAGAAATTACT 856
DB 781 CTCATGACGCGGTGTCGAGGGGATTCGCGATGATGAGCCCACTTCCAAAGAAATTACT 840
QY 857 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAACTGCTATGAT 916
DB 841 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAACTGCTATGAT 900
QY 917 CTGAGCGTGAAGAAAGCCCGCGAGCCAGAGCGAGTGTGCTGCGAGGCTCAAGCGG 976
DB 901 CTGAGCGTGAAGAAAGCCCGCGAGCCAGAGCGAGTGTGCTGCGAGGCTCAAGCGG 960
QY 977 GCGTTCGCCCCACCTTGATTAACGATACAGCTCTTCCGAGCTTCTCAACGCTGAGC 1036
DB 961 GCGTTCGCCCCACCTTGATTAACGATACAGCTCTTCCGAGCTTCTCAACGCTGAGC 1020
QY 1037 TCTGAGTTTCCCAAGCTGTGAGAGGCCCCGAGAGCTGACGCGGACCTCTGAGTGC 1096
DB 1021 TCTGAGTTTCCCAAGCTGTGAGAGGCCCCGAGAGCTGACGCGGACCTCTGAGTGC 1080
QY 1097 AAGCTGCAATGTCGCGGAGTGGGAAGAGCTCTCGGAGGATGCTCGGTGAGCTTCGCGC 1156
DB 1081 AAGCTGCAATGTCGCGGAGTGGGAAGAGCTCTCGGAGGATGCTCGGTGAGCTTCGCGC 1140
QY 1157 TTCTCTTCAGAGAGATCACTGTGCTGCTCTTTAGCGGAACTTCAACAGCATCTG 1216
DB 1141 TTCTCTTCAGAGAGATCACTGTGCTGCTCTTTAGCGGAACTTCAACAGCATCTG 1200


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QY 1217 GGTACCAAGACGTCAGAAAGAGAGCTTGTGGATGTCATCGTCTCCGGGACACCGC 1276
DB 1201 GGTACCAAGACGTCAGAAAGAGAGCTTGTGGATGTCATCGTCTCCGGGACACCGC 1260
QY 1277 AAACGTATGAAGATCTGCAAGCCGCGAGGACGTGACCTTGACCTGGACAGCGGTGCCAGC 1336
DB 1261 AAACGTATGAAGATCTGCAAGCCGCGAGGACGTGACCTTGACCTGGACAGCGGTGCCAGC 1320
QY 1337 CTGCTGACCTTGCGCGGTGAGAGCCCGGCGCAAGAGAGTGGCCCAATGGCTGTCTCAAC 1396
DB 1321 CTGCTGACCTTGCGCGGTGAGAGCCCGGCGCAAGAGAGTGGCCCAATGGCTGTCTCAAC 1380
QY 1397 AATGCCAACCCCACTTGACCAACCGTAAAGGGCTCCACCCGTTGCATAGGCGGTGAG 1456
DB 1381 AATGCCAACCCCACTTGACCAACCGTAAAGGGCTCCACCCGTTGCATAGGCGGTGAG 1440
QY 1457 AGGAGGAGTGGCGGAGTGTGCTGAGAGCTCTGCTGACCGAAGATGATGTCACCGCAAG 1516
DB 1441 AGGAGGAGTGGCGGAGTGTGCTGAGAGCTCTGCTGACCGAAGATGATGTCACCGCAAG 1500
QY 1517 GATGAGACCAAGTGAACAGCCCTCCACTTTGACGCCAGAAAGGGGATGAGTCTTGACCA 1576
DB 1501 GATGAGACCAAGTGAACAGCCCTCCACTTTGACGCCAGAAAGGGGATGAGTCTTGACCA 1560
QY 1577 CGGCTGCTGTTGAGAGAAAGACGCTCGGTCAACGAGGTGACCTTTGAGGGCCGAGCGCC 1636
DB 1561 CGGCTGCTGTTGAGAGAAAGACGCTCGGTCAACGAGGTGACCTTTGAGGGCCGAGCGCC 1620
QY 1637 ATGCAAGTGGCTCTGCAAGACCGGAGAGAAATATGTGCGCATCTGCTGCGCGAGGC 1696
DB 1621 ATGCAAGTGGCTCTGCAAGACCGGAGAGAAATATGTGCGCATCTGCTGCGCGAGGC 1680
QY 1697 GTGAGACGTGAGCGCTGCAAGAGAGATGCTGCGCACTGACCTAGCGTGCCTGGAG 1756
DB 1681 GTGAGACGTGAGCGCTGCAAGAGAGATGCTGCGCACTGACCTAGCGTGCCTGGAG 1740
QY 1757 GGCACACCTGCCCATGCTCAAGCTGTGCGCAAGACCGGAGGTGAGTGAACCGCCAG 1816
DB 1741 GGCACACCTGCCCATGCTCAAGCTGTGCGCAAGACCGGAGGTGAGTGAACCGCCAG 1800
QY 1817 AGCTGATGAGAGAGACGCTATGCACTGTGCGCAAGCGGAGGCACTACCGCGTGGCC 1876
DB 1801 AGCTGATGAGAGAGACGCTATGCACTGTGCGCAAGCGGAGGCACTACCGCGTGGCC 1860
QY 1877 CGCATCTTATGACCTGTGCTCCGACCTGCAACGCTGTGAGAGCTGTGCAACAGACCC 1936
DB 1861 CGCATCTTATGACCTGTGCTCCGACCTGCAACGCTGTGAGAGCTGTGCAACAGACCC 1920
QY 1937 CTGCAAGTGGCGCGGAGACGAGGACCAAGACCTGCAAGGCTGCTCTGATCGAGGC 1996
DB 1921 CTGCAAGTGGCGCGGAGACGAGGACCAAGACCTGCAAGGCTGCTCTGATCGAGGC 1980
QY 1997 GCTGGCAAGAGAGCGGTGACCTCAAGCGGCTACACCGCTTGCACCTGGCTCCCGCAAC 2056
DB 1981 GCTGGCAAGAGAGCGGTGACCTCAAGCGGCTTCAACCGGCTTGCACCTGGCTCCCGCAAC 2040
QY 2057 GGAACACCTGCCCATGCTCAAGCTGTGCGAGAGAGAGCGAGTGTGCGCCCGGAG 2116
DB 2041 GGAACACCTGCCCATGCTCAAGCTGTGCGAGAGAGAGCGAGTGTGCGCCCGGAG 2100
QY 2117 CCCCTGAACCAAGCGGCGCTGACCTGCTGCGCCCAAGGACCTCGAGGTGAGTGAAG 2176
DB 2101 CCCCTGAACCAAGCGGCGCTGACCTGCTGCGCCCAAGGACCTCGAGGTGAGTGAAG 2160
QY 2177 GAGTGGTCAAGCGCGCATGTCATTTGACCTGTTGACGAGACGAGGAGCTCAGCGCTGAC 2236
DB 2161 GAGTGGTCAAGCGCGCATGTCATTTGACCTGTTGACGAGACGAGGAGCTCAGCGCTGAC 2220
QY 2237 CTGCGCGCCCAAGGCGCGGACGAGACGAGAGTGGAGACCTCTGACGAGATGGGCGCAC 2296
DB 2221 CTGCGCGCCCAAGGCGCGGACGAGACGAGAGTGGAGACCTCTGACGAGATGGGCGCAC 2280
QY 2297 ATCAACCTGCAAGAGCTCAAGTTCAAGGCGGCGCATGGCCCGCGCACACTCTCTGCGG 2356
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DB 2281 ATCAACCTGCAAGAGCTCAAGTTCCAGAGGCGGCGCATGAGCCCGCGCACACTCTCGG 2340
QY 2357 CGAAGCAAGACCTTG 2371
DB 2341 CGAAGCAAGACCTTG 2355

RESULT 10
ADL67199
ID ADL67199 standard; DNA; 2355 BP.
XX
AC ADL67199;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human 14171 protein kinase coding region.
XX
KW Human; 14171 protein kinase; cancer; immunological disorder;
KW inflammation; heart failure; hypertension; atrial fibrillation;
KW viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
KW predictive medicine; forensic biology; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 1..2355
FT CDS /*tag=a
FT /product="Human 14171 protein kinase"
FT
PN US2004048305-A1.
XX
PD 11-MAR-2004.
XX
PF 10-SEP-2003; 2003US-00658904.
XX
PR 11-FEB-2000; 2000US-0182096P.
XX
PR 12-FEB-2001; 2001US-00781882.
XX
PA (MILL-) MILLENNium PHARM INC.
XX
PI Kapeller-Libermann R;
XX
DR MPI; 2004-226195/21.
XX
DR P-PSDB; ADL67198.
XX
PT New 14171 protein kinase and nucleic acid, useful for diagnosing or
PT treating diseases with aberrant expression of the 14171 protein kinase,
PT such as cancer, an immunological disorder, inflammation, heart failure
PT and hypertension.
XX
PS Claim 1; SEQ ID NO 3; 62pp; English.
XX
CC The invention provides novel human 14171 protein kinase polypeptides and
CC polynucleotides. The methods and compositions of the present invention
CC are useful for the diagnosis and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of a 14171 protein kinase
CC such as cancer, immunological disorder, inflammation, heart failure,
CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.
CC The invention can also be used in chromosome mapping, tissue typing,
CC predictive medicine, forensic biology and prognostic assays. The present
CC sequence is human 14171 protein kinase coding region.
XX
SQ Sequence 2355 BP; 464 A; 738 C; 759 G; 394 T; 0 U; 0 Other;

Query Match 61.0%; Score 2355; DB 12; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGGGCGAGCGGCGGACCCCATGGGCGCTGGCGCTGCGCACTTGACGCGGCGC 76
DB 1 ATGAGGGCGAGCGGCGGACCCCATGGGCGCTGGCGCTGCGCACTTGACGCGGCGC 60
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QY	77	GAGTTCA	CGGCGTGGAGAAAGATGGGCTTCGGGCGGCTTTCGGGCGAGGTGTA	CAAGATGCC	136
Db	61	GAGTTCA	CGGCGTGGAGAAAGATGGGCTTCGGGCGGCTTTCGGGCGAGGTGTA	CAAGATGCC	120
QY	137	CATGTCCA	CTGGAAAGACCTGGCTGGCCATCAAGGTCTCGCCAGCTGGACGTGACGAC	196	
Db	121	CATGTCCA	CTGGAAAGACCTGGCTGGCCATCAAGGTCTCGCCAGCTGGACGTGACGAC	180	
QY	197	AGGAGCGCA	TGAGAGCTTTTGGAAAGACCAGAAGATGAGATGGCCAAATTTCGTAC	256	
Db	181	AGGAGCGCA	TGAGAGCTTTTGGAAAGACCAGAAGATGAGATGGCCAAATTTCGTAC	240	
QY	257	ATCTCGCT	GTGTATGGCATCTGCCGGAACCTGTCCGCTGTGTATGAGTACATGGAG	316	
Db	241	ATCTCGCT	GTGTATGGCATCTGCCGGAACCTGTCCGCTGTGTATGAGTACATGGAG	300	
QY	317	ACGGGCTCC	TGGAAAGATGTGCTTGAGGCATTGGCCATGGGAATCTCCGGTTCCGA	376	
Db	301	ACGGGCTCC	TGGAAAGATGTGCTTGAGGCATTGGCCATGGGAATCTCCGGTTCCGA	360	
QY	377	ATCATCCACA	GAGACGGCGGTGGGCACTGACCTTCCGCACTGCAATGGCCCGCCACTCCTG	436	
Db	361	ATCATCCACA	GAGACGGCGGTGGGCACTGACCTTCCGCACTGCAATGGCCCGCCACTCCTG	420	
QY	437	CACCTGGA	ACTTCAGCCCGCGCAACATCTCTGTGATGCCCATACAGTCACAGATTTCT	496	
Db	421	CACCTGGA	ACTTCAGCCCGCGCAACATCTCTGTGATGCCCATACAGTCACAGATTTCT	480	
QY	497	GATTTTGGT	CTGGCCCAATGGCAA	CGGGGTGCCACTCGCATGACCTCAGCATGGATGGGCG	556
Db	481	GATTTTGGT	CTGGCCCAATGGCAA	CGGGGTGCCACTCGCATGACCTCAGCATGGATGGGCG	540
QY	557	CTGTTTGGCA	CAATGCGCTACCTCCCTCAGAAGCCATCAGGAGAAAGACCGGCTCTTC	616	
Db	541	CTGTTTGGCA	CAATGCGCTACCTCCCTCAGAAGCCATCAGGAGAAAGACCGGCTCTTC	600	
QY	617	GACACCAAG	CAGATGTATACAGCTTTCGATCTGTGGGCGGTGCTCACACAGAG	676	
Db	601	GACACCAAG	CAGATGTATACAGCTTTCGATCTGTGGGCGGTGCTCACACAGAG	660	
QY	677	AAGCGTTTG	CAGATGAGAAGAACTCTTGACATCAGTGTGAAGGTGTGAAGGGCCAC	736	
Db	661	AAGCGTTTG	CAGATGAGAAGAACTCTTGACATCAGTGTGAAGGTGTGAAGGGCCAC	720	
QY	737	CGCCCCGAG	CTGCGCCGCTGTCAGACCCCGGCGCGGCGGCTGCAAGCACTTATACGC	796	
Db	721	CGCCCCGAG	CTGCGCCGCTGTCAGACCCCGGCGGCGGCTGCAAGCACTTATACGC	780	
QY	797	CTCATGCA	GCGGTGTGCGCAGGGGGATCGCGAGTTAGGCCACCTTTCAGAAATTA	856	
Db	781	CTCATGCA	GCGGTGTGCGCAGGGGGATCGCGAGTTAGGCCACCTTTCAGAAATTA	840	
QY	857	TTTGAAC	CCGAGAGACTGTGTGTAAGAGCTGTATGACGAATGGAAGAACTGTCAATAT	916	
Db	841	TTTGAAC	CCGAGAGACTGTGTGTAAGAGCTGTATGACGAATGGAAGAACTGTCAATAT	900	
QY	917	CTGGA	CGTGAAGACCCCGGAGGCCAGAGACGAGTGTGCTGCGAGGCTCAAGCGG	976	
Db	901	CTGGA	CGTGAAGAGCCCGCGAGGCCAGAGACGAGTGTGCTGCGAGGCTCAAGCGG	960	
QY	977	GCCTCTG	CGCCCACTTGATACGACTACAGCCCTTTCGAGCTTCTTCA	CAGCTGGAC	1036
Db	961	GCCTCTG	CGCCCACTTGATACGACTACAGCCCTTTCGAGCTTCTTCA	CAGCTGGAC	1020
QY	1037	TTTGAAGTT	CCCAAGGCTGTCAAGGGCCCGAGAGGCTCAACCGCAGCTTCTTGAATCC	1096	
Db	1021	TTTGAAGTT	CCCAAGGCTGTGTAGGGCCCGAGAGGCTCAACCGCAGCTTCTTGAATCC	1080	
QY	1097	AAGCTG	CCATCGTCCGGCAGTGGAAAGAGCTCTGGAGGATGTCTCGATGACATCCGCC	1156	
Db	1081	AAGCTG	CCATCGTCCGGCAGTGGAAAGAGCTCTGGAGGATGTCTCGATGACATCCGCC	1140	
QY	1157	TTCTCTT	CCAGAGATCACTGTGCTCTTTGAGCGGAACTTCAACCAAGCATCTG	1216	

Db	1141	TTCTCTTCAGAGGATCACTGTCCGTCTCTTTGAGGGGAACTTACACAGGATCTG	1200
QY	1217	GGTACCAACAAGCGTCCAGAAAGAGCTTTGTGATGTCATCGTGTCCGGACAACAAC	1276
Db	1201	GGTACCAACAAGCGTCCAGAAAGAGCTTTGTGATGTCATCGTGTCCGGACAACAAC	1260
QY	1277	AAACTGATGAAGATCTCTGCACCGCCAGACGTGACCTTGGCACTGGACAAGCGGTGCCAGC	1336
Db	1261	AAACTGATGAAGATCTCTGCACCGCCAGACGTGACCTTGGCACTGGACAAGCGGTGCCAGC	1320
QY	1337	CTGCGCAACCTGGGCGGTGGAGGCGGGCAAGAGGAGTGCAGAGTGGAGTGGCTCTCAAC	1396
Db	1321	CTGCTGCACCTGGCGGTGGAGGCGGGCAAGAGGAGTGCAGAGTGGAGTGGCTCTCTCAAC	1380
QY	1397	AATGCCAACCCCAACCTGAGCAACCGTAGGGGCTCAACCCCGTTGCAATGGCCGTGAG	1456
Db	1381	AATGCCAACCCCAACCTGAGCAACCGTAGGGGCTCAACCCCGTTGCAATGGCCGTGAG	1440
QY	1457	AGAGAGGTGGCGGGGTGTCTGTGAGACTCTCTGTGGCAAGGAAGATCACTGTCAAGCCAAAG	1516
Db	1441	AGAGAGGTGGCGGGGTGTCTGTGAGACTCTCTGTGGCAAGGAAGATCACTGTCAAGCCAAAG	1500
QY	1517	GATGAGGACCAGTGGACAAGCCCTCACTTTGGCAGCCCAAGACGGGAGATGAGTCTAGACA	1576
Db	1501	GATGAGGACCAGTGGACAAGCCCTCACTTTGGCAGCCCAAGACGGGAGATGAGTCTAGACA	1560
QY	1577	CGCGCTGTGTGGAGAAAGACGCTTCGGTCAACAGAGGTGACCTTTGAGGGCCGGAACGCCC	1636
Db	1561	CGCGCTGTGTGGAGAAAGACGCTTCGGTCAACAGAGGTGACCTTTGAGGGCCGGAACGCCC	1620
QY	1637	ATGCACTGTGCCTTGCACAGCACGGGCAAGAGAAATTCGTGGCATTCCTGTCCGCCAGAGC	1696
Db	1621	ATGCACTGTGCCTTGCACAGCACGGGCAAGAGAAATTCGTGGCATTCCTGTCCGCCAGAGC	1680
QY	1697	GTGACACGTGAGACCTGCAAGGGCAAGATGCCGTGGCACTGACCTACGCTGCCTTGGCAG	1756
Db	1681	GTGACACGTGAGACCTGCAAGGGCAAGATGCCGTGGCACTGACCTACGCTGCCTTGGCAG	1740
QY	1757	GAGCAACCTGCCCATCTGTCAAGCTGTGCGCCAAAGAGCCGGGGGTGAGTGTGAACGCCAG	1816
Db	1741	GAGCAACCTGCCCATCTGTCAAGCTGTGCGCCAAAGAGCCGGGGGTGAGTGTGAACGCCAG	1800
QY	1817	ACGCTGATGAGGAGAGCGCCATTGCACTGTGGCCGCAACGCGGGGCACTTACCGGTGGCC	1876
Db	1801	ACGCTGATGAGGAGAGCGCCATTGCACTGTGGCCGCAACGCGGGGCACTTACCGGTGGCC	1860
QY	1877	CGCATCTCTCAATCGACCTGTGTCCGACGTCAACGTCGACGCTGAGGCAAGACACC	1936
Db	1861	CGCATCTCTCAATCGACCTGTGTCCGACGTCAACGTCGACGCTGAGGCAAGACACC	1920
QY	1937	CTGCACGTGGCCGCGGAGACGGGGCAACAGACACTGCGACGCTGCTCTTCATCTGAGGC	1996
Db	1921	CTGCACGTGGCCGCGGAGACGGGGCAACAGACACTGCGACGCTGCTCTTCATCTGAGGC	1980
QY	1997	GCTGGCAAGAGAGCCGTGACCTCAAGCGGCTTACAACCGCTTTCGCACTTGGCTCCCGCAAC	2056
Db	1981	GCTGGCAAGAGAGCCGTGACCTCAAGCGGCTTACAACCGCTTTCGCACTTGGCTCCCGCAAC	2040
QY	2057	GGAACACCTGGGCACTGTTCAAAGCTGTTCGAGGAGAAAGCCGATGTGCTGGCCCGGGGA	2116
Db	2041	GGAACACCTGGGCACTGTTCAAAGCTGTTCGAGGAGAAAGCCGATGTGCTGGCCCGGGGA	2100
QY	2117	CCCCGAAACAGACGCGCGCTGCACTGTGGCTGCCGCCCAAGGCACTCGAGAGTGGTGAAG	2176
Db	2101	CCCCGAAACAGACGCGCGCTGCACTGTGGCTGCCGCCCAAGGCACTCGAGAGTGGTGAAG	2160
QY	2177	GAGTTGTGTCAAGCGCCGATGTCAATTGACCTGTTTCCAGACAGGGGCTCAAGCGCTGCAC	2236
Db	2161	GAGTTGTGTCAAGCGCCGATGTCAATTGACCTGTTTCCAGACAGGGGCTCAAGCGCTGCAC	2220
QY	2237	CTGGCGCGGCAAGGCGCGGCAAGCAAGCGGTGAGACTCTGCTCAAGCAATGGGGCCAC	2296

DB 2221 CTGCGCGCCGACGGCGGACGACAGACGATGAGACTCTGTGACGAGCATGGGCGCAC 2280
QY 2237 ATCAACCTGACAGAGCTTCAAGTTCCAGGGCGGCGCCATGGCCCCGCGCACACTCTTGCGG 2356
DB 2281 ATCAACCTGACAGAGCTTCAAGTTCCAGGGCGGCGCCATGGCCCCGCGCACACTCTTGCGG 2340
QY 2357 CGAAGCAGACCTAG 2371
DB 2341 CGAAGCAGACCTAG 2355

RESULT 11
AAD64343
ID AAD64343 standard; DNA; 2355 BP.
AC AAD64343;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human protein kinase C-associated kinase (PKK) variant DNA #5.
XX
KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN US2003199462-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128174.
XX
PR 23-APR-2002; 2002US-00128174.
XX
PA (NMNE/) NMNEZ G.
PA (INOH/) INOHARA N.
PA (MUTO/) MUTO A.
XX
PI Nunez G, Inohara N, Muto A;
XX
DR WPI; 2003-852808/79.
XX
PT New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
PS Disclosure; SEQ ID NO 18; Opp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
XX
SQ Sequence 2355 BP; 463 A; 740 C; 761 G; 391 T; 0 U; 0 Other;

Query Match 60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

DB 121 CATGTCCACTGAAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCCTGACGTGACGAC 180
QY 197 AGGAGAGGCATGAGGCTTTTGAAAGAGCCAGAAAGATGAGAGATGGCAAGTTTCGTAC 256
DB 181 AGGAGAGGCATGAGGCTTTTGAAAGAGCCAGAAAGATGAGAGATGGCAAGTTTCGTAC 240
QY 257 ATCTGCTGTGTATGAGCATCTGCGCGAAACTGTGCGGCTGTGTCATGAGATCATGAG 316
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGAAACTGTGCGGCTGTGTCATGAGATCATGAG 300
QY 317 ACGGCTCTCCGAAAAGCTGTGGCTTCGAGGCAATTCGCAATGGATCTCGGTTCCGA 376
DB 301 ACGGCTCTCCGAAAAGCTGTGGCTTCGAGGCAATTCGCAATGGATCTCGGTTCCGA 360
QY 377 ATCATCCAGAGACGGGAGTGGGCAATGAATTCCTGACATGCAATGGCCCCGCACTCTG 436
DB 361 ATCATCCAGAGACGGGAGTGGGCAATGAATTCCTGACATGCAATGGCCCCGCACTCTG 420
QY 437 CACCTGACCTCAAGCCCGGCAACATCTGTGATGCCATCCGACTTACACAGTCAAGATTCT 496
DB 421 CACCTGACCTCAAGCCCGGCAACATCTGTGATGCCATCCGACTTACACAGTCAAGATTCT 480
QY 497 GATTTGGTCTGGCCAAATGTCACAGGCTGTCCCATCGCATGACCTCAGCATGATGGC 556
DB 481 GATTTGGTCTGGCCAAATGTCACAGGCTGTCCCATCGCATGACCTCAGCATGATGGC 540
QY 557 CTGTTTGGCAATCGGCTTACCTCCCTCCGAGGCAATCGAGGAAAGAGCGGCTTTC 616
DB 541 CTGTTTGGCAATCGGCTTACCTCCCTCCGAGGCAATCGAGGAAAGAGCGGCTTTC 600
QY 617 GACACCAAGCAGATGATACAGCTTTCGATCTGATCTGAGGCGTGTACACAGAG 676
DB 601 GACACCAAGCAGATGATACAGCTTTCGATCTGATCTGAGGCGTGTACACAGAG 660
QY 677 AAGCGTTTGGCAATGAAAGACATCTCTGCAATCATGTTGAAAGTGTGAGAGCGCAC 736
DB 661 AAGCGTTTGGCAATGAAAGACATCTCTGCAATCATGTTGAAAGTGTGAGAGCGCAC 720
QY 737 CGCCCCGAGCTGGCGCCGATGTCAGAGCCCGGCGGCGCTGACAGCACTGATACGC 796
DB 721 CGCCCCGAGCTGGCGCCGATGTCAGAGCCCGGCGGCGCTGACAGCACTGATACGC 780
QY 797 CTCATGACGCGTCTGTCAGAGGAGATCCGCAATGAGCCCACTTCCAGAAATTAAT 856
DB 781 CTCATGACGCGTCTGTCAGAGGAGATCCGCAATGAGCCCACTTCCAGAAATTAAT 840
QY 857 TCTGAACCGAGACCTGTGTGAAAGCTGTATGACGATGAAAGAAATCTGCTCATGAT 916
DB 841 TCTGAACCGAGACCTGTGTGAAAGCTGTATGACGATGAAAGAAATCTGCTCATGAT 900
QY 917 CTGACGTAAGAAAGCCCGCGAGGCCAGAGGAGGATGCTGCGAGGCTCAAGCGG 976
DB 901 CTGACGTAAGAAAGCCCGCGAGGCCAGAGGAGGATGCTGCGAGGCTCAAGCGG 960
QY 977 GCTCTGCCCCCACTTGTGATTAACGACTTCCAGACTTCTCTCAACAGCTGAGC 1036
DB 961 GCTCTGCCCCCACTTGTGATTAACGACTTCCAGACTTCTCTCAACAGCTGAGC 1020
QY 1037 TCTGAAGTTTCCAGGCTGTGAGAGGCCCGAGAGACTCAAGCCGAGCTCTCTGAGTCC 1096
DB 1021 TCTGAAGTTTCCAGGCTGTGAGAGGCCCGAGAGACTCAAGCCGAGCTCTCTGAGTCC 1080
QY 1097 AAGCTGCATGATCCGAGAGTGGGAAGAGGCTCTCGGAGGATGCTGAGTGGATCCGGC 1156
DB 1081 AAGCTGCATGATCCGAGAGTGGGAAGAGGCTCTCGGAGGATGCTGAGTGGATCCGGC 1140
QY 1157 TTCTCTTCCAGAGATCATGTCGCTCTCTTTGAGCGGAAACCTTCAACAGAGATCTG 1216
DB 1141 TTCTCTTCCAGAGATCATGTCGCTCTCTTTGAGCGGAAACCTTCAACAGAGATCTG 1200
QY 1217 GGTACCAAGAGCTTCAAGAAAGAAAGCTTGTGATGCACTGTGTC -GGACACCAAG 1275
DB 1201 GGTACCAAGAGCTTCAAGAAAGAAAGCTTGTGATGCACTGTGTC -GGACACCAAG 1259

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QY 1276 CAAATGATGAAGATCTGCAAGCCGAGAGCGTGAAGCTTGGCACTGGACAGCGGTGCCAG 1335
DB 1260 CAAACTGATGAAGATCTTGCAGCCGAGAGCGTGAAGCTTGGCACTGGACAGCGGTGCCAG 1319
QY 1336 CCGTGGCAAGCTGGCGGTGGAGGCGGGGCAAGAGAGTGGCGGCAAGTGGCTGCTGCTCA 1395
DB 1320 CCGTGGCAAGCTGGCGGTGGAGGCGGGGCAAGAGAGTGGCGGCAAGTGGCTGCTGCTCA 1379
QY 1396 CAATGCCAACCCCAACTGAGCAACCGTGAAGGAGCTTCAACCCGTTGCAATGAGCGGTGA 1455
DB 1380 CAATGCCAACCCCAACTGAGCAACCGTGAAGGAGCTTCAACCCGTTGCAATGAGCGGTGA 1439
QY 1456 GAGGAGGGGTGGCGGGGTGTGTGTGAGTCTTGTGCGGCAAGAGATGATGATGATGATG 1515
DB 1440 GAGGAGGGGTGGCGGGGTGTGTGTGAGTCTTGTGCGGCAAGAGATGATGATGATGATG 1499
QY 1516 GGATGAGGACCAAGTGAACAGCCCTTCACTTTGACGCCAAGACGGGGATGATGATGATG 1575
DB 1500 GGATGAGGACCAAGTGAACAGCCCTTCACTTTGACGCCAAGACGGGGATGATGATGATG 1559
QY 1576 ACGGCTGTGTTGAGAGAGAGCGCTCGGTCAACGAGGTGATCTTTGAGGGCCGAGCGCC 1635
DB 1560 ACGGCTGTGTTGAGAGAGAGCGCTCGGTCAACGAGGTGATCTTTGAGGGCCGAGCGCC 1619
QY 1636 CATGCACTGTGGCTGTCAGCAAGGCGAGAGAAATATGTGTGCGCATCTGTGCGCGAGAG 1695
DB 1620 CATGCACTGTGGCTGTCAGCAAGGCGAGAGAAATATGTGTGCGCATCTGTGCGCGAGAG 1679
QY 1696 CCGTGAAGTGAAGCGTCAAGGAGAGATGCTGGCTGCGCACTGAAGCTGCGCTGAGGA 1755
DB 1680 CCGTGAAGTGAAGCGTCAAGGAGAGATGCTGGCTGCGCACTGAAGCTGCGCTGAGGA 1739
QY 1756 GGGGCACTGCGCCATGCTGCTGAGCTGGCTGGCAAGAGCGCGGGGTGATGTGAACGCCCA 1815
DB 1740 GGGGCACTGCGCCATGCTGCTGAGCTGGCTGGCAAGAGCGCGGGGTGATGTGAACGCCCA 1799
QY 1816 GACGCTGATGAGGAGAGCGCCATTTGCACTCTGGCCGCAAGCGCGGGCACTACCGCTGGC 1875
DB 1800 GACGCTGATGAGGAGAGCGCCATTTGCACTCTGGCCGCAAGCGCGGGCACTACCGCTGGC 1859
QY 1876 CCGCATCTTCATGACCTGTGCTCCGACGTCAAGCTGTGAGCTGAGCTGAGCAAGACACC 1935
DB 1860 CCGCATCTTCATGACCTGTGCTCCGACGTCAAGCTGTGAGCTGAGCTGAGCAAGACACC 1919
QY 1936 CCTGCACTGTGGCGCGGAGAGCGGGGCAACGAGCACTGCGAGGCTCTCTGTCATGCGGG 1995
DB 1920 CCTGCACTGTGGCGCGGAGAGCGGGGCAACGAGCACTGCGAGGCTCTCTGTCATGCGGG 1979
QY 1996 CCGTGGCAAGAGAGCGCGTGAAGCTTGAAGCGGCTTACCGCTTGTGCACTGTGCTGCCG 2055
DB 1980 CCGTGGCAAGAGAGCGCGTGAAGCTTGAAGCGGCTTACCGCTTGTGCACTGTGCTGCCG 2039
QY 2056 CGGACACTGGGCGCACTGTCAAGCTGTGCGAGGAGAGAGCGGATGTGTGGCCCGGGG 2115
DB 2040 CGGACACTGGGCGCACTGTCAAGCTGTGCGAGGAGAGAGCGGATGTGTGGCCCGGGG 2099
QY 2116 ACCCTGAAACCAAGCGGCGCTGCACTGTGCTGCCGCAAGGCACTCGAGGTGTGGA 2175
DB 2100 ACCCTGAAACCAAGCGGCGCTGCACTGTGCTGCCGCAAGGCACTCGAGGTGTGGA 2159
QY 2176 GAGGTGTGTGAGCGCGCGATGTCAATTGAAGCTTGTGAGAGAGAGAGGCTTCAAGCGGCTG 2235
DB 2160 GAGGTGTGTGAGCGCGCGATGTGTCAATTGAAGCTTGTGAGAGAGAGAGGCTTCAAGCGGCTG 2219
QY 2236 CCGTGGCGGCGCGAGGCGCGGCAAGAGAGGAGAGAGCTTGTCAAGAGAGAGGAGGAGG 2295
DB 2220 CCGTGGCGGCGCGAGGCGCGGCAAGAGAGGAGAGAGCTTGTCTCAAGGAGAGGAGGAGG 2279
QY 2296 CATCAACCTGCAAGAGCTTCAAGTTTCAAGGCGGCGCATGAGCCCGCGCCCACTCTGCG 2355
DB 2280 CATCAACCTGCAAGAGCTTCAAGTTTCAAGGCGGCGCATGAGCCCGCGCCCACTCTGCG 2339
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QY 2356 GCGAAGCAAGACTTAG 2371
DB 2340 GCGAAGCAAGACTTAG 2355

RESULT 12
AAB64340
ID AAB64340 standard; DNA; 2355 BP.
XX
AC AAB64340;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human protein kinase C-associated kinase (PKK) variant DNA #2.
XX
KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN US2003199462-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128174.
XX
PR 23-APR-2002; 2002US-00128174.
XX
PA (NUNEZ/) NUNEZ G.
PA (INOCH/) INOHARA N.
PA (MUTO/) MUTO A.
PI Nunez G, Inohara N, Muto A;
XX
DR WPI; 2003-852808/79.
XX
PT New nucleic acid encoding RICK3, useful in preparing a composition for
XX inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
PS Disclosure; SEQ ID NO 15; Opp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
XX
SQ Sequence 2355 BP; 462 A; 740 C; 761 G; 392 T; 0 U; 0 Other;
XX

Query Match 60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 17 ATGAGAGGCGAGCGGCGGAGCCCAATGGGCGCTGGCGCTGCGCACTTTCAGCGGGG 76
DB 1 ATGAGAGGCGAGCGGCGGAGCCCAATGGGCGCTGGCGCTGCGCACTTTCAGCGGGG 60
QY 77 GAGTTCAAGGCGCTGGAGAGAGGTGGGCTCGGGCGGCTTGGGCAAGGTGAAGGTCGCG 136
DB 61 GAGTTCAAGGCGCTGGAGAGAGGTGGGCTCGGGCGGCTTGGGCAAGGTGAAGGTCGCG 120
QY 137 CATGTCACTGGAAGACTTGGCTGGCCATCAAGTGTGCGCCAGCTGAGCGTGAAGAC 196
DB 121 CATGTCACTGGAAGACTTGGCTGGCCATCAAGTGTGCGCCAGCTGAGCGTGAAGAC 180
QY 197 AGGAGCGCATGAGCTTTTGGAGAGAGCAAGAGATGAGAGATGAGCAAGTTTGGCTAC 256
DB 181 AGGAGCGCATGAGCTTTTGGAGAGAGCAAGAGATGAGAGATGAGCAAGTTTGGCTAC 240
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AAD64341
ID AAD64341 standard; DNA; 2355 BP.
AC AAD64341;
XX
XX
DT 12-FEB-2004 (first entry)
XX
XX Human protein kinase C-associated kinase (PKK) variant DNA #3.
DE Human protein kinase C-associated kinase (PKK) variant DNA #3.
XX
XX Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; de.
XX
XX Homo sapiens.
OS
XX US2003199462-A1.
PN
XX
XX 23-OCT-2003.
PD
XX 23-APR-2002; 2002US-00128174.
PF
XX 23-APR-2002; 2002US-00128174.
PR
XX 23-APR-2002; 2002US-00128174.
XX
XX (NUNE/) NUNEZ G.
PA (INOH/) INOHARA N.
PA (MUTO/) MUTO A.
XX
XX Nunez G, Inohara N, Muto A;
PI
XX
XX WPI; 2003-852808/79.
DR
XX
XX
XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
XX
XX Disclosure; SEQ ID NO 16; Opp; English.
PS
XX
XX
XX The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
CC
SQ Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;

Query Match 60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Query
17 ATGAGAGGCGACGAGCGGAGCCCATGAGGCGCTGCGTGCACCTTGAACGCGGAGC 76
1 ATGAGAGGCGACGAGCGGAGCCCATGAGGCGCTGCGTGCACCTTGAACGCGGAGC 60
77 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 136
61 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 120
77 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 136
61 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 120
137 CATGTCCATGAGGAGAGCTGCGTGCATCAAGTGTGCGCCGAGCTGCAGCGTGCAGC 196
121 CATGTCCATGAGGAGAGCTGCGTGCATCAAGTGTGCGCCGAGCTGCAGCGTGCAGC 180
197 AGGAGCGCATGAGAGCTTTTGAAGAGCCAGAGAGTGAATGAGTGGCAATTTGCTAC 256
181 AGGAGCGCATGAGAGCTTTTGAAGAGCCAGAGAGTGAATGAGTGGCAATTTGCTAC 240
257 ATCTGCTGTGTATGAGCATCTGCGGAACTGTGCGCTGGTCAATGAGTACATGAGAG 316
241 ATCTGCTGTGTATGAGCATCTGCGGAACTGTGCGCTGGTCAATGAGTACATGAGAG 300
317 ACGGAGCTCCCTGAGAAAGCTGTGCTTGCAGGCAATGAGTGGCAATGAGTGGTCCGA 376

Query
17 ATGAGAGGCGACGAGCGGAGCCCATGAGGCGCTGCGTGCACCTTGAACGCGGAGC 76
1 ATGAGAGGCGACGAGCGGAGCCCATGAGGCGCTGCGTGCACCTTGAACGCGGAGC 60
77 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 136
61 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 120
77 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 136
61 GAGTTCAACGAGGCTGAGGAGAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAGAGTGC 120
137 CATGTCCATGAGGAGAGCTGCGTGCATCAAGTGTGCGCCGAGCTGCAGCGTGCAGC 196
121 CATGTCCATGAGGAGAGCTGCGTGCATCAAGTGTGCGCCGAGCTGCAGCGTGCAGC 180
197 AGGAGCGCATGAGAGCTTTTGAAGAGCCAGAGAGTGAATGAGTGGCAATTTGCTAC 256
181 AGGAGCGCATGAGAGCTTTTGAAGAGCCAGAGAGTGAATGAGTGGCAATTTGCTAC 240
257 ATCTGCTGTGTATGAGCATCTGCGGAACTGTGCGCTGGTCAATGAGTACATGAGAG 316
241 ATCTGCTGTGTATGAGCATCTGCGGAACTGTGCGCTGGTCAATGAGTACATGAGAG 300
317 ACGGAGCTCCCTGAGAAAGCTGTGCTTGCAGGCAATGAGTGGCAATGAGTGGTCCGA 376

Db 301 ACGGAGCTCCCTGAGAAAGCTGCTGCGTTCGAGGCCATTGCCATGGAGATCTCCGGTTCGA 360
377 ATCATTCACGAGAGCGGCGGTGAGATGAATCTTCCGACATGAGGCCCGCACTCTCG 436
361 ATCATTCACGAGAGCGGCGGTGAGATGAATCTTCCGACATGAGGCCCGCACTCTCG 420
437 CACCTGAGACTCAAGCCCGGAGACATCTGCTGATGCCCACTACAGATCAAGATTTCT 496
421 CACCTGAGACTCAAGCCCGGAGACATCTGCTGATGCCCACTACAGATCAAGATTTCT 480
497 GATTTGTGTGCGCAAGTGAAGAGAGTGGCTGTCCCATCTGCAATGACCTGAGTGAATGAGC 556
481 GATTTGTGTGCGCAAGTGAAGAGAGTGGCTGTCCCATCTGCAATGACCTGAGTGAATGAGC 540
557 CTGTTGGCAATGAGTGGCTTACCTCCCTCAGAGGCAATCAGGAGAGAGCGGCTCTTC 616
541 CTGTTGGCAATGAGTGGCTTACCTCCCTCAGAGGCAATCAGGAGAGAGCGGCTCTTC 600
617 GACACCAAGCAGATGATTAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 676
601 GACACCAAGCAGATGATTAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 660
677 AAGCGTTTGAAGATGAGAGAGACATCTGCAATCATGATGATGATGATGATGATGATGATGAT 736
661 AAGCGTTTGAAGATGAGAGAGACATCTGCAATCATGATGATGATGATGATGATGATGATGATGAT 720
737 CGCCCGGAGCTGCGCCGCTGTGAGAGCCCGGCGGCGGCTGAGGCACTGATAGGC 796
721 CGCCCGGAGCTGCGCCGCTGTGAGAGCCCGGCGGCGGCTGAGGCACTGATAGGC 780
797 CTGATGAGCGGTGCTGAGAGGAGGATCCGAGATGATGATGATGATGATGATGATGATGATGAT 856
781 CTGATGAGCGGTGCTGAGAGGAGGATCCGAGATGATGATGATGATGATGATGATGATGATGAT 840
857 TCTGAACCGAGAGCTGTGTGTAAGAGCTGATGATGATGATGATGATGATGATGATGATGAT 916
841 TCTGAACCGAGAGCTGTGTGTAAGAGCTGATGATGATGATGATGATGATGATGATGATGAT 900
917 CTGAGAGTGAAGAGGCGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 976
901 CTGAGAGTGAAGAGGCGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
977 GCGTGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1036
961 GCGTGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
1037 TCTGAGATTTCCAGAGCTGTGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1096
1021 TCTGAGATTTCCAGAGCTGTGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
1097 AAGCTGCCATGCTGCGGAGTGGAGAGAGGCTCTCGGGGGTGTCTCGGTGAGACTCCGCG 1156
1081 AAGCTGCCATGCTGCGGAGTGGAGAGAGGCTCTCGGGGGTGTCTCGGTGAGACTCCGCG 1140
1157 TTTCTGTCAGAGAGATCACTGTGCTGCTTGTGAGCGGAGAACTTCAACAGCATCTG 1216
1141 TTTCTGTCAGAGAGATCACTGTGCTGCTTGTGAGCGGAGAACTTCAACAGCATCTG 1200
1217 GGTACCAAGAGAGCTGCAAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1275
1201 GGTACCAAGAGAGCTGCAAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1259
1276 CAAACTGATGAAGATCTGCAAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1335
1260 CAAACTGATGAAGATCTGCAAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1319
1336 CCGTGCAGCACTGAGCGGTGAGAGGCGGAGAGAGAGTGGCAATGAGGCTGCTCA 1395
1320 CCGTGCAGCACTGAGCGGTGAGAGGCGGAGAGAGAGTGGCAATGAGGCTGCTCA 1379
1396 CAATGCAACCCCAACTGAGCAACCTGATGAGGAGCTCAACCCGTTGCAATGAGCGGTGGA 1455
1380 CAATGCAACCCCAACTGAGCAACCTGATGAGGAGCTCAACCCGTTGCAATGAGCGGTGGA 1439

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QY 1456 GAGGAGGCTGCGGGGTGCTGCTGAGCTCTGCTGGCAAGGAAGATCAAGTGTCAAGCCAA 1515
DB 1440 GAGGAGGGGTGCGGGGTGCTGCTGAGCTCTGCTGGCGGGAAGATCAGTGTCAAGCCAA 1499
QY 1516 GATATGAGGACAGTGGACAGCCCTCCACTTTGTCAGAGCCGGAACGGGGAGTGAAGTTCAGAC 1575
DB 1500 GGATATGAGACAGTGGACAGCCCTCCACTTTGTCAGAGCCGGAACGGGGAGTGAAGTTCAGAC 1559
QY 1576 ACGGCTGCTGTTGAGAAAGAACGCTTCGGTCAACAGAGTGAAGTTGAGGGCGGAGCGCC 1635
DB 1560 ACGGCTGCTGTTGAGAAAGAACGCTTCGGTCAACAGAGTGAAGTTGAGGGCGGAGCGCC 1619
QY 1636 CATGCAAGTGGCTGCTGCAAGAGGAGGAGGAGAAATTCGTGCCATTCCTGCTGCGGAGG 1695
DB 1620 CATGCAAGTGGCTGCTGCAAGAGGAGGAGGAGAAATTCGTGCCATTCCTGCTGCGGAGG 1679
QY 1696 CGTGAAGTGAAGCTGCAAGGAGGAGATGCTGCTGCAAGAGCTGCACTAGCGCTGCTGCA 1755
DB 1680 CGTGAAGTGAAGCTGCAAGGAGGAGATGCTGCTGCAAGAGCTGCACTAGCGCTGCTGCA 1739
QY 1756 GGGGCAAGCTGCAAGCTGCTGCAAGCTGCTGCAAGAGCGGGGGTGAAGTGAAGCGCCA 1815
DB 1740 GGGGCAAGCTGCAAGCTGCTGCAAGCTGCTGCAAGAGCGGGGGTGAAGTGAAGCGCCA 1799
QY 1816 GACGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1875
DB 1800 GACGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1859
QY 1876 CCGCATCTCATGCAAGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAGGAG 1935
DB 1860 CCGCATCTCATGCAAGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAGGAG 1919
QY 1936 CCGCATCTCATGCAAGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAGGAG 1995
DB 1920 CCGCATCTCATGCAAGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAGGAG 1979
QY 1996 CCGCATCTCATGCAAGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAGGAG 2055
DB 1980 CCGCATCTCATGCAAGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAGGAG 2039
QY 2056 CCGCATCTCATGCAAGCTGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAG 2115
DB 2040 CCGCATCTCATGCAAGCTGCTGCTGCTGCAAGCTGCTGCAAGAGCTGCTGCAAGAGGAGGAG 2099
QY 2116 ACCCTGGAACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2175
DB 2100 ACCCTGGAACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2159
QY 2176 GGAAGTTGTCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2235
DB 2160 GGAAGTTGTCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2219
QY 2236 CCGCATCTCATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2295
DB 2220 CCGCATCTCATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2279
QY 2296 CATCAACCTGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2355
DB 2280 CATCAACCTGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2339
QY 2356 GGGAGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2371
DB 2340 GGGAGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2335
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RESULT 14
AAB64344
ID AAB64344 Standard; DNA; 2355 BP.
AC AAB64344;
XX
DT 12-FEB-2004 (first entry)
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```
XX
DE Human protein kinase C-associated kinase (PKK) variant DNA #6.
XX
KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
OS Homo sapiens.
PN US2003199462-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128174.
XX
PR 23-APR-2002; 2002US-00128174.
XX
PA (NUNEZ/) NUNEZ G.
PA (INOH/) INOHARA N.
XX (MUTO/) MUTO A.
PI Nunez G, Inohara N, Muto A;
XX
DR WPI; 2003-852808/79.
XX
PT New nucleic acid encoding RICK3, useful in preparing a composition for
XX inhibiting PKK induced NF-kB activation for treating hyperglycaemia.
XX
PS Disclosure; SEQ ID NO 19; Opp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia.
CC The invention is also used in gene therapy. The present sequence is human
XX PKK variant DNA
XX
SQ Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;
XX
Query Match 60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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QY 17 ATGAGGAGCGAGCGGCGGAGCCCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 76
DB 1 ATGAGGAGCGAGCGGCGGAGCCCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 77 GAGTTCAACGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 136
DB 61 GAGTTCAACGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 137 CATGTCACATGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196
DB 121 CATGTCACATGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 197 AGGAGGCGCATGAGAGCTTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 256
DB 181 AGGAGGCGCATGAGAGCTTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 257 ATTCGCTGCTGTAAGGATGCTGCGGAGACCTGTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
DB 241 ATTCGCTGCTGTAAGGATGCTGCGGAGACCTGTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 317 ACGGCTGCTGTAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
DB 301 ACGGCTGCTGTAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 377 ATCATTCAGAGAGCGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 436
DB 361 ATCATTCAGAGAGCGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
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QY	437	CACCTGGACCTTCAGAGCCCGCGGAAACATCTGTGTGAATGCCCATTCACAGCTCAAGATTTC	436
Db	421	CACCTGGACCTTCAGAGCCCGCGGAAACATCTGTGTGAATGCCCATTCACAGCTCAAGATTTC	480
QY	497	GATTTTGGTCTGGCCCAAGTGGACAAGGCGTGGCCCACTCGCATGATCACTCAGCATGGATGGC	556
Db	481	GATTTTGGTCTGGCCCAAGTGGACAAGGCGTGGCCCACTCGCATGATCACTCAGCATGGATGGC	540
QY	557	CTGTTTGGCACATGCGCTTACCTCCCTTCAGAGCGCATCAGAGGAAAGCGGCTCTTC	616
Db	541	CTGTTTGGCACATGCGCTTACCTCCCTTCAGAGCGCATCAGAGGAAAGCGGCTCTTC	600
QY	617	GACACCAAGCACGATGTTTACAAGCTTTTGGCATCTGTGATCTTGGGGCGTGTCAACAAG	676
Db	601	GACACCAAGCACGATGTTTACAAGCTTTTGGCATCTGTGATCTTGGGGCGTGTCAACAAG	660
QY	677	AAGCGTTTGGAGATGAGAGAAGAACATCTTGACACATCATGTGTGAAGTGTGAAGGGCAC	736
Db	661	AAGCGTTTGGAGATGAGAGAAGAACATCTTGACACATCATGTGTGAAGTGTGAAGGGCAC	720
QY	737	CGCCCGGAGCTGCGCGCCGCTGTGACAGAGCCCGCGCGGCTTGACGACCTGTATACG	796
Db	721	CGCCCGGAGCTGCGCGCCGCTGTGACAGAGCCCGCGCGGCTTGACGACCTGTATACG	780
QY	797	CTCATGCAAGCGGTGTGGCAGGGGGGATCCGGGAGTTTAGGCCCACTTTCAGAAATTAATCT	856
Db	781	CTCATGCAAGCGGTGTGGCAGGGGGGATCCGGGAGTTTAGGCCCACTTTCAGAAATTAATCT	840
QY	857	TCTGAAACCGAGGACCTGTGTGAAGGCTGATGACGAAGTGAAGAAACGCTCATGAT	916
Db	841	TCTGAAACCGAGGACCTGTGTGAAGGCTGATGACGAAGTGAAGAAACGCTCATGAT	900
QY	917	CTGACAGTGAAGAAAGCCCCCGGAGCCACAGAGCGAGGTGTGCTGCGAGGCTCAAGCG	976
Db	901	CTGACAGTGAAGAAAGCCCCCGGAGCCACAGAGCGAGGTGTGCTGCGAGGCTCAAGCG	960
QY	977	GCTCTGCCCCCACTTGTGATTAACGATCAAGCTCTTCGAGCTTCTTCAACAGCTGAC	1036
Db	961	GCTCTGCCCCCACTTGTGATTAACGATCAAGCTCTTCGAGCTTCTTCAACAGCTGAC	1020
QY	1037	TCTGAGTTCCTCCAGGCTGTGAGGGGCCCGAGGAGCTCAGCGGAGCTCCTCGAGTCC	1096
Db	1021	TCTGAGTTCCTCCAGGCTGTGAGGGGCCCGAGGAGCTCAGCGGAGCTCCTCGAGTCC	1080
QY	1097	AAGCTGCATCGTCCGGCAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGAATCTCGCC	1156
Db	1081	AAGCTGCATCGTCCGGCAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGAATCTCGCC	1140
QY	1157	TTCTCTTCAGAGATCACTGTGCTTTCCTTTGAGCGGAAACCTTCAACAGCGATCTG	1216
Db	1141	TTCTCTTCAGAGATCACTGTGCTTTCCTTTGAGCGGAAACCTTCAACAGCGATCTG	1200
QY	1217	GGTACCAACAAGCTTCGAGAGAAAGAAACCTTGTGATTCGATTCGATCC-GGACAACAG	1275
Db	1201	GGCACCAAC-AGACGTTCAGAAAGAAAGAAACCTTGTGATTCGATTCGATTCGAGAG	1259
QY	1276	CAAACTGATGAAGATCTGTCAGCCCGCAGACGTGACCTTGACCTGACCAACGGGTGCAG	1335
Db	1260	CAAACTGATGAAGATCTGTCAGCCCGCAGACGTGACCTTGACCTGACCAACGGGTGCAG	1319
QY	1336	CCTGCTGCACTTGCGCGTGTGAAGCGCGGCGAAGAGATGTGCGCAATGTGGTCTTC	1395
Db	1320	CCTGCTGCACTTGCGCGTGTGAAGCGCGGCGAAGAGATGTGCGCAATGTGGTCTTC	1379
QY	1396	CAATGCCCAACCCCAACCTGAGGAAACCGTATGGGGCTTCAACCCCTTGGACATGGCGTGG	1455
Db	1380	CAATGCCCAACCCCAACCTGAGGAAACCGTATGGGGCTTCAACCCCTTGGACATGGCGTGG	1439
QY	1456	GAGAGAGGTGCGGGGTGTGTGGAAGCTCCTGTGTGACAGGAAGATCAATGTCAACGCCAA	1515
Db	1440	GAGAGAGGTGCGGGGTGTGTGGAAGCTCCTGTGTGCGGGAAGATCAATGTCAACGCCAA	1499
QY	1516	GGATAGAGCAGGTGGACAGCCCTTCACTTTGACGCCCAAGACGGGGATGATGTACAC	1575

Db	1500	GGAATGAGAGACCAAGTGGACAAGCCCTCCACTTTGGACGCCAGAACGGGGATGAGTCTAGAC	155.9
OY	1576	ACGGCTGCTGTTGGAGAAAGAACGCTCTCGGTCAACAGAGTGGACTTTGAGGGCCCGACGCC	163.5
Db	1560	ACGGCTGCTGTTGGAGAAAGAACGCTCGGTCAACAGAGTGGACTTTGAGGGCCCGACGCC	161.9
OY	1636	CATCAGCTAGGGCCCTGGCCAGCAACGGGCAAGGAATATGTTGGATCCCTGCTGGCCGAGG	169.9
Db	1620	CATCAGCTAGGGCCCTGGCCAGCAACGGGCAAGGAATATGTTGGATCCCTGCTGGCCGAGG	167.79
OY	1696	CGTGAACGTGAGCGCTGACAGGGCAAGATGCTGCTGCCACTGCACTAACGCTGCTGGCA	175.5
Db	1660	CGTGAACGTGAGCGCTGACAGGGCAAGATGCTGCTGGCTGCCTGCACTAACGCTGCTGGCA	173.9
OY	1756	GGGGCACTGCGCCATCGTCAAGCTGCTGGCCAGACAGCCGGGGGTGAGTGTAAACGCCCA	181.5
Db	1740	GGGGCACTGCGCCATCGTCAAGCTGCTGGCCAGACAGCCGGGGGTGAGTGTAAACGCCCA	179.9
OY	1816	GAACCTGAGATGGGAGAGACGCATTGGACACTGGGCCGACAGGGCGGGGCACTACCGAGTGGC	187.57
Db	1800	GACCTGTGATGGGAGAGACGCATTGGACACTGGGCCGACAGGGCGGGGCACTACCGAGTGGC	185.8
OY	1876	CCGATCCCTCATCCACCTGTGCTCCGACGTTCACAGCTCTGACAGCTGTGGGCAAGACAC	193.9
Db	1860	CCGATCCCTCATCCACCTGTGCTCCGACGTTCACAGCTCTGACAGCTGTGGGCAAGACAC	191.9
OY	1936	CTTGCACGTGGCCGCGGAGACGGGGCAACAGAGCACTGCCAGGCTGCTCTGCATCGGGG	199.9
Db	1920	CTTGCACGTGGCCGCGGAGACGGGGCAACAGAGCACTGCCAGGCTGCTCTGCATCGGGG	197.79
OY	1996	CGCTGGCAGAGAGGCGCTGACCTTGAAGACGCTTACACCGCTTTGGACCTGGCTGCCCGGAA	205.5
Db	1980	CGCTGGCAGAGAGGCGCTGACCTTGAAGACGCTTACACCGCTTTGGACCTGGCTGCCCGGAA	203.9
OY	2056	CGGACACCTGGCCACTGTCAAGCTGCTTGTGAAGAGAGAGGCCGATGTGCTGGCCCGGGG	211.5
Db	2040	CGGACACCTGGCCACTGTCAAGCTGCTTGTGTGAAGAGAGAGGCCGATGTGCTGGCCCGGGG	209.9
OY	2116	ACCCCTGAACCAAGACGGGCGCTGCACTTGGCTGCCGCCACGGGCACTTGGAGTGTGGA	217.5
Db	2100	ACCCCTGAACCAAGACGGGCGCTGCACTTGGCTGCCGCCACGGGCACTTGGAGTGTGGA	215.5
OY	2176	GGAAGTTGTCACGCGCCGATGTTCATTGACCTTGTGAGAGAGAGGGGCTCAACGCGCTGCA	223.3
Db	2160	GGAAGTTGTCACGCGCCGATGTTCATTGACCTTGTGAGAGAGAGGGGCTCAACGCGCTGCA	221.5
OY	2236	CTGGCGGCCCAAGGGCCGGGCAACGACAGAGGATGAGACTGTGCTCAGGCAATGGGGCCCA	229.5
Db	2220	CTGGCGGCCCAAGGGCCGGGCAACGACAGAGGATGAGACTGTGCTCAGGCAATGGGGCCCA	227.7
OY	2296	CATCAACCTGAGAGACCTCAAGTTTCAAGGGCGGCGCATGAGCCCGCGCACACTTCTTGG	235.5
Db	2280	CATCAACCTGAGAGACCTCAAGTTTCAAGGGCGGCGCATGAGCCCGCGCACACTTCTTGG	233.3
OY	2356	GCGAAGCAAGACTTAG 2371	
Db	2340	GCGAAGCAAGACTTAG 2355	
RESULT 15			
AAD64329			
ID	AAD64329 standard; DNA; 2355 BP.		
XX	AAD64329;		
AC	12-FEB-2004 (first entry)		
DT	Human protein kinase C-associated kinase (PKC) DNA.		
XX	Human: cellular signalling; protein kinase C-associated kinase; PKC; DIK;		
XX	RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; gene; db.		
KW			
XX			

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 1..2355
 FT /*tag= a
 FT /product= "Human PKK protein"
 XX
 PN US2003199462-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 23-APR-2002; 2002US-00128174.
 XX
 PR 23-APR-2002; 2002US-00128174.
 XX
 PA (NUNEZ/ NUNEZ G.
 PA (INOH/ INOHARA N.
 XX (MUTO/) MUTO A.
 PI Nunez G, Inohara N, Muto A;
 XX
 DR WPI; 2003-852808/79.
 DR P-PSDB; ABW02412.
 XX
 PT New nucleic acid encoding RICK3, useful in preparing a composition for
 PT inhibiting PKK induced NF-kB activation for treating hyperglycemia.
 XX
 PS Disclosure; SEQ ID NO 1; Opp; English.
 XX
 CC The invention relates to methods and compositions for modulating cellular
 CC signaling. In particular the present invention relates to protein kinase
 CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
 CC encoding such proteins. The invention further relates to the use of PKK
 CC and RICK3 proteins in modulating NF-kappaB signaling. Nucleic acid
 CC molecules of the invention are useful in preparing a composition for
 CC inhibiting PKK induced NF-kappaB activation for treating hyperglycemia.
 CC The invention is also used in gene therapy. The present sequence is human
 CC PKK DNA
 XX
 SQ Sequence 2355 BP; 462 A; 740 C; 762 G; 391 T; 0 U; 0 Other;
 Query Match 60.2%; Score 2325.6; DB 10; Length 2355;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2350; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 437 CACCTGACCTCAAGCCCGGAAATCTCTGTGATGCCCACTACACGTCGAAGTTTCT 496
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 Db 421 CACCTGACCTCAAGCCCGGAAATCTCTGTGATGCCCACTACACGTCGAAGTTTCT 480
 QY 497 GATTTTGGTCTGGCCAAGTGCAGAGGCTGTCCCATCTGCATGACCTCAGCATGATGCG 556
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 Db 481 GATTTTGGTCTGGCCAAGTGCAGAGGCTGTCCCATCTGCATGACCTCAGCATGATGCG 540
 QY 557 CTGTTTGGCAATCGGCTTACCTCCCTCCAGAGGCACTCAGGGAAGAGCCGCTCTTC 616
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 Db 541 CTGTTTGGCAATCGGCTTACCTCCCTCCAGAGGCACTCAGGGAAGAGCCGCTCTTC 600
 QY 617 GACACCAAGCAGATGATACAGCTTTCATCTGATGAGGCGCTGTCCACAGAG 676
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 Db 601 GACACCAAGCAGATGATACAGCTTTCATCTGATGAGGCGCTGTCCACAGAG 660
 QY 677 AAGCGTTTGCAGATGAGAGAACATCTCTGCATCATGTGTGAAGGTGTGAAGGCCAC 736
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 Db 661 AAGCGTTTGCAGATGAGAGAACATCTCTGCATCATGTGTGAAGGTGTGAAGGCCAC 720
 QY 737 CGCCCGAGCTGCGCGCGGTGTGCAGAGCCCGCGCGGCTTGCAGCACTGTATACG 796
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 Db 721 CGCCCGAGCTGCGCGCGGTGTGCAGAGCCCGCGCGGCTTGCAGCACTGTATACG 780
 QY 797 CTGATGACAGCGTGTGCAAGGAGATCCGAGATTAGGCCCATCTTCAAGAAATTACT 856
 |||||
 Db 781 CTGATGACAGCGTGTGCAAGGAGATCCGAGATTAGGCCCATCTTCAAGAAATTACT 840
 QY 857 TCTGAATCCGAGACTGTGTGAATAAGCTGTATGACAGATGAAGAAATCTGTCATGAT 916
 |||||
 Db 841 TCTGAATCCGAGACTGTGTGAATAAGCTGTATGACAGATGAAGAAATCTGTCATGAT 900
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 Db 901 CTGACAGTGAATAAGCCCGCGAGCCAGAGAGCAGAGGTGTGCTGCGAGGCTCAAGCG 960
 QY 977 GCCTGTGCCCCACCTTGATGATACGATACAGCTCTCCAGCTTCTCAACAGTGAAC 1036
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 Db 961 GCCTGTGCCCCACCTTGATGATACGATACAGCTCTCCAGCTTCTCAACAGTGAAC 1020
 QY 1037 TCTGAGTTTCCAGGCTGTGAGAGGCCCGAGAGGCTCAGCCGCACTCTCTGATGCC 1096
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 Db 1081 AAGCTGCATGTCCGAGAGGAGAGAGGCTCTCGGAGGAGTCTCGATGAGCACTCCGCC 1140
 QY 1157 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCAACCAAGCATCTG 1216
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 Db 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCAACCAAGCATCTG 1200
 QY 1217 GGTACCAAGAGCTTCCAGAAAGAAAGCTTGTGATGCCATCTGTGTCC -GGACACCAAG 1275
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 Db 1201 GGTACCAAGAGCTTCCAGAAAGAAAGCTTGTGATGCCATCTGTGTCCGGGGAACACCAAG 1259
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 Db 1320 CCGTGTGACCTTGGCGGTGTGAGAGCGCGGCAAGAGATGCGCAAGTGGCTGTCTCAA 1379
 QY 1396 CAATGCCAACTCCAACTGTAGCAACCTGTAGGGGCTCCACCCGTTTGACATGCGCGTGA 1455
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 Db 1380 CAATGCCAACTCCAACTGTAGCAACCTGTAGGGGCTCCACCCGTTTGACATGCGCGTGA 1439
 QY 1456 GAGAGGGTGTGGGGTGTGCTGTGAGCTCTCTGCTGCAACGGAAGATCACTGTCAACGCGCAA 1515
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 Db 1440 GAGAGGGTGTGGGGTGTGCTGTGAGCTCTCTGCTGCAACGGAAGATCACTGTCAACGCGCAA 1499
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Db 1500 GATATGAGACGATGACAGCCCTTCACTTTCAGCCAGAACGAGGACGATCTAGCAC 1559
QY 1576 ACGGCTGCTGTTGAGAGAGAACGCTCGTCAACGAGGTGACTTTGAGGGCCGAGCGCC 1635
Db 1560 ACGGCTGCTGTTGAGAGAGAACGCTCGTCAACGAGGTGACTTTGAGGGCCGAGCGCC 1619
QY 1636 CATGCACTGTCCTGCGACGAGGAGAGATATCGTGGCATCTGCTGCGCGAGG 1695
Db 1620 CATGCACTGTCCTGCGACGAGGAGAGATATCGTGGCATCTGCTGCGCGAGG 1679
QY 1696 CGTGAACGTGACCTGACAGGGAGATGCTGGCTGGCCACTAGCTGCTGGCA 1755
Db 1680 CGTGAACGTGACCTGACAGGGAGATGCTGGCTGGCCACTAGCTGCTGGCA 1739
QY 1756 GAGCCACCTGCCATCGTCAAGCTGTGGCAAGCAGCCGGGGGTGAGTGTGACGCCA 1815
Db 1740 GAGCCACCTGCCATCGTCAAGCTGTGGCAAGCAGCCGGGGGTGAGTGTGACGCCA 1799
QY 1816 GACGCTGATGAGAGAGACGCAATTGCACTGGCCGCAAGCCGGGGCACTACCGCTGGC 1875
Db 1800 GACGCTGATGAGAGAGACGCAATTGCACTGGCCGCAAGCCGGGGCACTACCGCTGGC 1859
QY 1876 CCGCATCTCATGCACTGTGCTCCGACGTTCAACGTTGCAAGCTGCTGGCAAGACACC 1935
Db 1860 CCGCATCTCATGCACTGTGCTCCGACGTTCAACGTTGCAAGCTGCTGGCAAGACACC 1919
QY 1936 CCGCATCTGAGCCGAGAGACGGGGCAACGAGCACTGCAAGCTGCTGCTGATGGGG 1995
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QY 1996 CCGTGGCAAGAGGCGGTGACTCAGACGAGCTACCGCTCTGCACTTGGCTGCGCAA 2055
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QY 2056 CCGACACCTGGGCCACTGTCAAGCTGTTGAGAGAGAGCCGATGTGCTGGCCGGGG 2115
Db 2040 CCGACACCTGGGCCACTGTCAAGCTGTTGAGAGAGAGCCGATGTGCTGGCCGGGG 2099
QY 2116 ACCCTGAACAGACGGGCTGCACTGGCTGCGCCACGGGCACTCGAGGTGTGGA 2175
Db 2100 ACCCTGAACAGACGGGCTGCACTGGCTGCGCCACGGGCACTCGAGGTGTGGA 2159
QY 2176 GAGTTGTCAAGGCGGATGTCAATTGACTTGTGACGAGCAGGGGCTCAGCGCTGCA 2235
Db 2160 GAGTTGTCAAGGCGGATGTCAATTGACTTGTGACGAGCAGGGGCTCAGCGCTGCA 2219
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Db 2220 CCGGCGGCGCCAGGCGCGGACGCAAGAGGTGAGACTGCTCAGGCTAGGGGCCCA 2279
QY 2296 CATCAACTGCAAGGCTCAAGTTCCAGGGCGGCACTGGCCCGCCGCCACACTCTGCG 2355
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QY 2356 GCGAGCAAGACCTAG 2371
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Search completed: September 15, 2005, 18:09:52
Job time : 1879.97 secs

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 genomic survey sequence.
 ACCESSION AY419490
 VERSION AY419490.1 GI:39775447
 KEYWORDS GSS.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 REFERENCE
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE
 Inferred nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302

REFERENCE 2 (bases 1 to 2173)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT
 These sequences were made by sequencing genomic exons and ordering
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 Db 61 CTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 QY 319 GGGCTCCTGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
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Qy	1039	TGGAGTTTCCAGAGGTTCGAGGGCCCGAGAGGCTCAGCGGACCTCTGAGTCCAA	1098
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Db	AY419491	Pan troglodytes ANRD3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	
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GSS.			
Qy	Pan troglodytes (chimpanzee)		
Db	Pan troglodytes		
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Db	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
Qy	REFERENCE		
Db	1 (bases 1 to 1901)		
Qy	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.		
Db	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
Qy	JOURNAL		
Db	Science 302 (5652), 1960-1963 (2003)		
Qy	PUBMED		
Db	14671302		
Qy	REFERENCE		
Db	2 (bases 1 to 1901)		
Qy	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.		
Db	Direct Submission		
Qy	JOURNAL		
Db	Submitted (16-NOV-2003) Celera Genomics, 45 west Gude Drive, Rockville, MD 20850, USA		
Qy	COMMENT		
Db	These sequences were made by sequencing genomic exons and ordering them based on alignment.		
Qy	FEATURES		
Db	source		
Qy	gene		
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gene tries
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2173)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
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Best Local Similarity 84.2%; Pred. No. 0;
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Qy 1458 GGAAGGTGCGGGGTGTGTGAGAGCTCTGCTGAGCAGAGATCAAGTGTCAAGCGCAAGG 1517
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Db		1920	CCCTGAATTCAGACAGCACTGTGACCTGGCTGTGCTGCCCTGGACATCAGAGGTGTATAAG	1979
OY		2178	AGTTGGTCAGGCGCGATGTCTCAATTCAGCTGTTCACAGACAGAGGGGCTCAGCGCTGTGACC	2237
Db		1980	AGCTGTGATGATGCTGACCTCACTTAATCCTGTCTGATGAGACAGGGGCTCAGCGCACTGACCC	2039
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Db		2040	TGGCTGTCTCAGGGCAGGCGATTCAACAGACTGTGGAGACACTGCTCTCAACATGACACACACA	2099
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ACCESSION VERSION KEYWORDS SOURCE		AK077233.1	GI:26097247	
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		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE				
AUTHORS		Carninci,P. and Hayashizaki,Y.		
TITLE		High-efficiency full-length cDNA cloning		
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE		99279253		
PUBMED		10349636		
REFERENCE				
AUTHORS		2		
		Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,		
		Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
		Normalization and subtraction of cap-trapper-selected cDNAs to		
		prepare full-length cDNA libraries for rapid discovery of new genes		
		Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL		20499374		
MEDLINE		11042159		
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		Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P.,		
		Komno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,		
		Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,		
		Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K.,		
		Fujitake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M.,		
		Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,		
		Okazaki,Y., Muramatsu,M., Inoue,Y., Kite,A. and Hayashizaki,Y.		
		Riken integrated sequence analysis (RISA) System--384-format		
		sequencing pipeline with 384 multicapillary sequencer		
		Genome Res. 10 (11), 1757-1771 (2000)		
JOURNAL		20530913		
MEDLINE		11076861		
PUBMED				
REFERENCE				
AUTHORS		4		
		The RIKEN Genome Exploration Research Group Phase II Team and the		
		PANTOM Consortium.		

REFERENCE	TITLE	AUTHORS	JOURNAL	COMMENT	FEATURES
Functional annotation of a full-length mouse cDNA collection					
Nature 409, 685-690 (2001)					
5	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
Nature 420, 563-573 (2002)					
6 (bases 1 to 3741)					
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Hayashida, K., Hayatsu, N., Hiramatsu, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramatsu, T., Hara, A., Hashizume, W., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kondo, M., Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, Y., Nishii, K., Nomura, K., Numasaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazawa, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.					
Submitted (16-APR-2002)					
Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)					
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.					
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.					
Please visit our web site for further details.					
URL: http://genome.gsc.riken.jp/					
URL: http://fantom.gsc.riken.jp/					
Location/Qualifiers					
1..3741					
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/db_xref="taxon:10090"					
/clone="5031407D20"					
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/dev_stage="11 days pregnant adult"					
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ORIGIN					
misc_feature					
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Best Local Similarity	83.0%	Pred. No. 0;			
Matches 1884;	Conservative	0;	Mismatches 373;	Indels 13;	Gaps 6
191	GACGACGAGGAGCCATGAGACTTTTGGAAAGAACCAAGATGAGATGCCAAGTTT	250			
406	GACTTAAAGGAAACAAATGAGCTCTCTGAGGAGAACTTAAAGATGAGATGCCAAGTTT	465			
251	CGTACATCTGCTGCTGTATGATGAGATCTGCGCGAACCCTGTGCGCTGTCTATGAGATAC	310			
466	CGATACATTTTACCTGCTGTATGAGGCAATATGACAGAAACCTGTGCGCTGTCTATGAGATAC	525			
311	ATGAGAGAGGCTCTCTGGAAGAAACCTGTGCTCTGAGGCAATGAGATGAGATCTCGG	370			
526	ATGAGAGAGGCTCTCTGGAAGAAACCTGTGCTCTGAGGCAATGAGATGAGATCTCGG	585			
371	TTTGGATCATCAACGAGACGCGCGTGGGACATGAACTTCTGCACTGAGATGCCCGGCA	430			
586	TTTGGATCATCAACGAGACGCGCGTGGGACATGAACTTCTGCACTGAGATGCCCGGCA	645			

QY 431 CTCCTGCACTTGAAGCCGCGAACAATCTGCTGANTGCCCCACTACAGTCAAG 490
DB 646 CTGCTGCACTTGAAGCCGCGAACAATCTGCTGANTGCCCCACTACAGTCAAG 705
QY 491 ATTTCTGATTTTGTCTGCGCAAGTGAACAGGCTGTCCACTCGCATGACTCAGCATG 550
DB 706 ATTTCTGACTTTGGCTGGCCAGTGAATGGCAATGCTCCACTCTCATGACCTCAGCATG 765
QY 551 GATGCGCTGTTTGGCAATGCTCTACTCTCCAGAGCGCATGAGGAGAGAGCCGG 610
DB 766 GATGCGCTGTTTGGCAATGCTCTACTCTCCAGAGCGCAATCTGAGAGAGCGCG 825
QY 611 CTCTTGCACCAAGCAGATGATATACGCTTTGCGATGCTATGAGGAGGCTGCTCA 670
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DB 1185 CGCTCAAGCGGGGCTTGCAGCCCACTTGCATACGACTACAGGCTTCCGAGTGTCTG 1244
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QY 1265 -CGGACACCGAGCAATGATGATGATCTGAGCGCAGAGCGTGTGAGCTGTGGA 1323
DB 1484 AGGGAGCAACAGCAGAGCTGATGAATCTTACAGCCCAAGATGTGACTTGTGTGA 1543
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QY 1683 TGCTGCGCGAGAGCGTGAAGCTGAGCTGCAAGGCAAGATGCTGTGCTGCACTGCACT 1742
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QY 1743 AGCTGCTGTGCAAGGCGCACTGTCCATCTGCAAGCTGTGCGCAAGAGCTCGGGGTGA 1802
DB 1964 ATGCTGCTGTGCAAGGCGCACTTCCATTTGAAGCTGTGAGCAAGCAGCTGGGGTGA 2023
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DB 2024 GTGTGAATGCCCAAGCACTGAAGGAGAGACCCCTGCACTGTGCTGAGAGGGGC 2083
QY 1863 ACTACCGGTGAGCCCGCATCTCATGCACTGTGCTCGAGCTGCAAGCTGTGCAAGCTGTG 1922
DB 2084 ATTAACCGTGTGCTGTGCAATTTCTGATTGACCTGTGCTGTGATGTTAAACATGTGAGCGCTAC 2143
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DB 2144 AGGCAACAGACCTTCTCATGTTGCTGCAAGAGTGAACACATGATGCTGCGAGGCTAC 2203
QY 1983 TCTGCAATCGGGGGGCTGTGCAAGAGGCGGTCGCTGCAAGAGCTGCAAGCTGTGCAAGC 2042
DB 2204 TCTTGCATCTGTGTGTGTGTGCAAGAGGCTTTGACTCAGAGAGGCTTAATCTGCTTGCAC 2263
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DB 2264 TGGCAGGCGCAAGATGGAACCTGTGCTGTGCAAGCTGTGCTGTGAGAGAGGCTGTAG 2323
QY 2103 TGTGTGCGCGGGGAGCCCTTGAACAGAGCGGCTGTGCACTGTGCTGCGGCCAGCT 2162
DB 2324 TGTGTGCTGCGGGGTGCTGCTGATGACAGAGCTGTGCACTGTGCTGCGGCCAGCT 2383
QY 2163 CGAGGTGTGGAAGATGTGTGTGAGCGCGCATGTCAATGACCTGTGTGAGCAGAGAGGGC 2222
DB 2384 CAGAGGTGTGAAGAGCTGTGTGAGTGTGACTTGTGACTTGTGTGATGAGAGGGCC 2443
QY 2223 TCAGCGCGCTGCACTGTGCGCGCCAGAGGCGCGCAACGACAGAGGTGAGACTGTCTCA 2282
DB 2444 TCAGCGCACTGTGCACTGTGCTGTGAGGGAGGCAATTCAGACTGTGAGAGCACTGTCTCA 2503
QY 2283 GGCATGGGGCCCAATCACTGTGCAAGCTTCAAGTTTCAAGGGGGGCTATGGCCCGCG 2342
DB 2504 AACATGAGCAACATCACTGTGCAAGTCTCAAGTTTCAAGAGGCGCAAGGCTGTGTG 2563
QY 2343 CCACATCTGTGCGGAGAGCAAGCACTGTGCTGTGCTGTGCGAGAGACGGGGGTCCAGT 2402
DB 2564 CCAGTGTCTTCCAGCGCAGAGACTGAGT---TGCACCACAAAACAGAGGCTCGGTG 2620
QY 2403 GGGGCTTGTGTCTGTGTGTGTGTCTGTGTGGAGTGAAGAGATCTGTGCG 2452
DB 2621 TAGGCTTGTGAACATCTTGTGTCTGTGTGAGGAGAGAAATGTCTGTGG 2670

RESULT 6
BM924233 1119 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6630417 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760485
DEFINITION 5', mRNA sequence.
ACCESSION BM924233
VERSION BM924233.1 GI:19374612
KEYWORDS EST.

QY 428 CCACTCTGCACTGGACTCAAGCCCGGCAATCTGTCTGATGSCCACTACCAAGTC 487

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

QY 3695 TTCATGCGAGAAATATCCAAAGCTGTGAAACTGGCTATGTTTAAATATGCTCATGT 3754
|
|
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Db 161 TTCATATGCGAGAAATATCCAAAGCTGTGAAACTGGCTATGTTTAAATATGCTCATGT 102
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QY 3755 GCGTTTACCTGTTGTGTGACCTGCGTAGGAGGACCAAGATGTCATTTGATGTCATTAAGC 3814
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Db 101 GCGTTTACCTGTTGTGTGACCTGCGTAGGAGGACCAAGATGTCATTTGATGTCATTAAGC 42
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QY 3815 AAAGTACTTGCTTACTTTTGTGAACTGAAAAAATGAAAAAATGAAAAAATGAAAAA 3855
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RESULT 10
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LOCUS 56053082H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630278
ACCESSION CD630278.1 GI:40278544
VERSION
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Pu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Pu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source 1..716
/organism="Homo sapiens"
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/clone_lib="FLP"
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Matches 697; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Db 16 GCTGCAAGAGAGCGGTGACCTCA-GAGGGCTACACCGCTCTGCACTGGCTGCCGCGAA 75
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QY 2056 CGACACCTGGCGCACTGTCAAGCTGTTGTCAGAGAAAGCCGATGTCCTGGCCGCGG 2115
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Db 76 CGACACCTGGCGCACTGTCAAGCTGTTGTCAGAGAAAGCCGATGTCCTGGCCGCGG 135
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QY 2116 ACCCTGAAACCAAGAGCGCTGCACTGCTGCCGCCCACTGGAGAGTGTGTGA 2175
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QY 2236 CCTGGCCGCCCGAGCGCGCGAGCAAGAGCGTGAAGTCTGCTCAGGATGAGGAGCA 2295
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QY 2416 TGTCTGTGTCTCTGTGAGAGATGAACGATCTGCTGAGGAGCCCGCTGTGCTTAACT 2475
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Db 496 AAATGTTAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 555
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QY 2536 TGTCCCTCCAGGTGAAGTGTGCTCAGATGACATGTCGCTCCATCATGATCAGTACGCA 2595
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|
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RESULT 11
LOCUS BM979316/c 705 bp mRNA linear EST 21-FEB-2003
DEFINITION UI-CF-DUI-adr-o-17-0-UI.s1 UI-CF-DUI Homo sapiens cDNA clone
UI-CF-DUI-adr-o-17-0-UI 3', mRNA sequence.
ACCESSION BM979316
VERSION BM979316.1 GI:19599640
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 705)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Ogen Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.
FEATURES
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/organism="Homo sapiens"
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/dev stage="Adult"
/lab_host="MDH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Scov I; Site 2: Not I;
UI-CF-DUI is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells The

library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is GACTGTAGC.
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-DUI
TAG_SEQ=GACTGTAGC"

ORIGIN

Query Match 17.6%; Score 680.8; DB 5; Length 705;
Best Local Similarity 99.3%; Pred. No. 2.4e-157;
Matches 693; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB TTTAAATTCCTCTTGTAACTCAGTGTGGGAGCTGAGGCGGACCCCTCAGGTCCG 640
QY 3221 TGAAGTGCACCACTCTTGGGAGAGGTGAGGAGAGGCTGTCTTTATCTCCACAG 3280
DB TGAAGTGCACCACTCTTGGGAGAGGTGAGGAGAGGCTGTCTTTATCTCCACAG 581
QY 3281 CAGTATGAGATGAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGTATGAT 3340
DB CAGTATGAGATGAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGTATGAT 521
QY 3341 GCACTGCTCAGCTGACACCTTCCAGCTCATTTTGTAGGTGATTTGGATAGGAT 3400
DB GCACTGCTCAGCTGACACCTTCCAGCTCATTTTGTAGGTGATTTGGATAGGAT 461
QY 3401 AGCTTTTGGGAGTATGGGGGAGGTCTTGCACCTGTTTGCAGAGTGTCTCCGACCT 3460
DB AGCTTTTGGGAGTATGGGGGAGGTCTTGCACCTGTTTGCAGAGTGTCTCCGACCT 401
QY 3461 CAGCAGTTTGGGAGTGTGGCCCGAGGCGGTTCTTGTGATGTAAGAATGTGGCCATCTAGC 3520
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QY 3521 CTGCTAACTTCACTGTCACCTGTGTCCATAGGGTCTTGTGAATCTGTATTGAT 3580
DB CTGCTAACTTCACTGTCACCTGTGTCCATAGGGTCTTGTGAATCTGTATTGAT 281
QY 3581 AAGTTTGTGCAAGCGTACCTGCGTGAACAATGTACCGTGGCTGTATATGATAG 3640
DB AAGTTTGTGCAAGCGTACCTGCGTGAACAATGTACCGTGGCTGTATATGATAG 221
QY 3641 AGATTGATTAATTAATGACATGATGTTAATGTAATCTGTGGGAGAGATCTTTCCAT 3700
DB AGATTGATTAATTAATGACATGATGTTAATGTAATCTGTGGGAGAGATCTTTCCAT 161
QY 3701 GGCAGGAATATATCAAGCTGTGAACTGTGCTAATGTTTAATATGCTCATGTGCTTT 3760
DB GGCAGGAATATATCAAGCTGTGAACTGTGCTAATGTTTAATATGCTCATGTGCTTT 101
QY 3761 ACTGTTGTGTGACGTGTGAGGAGCAAGAGTTCCATTTGATGTAATTAACCAAGTA 3820
DB ACTGTTGTGTGACGTGTGAGGAGCAAGAGTTCCATTTGATGTAATTAACCAAGTA 41
QY 3821 CTGCTCACTTTTGTGAAGCTGAAAAAATTTTAAAAA 3858
DB CTGCTCACTTTTGTGAAGCTGAAAAAATTTTAAAAA 3

RESULT 12 685 bp mRNA linear EST 11-OCT-2001
BI688710
LOCUS BI688710
DEFINITION 6033904P1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402051 5',
mRNA sequence.

ACCESSION BI688710 GI:16042383
VERSION BI688710.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
<http://image.jhmi.gov>
Plate: LLM12025 row: c column: 12
High quality sequence stop: 680.
Location/Qualifiers

FEATURES

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/clone="IMAGE:5402051"
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/clone_1ib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.4%; Score 671.4; DB 4; Length 685;
Best Local Similarity 99.6%; Pred. No. 5.1e-155;
Matches 684; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 2610 GGACGGTGGTCAAGATCAATTCGTTGCTCTTAATGGGCTGAGGCTGCTCTCA 2669
DB 1 GGACGGTGGTCAAGATCAATTCGTTGCTCTTAATGGGCTGAGGCTGCTCTCA 60
QY 2670 GTGATGAAGCCCGAGCGGTGAAGATCACTCTCTTGAAGCCACCTTGGGTTG 2729
DB 61 GTGATGAAGCCCGAGCGGTGAAGATCACTCTCTTGAAGCCACCTTGGGTTG 120
QY 2730 CTGAGCTCAACAGTCTTGAAGGAGGTGAGGAGAACTGTCTTTTATCTTCAATCAT 2789
DB 121 CTGAGCTCAACAGTCTTGAAGGAGGTGAGGAGAACTGTCTTTTATCTTCAATCAT 180
QY 2790 GACGGTGGCAGAGAGGCTGTCTTAAAGTTCCATGAAATGTTTATTAATAATCTTA 2849
DB 181 GACGGTGGCAGAGAGGCTGTCTTAAAGTTCCATGAAATGTTTATTAATAATCTTA 240
QY 2850 AGAGATGATATACCTTATCAGCTGTGCTGAAACCTGTTAAAAATGTTATTAATGGA 2909
DB 241 AGAGATGATATACCTTATCAGCTGTGCTGAAACCTGTTAAAAATGTTATTAATGGA 300
QY 2910 TAGCTAGTCTTAAATGATGCTAATGATGAGGCTTGTGAAACAAATGTTTATG 2969
DB 301 TAGCTAGTCTTAAATGATGCTAATGATGAGGCTTGTGAAACAAATGTTTATG 360
QY 2970 CAAAGAGAAAGAAATGTAGCAGCAGCTTGGGGGCGTATGTGCGCAGCTCTTAAC 3029
DB 361 CAAAGAGAAAGAAATGTAGCAGCAGCTTGGGGGCGTATGTGCGCAGCTCTTAAC 420
QY 3030 CATTCAGTCTATTAATCTTGGTGAAGTCTTGTGACCAACACACACAGTGGCCACATGG 3089
DB 421 CATTCAGTCTATTAATCTTGGTGAAGTCTTGTGACCAACACACACAGTGGCCACATGG 480

OY	3090	TACTAGCGCCGGTGTGTTCTTCGTGCCTAAGAATTTTTGGCACTCAGAGCCACAGC	3148
Dd	481	TACTAGCTGCCGTTCTGTTCTTCGTGCCTAAGATTTTTGGCACTCAGAGCCACAGC	540
OY	3150	CTAAGAGTCATTAAAAAAATTCCTCCCTTGTAACCTCAGTGTCTGGGACTGAGCGAGCC	3208
Dd	541	CTAAGAGTCATTAAAAAAATTCCTCCCTTGTAACCTCAGTGTCTGGGACTGAGCGAGCC	600
OY	3210	CCTCAGGTGCGCTGGAGGTGCAACAAGTCTTGGGGAAAGAAGTCAGAGAAAGCTGTGTTTTT	3268
Dd	601	CCTCAGGTGCGCTGGAGGTGCAACAAGTCTTGGGGAAAGAAGTCAGAGAAAGCTGTGTTTTT	658
OY	3270	ATCTCACACGCGCATATGATAAGATAAAA	3296
Dd	659	ATCTCACACGCGCATATGATAAGATAACA	685

RESULT 13

LOCUS B1868794 665 bp mRNA linear EST 11-OCT-2003
DEFINITION G03391950F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:5402052 5',
mRNA sequence.

ACCESSION	BI868794	GI:16042467
VERSION	BI868794.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 665)
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Place: LHAM12025 row: c column: 13
High quality sequence stop: 663.

FEATURES	Location/Qualifiers
source	1. .665

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/organism="Homo sapiens"
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/clone="IMAGE:5402052"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NIH MGc 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH MGc library."

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ORIGIN

Query Match	17.2%;	Score 665;	DB 4;	Length 665;
Best Local Similarity	100.0%;	Pred. No. 2e-153;		
Matches 665;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Db	1	GGACCGTGGGTGAGATCATTTGCTGTGCTCTAAATGGGTGCTGAGGCTGGTCTCTCA	60
Qy	2670	GTGATGAGACCCGAGCGCTGGAAGCATCTCTCTCTGAGGCGAGCCACTTGGGTG	2725
Db	61	GTGATGAGACCCGAGCGCTGGAAGCATCTCTCTCTGAGGCGAGCCACTTGGGTG	120

QY	2730	TTGAGAGCTCACCACTCTTGGAGGAGGAGGAGGAGGAGAACTGGTCTTTTATCTTCATCAT	278
Db	121	CTGAGAGCTCACCAAGTCTTGGAGGAGGAGGAGGAGGAGAACTGGTCTTTTATCTTCATCAT	180
QY	2790	GACGATGGGCGAGAGAGGCGCTGTCTTAAAGTTCCATGGAATGTGTTTATATAAATATCTTA	2849
Db	181	GACGATGGGCGAGAGAGGCGCTGTCTTAAAGTTCCATGGAATGTGTTTATATAAATATCTTA	240
QY	2850	AGAGATGAAATCCTTATCAGCTGTGCTTGAAACCTGTATAAATGTTTCATTAACATTGGA	2909
Db	241	AGAGATGAAATCCTTATCAGCTGTGCTTGAAACCTGTATAAATGTTTCATTAACATTGGA	300
QY	2910	TAGCTAGTGTCTTAATAGATGGAGCTAAGAGAGGAGTTGGCTTTGAAAAAACAATGTTTATG	2969
Db	301	TAGCTAGTGTCTTAATAGATGGAGCTAAGAGAGGAGTTGGCTTTGAAAAAACAATGTTTATG	360
QY	2970	CAACAAGGAACGAATGTGTAGCAGCGAGCTTTGACGAGGAGTATGTGTGGCCAGCTTTAAC	3029
Db	361	CAACAAGGAACGAATGTGTAGCAGCGAGCTTTGACGAGGAGTATGTGTGGCCAGCTTTAAC	420
QY	3030	CATTCAGATCTAATTACTTGGGTGAGTCTTGTGGAACAACAACAACAGCTGCCACATGG	3089
Db	421	CATTCAGATCTAATTACTTGGGTGAGTCTTGTGGAACAACAACAACAGCTGCCACATGG	480
QY	3090	TACTAGAGCGCGGTTCGTTTCGATGGCCTAAGATGTTTGGCAACTCTAGAGCCACAGCG	3149
Db	481	TACTAGAGCGCGGTTCGTTTCGATGGCCTAAGATGTTTGGCAACTCTAGAGCCACAGCG	540
QY	3150	CTAAGAGATCATTAATAAAATTTCTCCCTTGTGAACCTCAGTGTGGGGAATGAAGGCGAGCC	3209
Db	541	CTAAGAGATCATTAATAAAATTTCTCCCTTGTGAACCTCAGTGTGGGGAATGAAGGCGAGCC	600
QY	3210	CCTCAGATCGCTGAGAGTCAACCAAGCTTTGGGGAAGAAGTGCAGAGGAAGCTGTGTTTTT	3269
Db	601	CCTCAGATCGCTGAGAGTCAACCAAGCTTTGGGGAAGAAGTGCAGAGGAAGCTGTGTTTTT	660
QY	3270	ATCTC 3274	
Db	661	ATCTC 665	

RESULT 14

LOCUS	830 bp	mrna	linear	EST 24-JAN-2001
DEFINITION	602300806F1 NIH_MGC_87 Homo sapiens CDNA	clone IMAGE:4402320	5'	
	mrna sequence.			

ACCESSION	BC031653
VERSION	BC031653.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 830)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

CDNA library Preparation: Life Technologies, Inc.
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM0110 row: 1 column: 01
High quality sequence stop: 646.

FEATURES	Location/Qualifiers
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1. .830
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/mol_type="mRNA"
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 /lab_host="MDH10B (phage-resistant)"
 /clone_lib="NIH MGC 87"
 /note="Organ: breast; Vector: PCMV-Spore; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 16.9%; Score 651.2; DB 4; Length 830;
 Best Local Similarity 93.8%; Pred. No. 5.6e-150;
 Matches 765; Conservative 0; Mismatches 43; Indels 8; Gaps 8;

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61 GGCACCTGACAGCGCGGTGCGACCTGCTGACCTGGCGGTGAGAGCCCGGACAGAGAGT 120
1374 GGGCCAAAGGCGTCTGCTCAACATGCAACCCCAACCTGAGCAACGCTAGGGGCTCA 1433
121 GCGCAAGTGGCTGCTGCTCAACATGCAACCCCAACCTGAGCAACGCTAGGGGCTCA 180
1434 CCCGTCGACATGAGCCGTGAGAGAGGAGTGGGAGTGTCTGTGAGTCTCTGCTGAC 1493
181 CCCGTCGACATGAGCCGTGAGAGAGGAGTGGGAGTGTCTGTGAGTCTCTGCTGAC 240
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241 GGAAGATCATGTCTCAACGCCAAGATGAGAGCAAGTGAACAGCCTTCCACTTTCAGCC 300
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301 AAGAAGGAGATGATGCTAGACACAGCGCTGCTGTGAGAAAGACGCTGCTCAAGAG 360
1614 TGGAATTTGAGGGCCGACGCGCATGACAGTGGCTGCGACGACGAGGAGAAATATG 1673
361 TGGAATTTGAGGGCCGACGCGCATGACAGTGGCTGCGACGAGGAGGAGAAATATG 420
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1734 CACTGACATACGCTGCTGCGAGGCGACCTGCGCATGCTCAAGCTGCGCAAGCAGC 1793
481 CACTGACATACGCTGCTGCGAGGCGCA-CTGCCATTCGTCAAGCTGCTGCG-CAAGCAGC 538
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599 CAGCGGGGACATACGCGGTGCG-CCGATTCATCATGACCTGTGCTCGACGTCGCAAGT 657
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1970 ACTGCAAGGCTGCTCTGATCTGAGTGGGGGCGCTGAGCAAGAGGCGCTGACGCTTAC 2029
718 ACTGCAAGGCTGCTCTGATCTGAGTGGGGGCGCTGAGCAAGAGGCGCGACGCTTCCAGACGGT 777
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778 ACCCGTTTGGCCCTGCTGTCGCGAAGCGGCACTG 813

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RESULT 15

BM980861/c
 LOCUS 657 bp mRNA linear EST 21-FEB-2003
 DEFINITION UI-CF-EN1-ade-1-02-0-UI.161 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-ade-1-02-0-UI 3', mRNA sequence.
 ACCESSION BM980861
 VERSION BM980861
 KEYWORDS BM980861.1 GI:19602752
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 657)
 TITLE Bernaldo, M.F., Lennon, G., and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704447
 PUBMED 8889548

COMMENT
 Contact: McCray, PB

McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
 source location/Qualifiers

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 /db_xref="taxon:9606"
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 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
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 /dev_stage="Adult"
 /lab_host="MDH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EN1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was ligated to an EcoR I adaptor, digested with Not
 I, and cloned directionally into pT7T3-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CTGCTCAGCT.
 TAG TISSUE=Human Lung Epithelial Cell lines untreated LPS
 6hr to LPS 24h
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 TAG_SEQ=CTGCTCAGCT"

ORIGIN

Query Match 16.8%; Score 649.6; DB 5; Length 657;
 Best Local Similarity 99.2%; Pred. No. 1.3e-149;
 Matches 652; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 3541 TGTGTCCCATAGGAGTGTCTGATATCTGTATTAAGATTAAGTTTGTGCAAGACGTGA 3600
 QY 3601 CCTGTGCGCAACATGATACCGTGTCTGTATATGATAGATTTGATTAATTAAGTCA 3660
 DB 3601 CCTGTGCGCAACATGATACCGTGTCTGTATATGATAGATTTGATTAATTAAGTCA 3660
 QY 3661 TGTATGTTAATGTAATCTGTGCGCAGAGTACTTTTCCATGCGCAGAAATATCCAGCTG 3720
 DB 3661 TGTATGTTAATGTAATCTGTGCGCAGAGTACTTTTCCATGCGCAGAAATATCCAGCTG 3720
 QY 3721 TTGAACCTGCTATGTTTTATATATGCTCAATGTCCTTTAATGTTGTGTGACTGCGTG 3780
 DB 3721 TTGAACCTGCTATGTTTTATATATGCTCAATGTCCTTTAATGTTGTGTGACTGCGTG 3780
 QY 3781 AGGACCAAGAGTTCATTTGATGTCAATTAAGCAAGATCTTGTCTTATTTTGAANC 3840
 DB 3781 AGGACCAAGAGTTCATTTGATGTCAATTAAGCAAGATCTTGTCTTATTTTGAANC 3840
 QY 3841 TGAATAAAAAAAAAAAGG 3860
 DB 3841 TGAATAAAAAAAAAAAGG 3860

RESULT 2
 US-09-949-016-1103
 ; Sequence 1103, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 1103
 ; LENGTH: 3879
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-1103

Query Match 98.6%; Score 3804.2; DB 4; Length 3879;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 3811; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
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 DB 39 GACGTGCGGATGAGGCGAGCGGCGGAGCCCATAGGCGCTGCGTGGCACTT 98
 QY 67 CGAGCGGCGAGTTTACGCGGCTGGAAGAGTGTGCGCTTGGGCAAGTGA 126
 DB 99 CGAGCGGCGAGTTTACGCGGCTGGAAGAGTGTGCGCTTGGGCAAGTGA 158
 QY 127 CAAGTGTGCGGATGTCACCTGGAAGACTGTGCGCATCAAGTGTGCGGCGCTGCA 186
 DB 159 CAAGTGTGCGGATGTCACCTGGAAGACTGTGCGCATCAAGTGTGCGGCGCTGCA 218
 QY 187 CCGTCAAGCAAGGAGCGCATGAGCTTTTGAAGAGCAAGCAAGATGAGATGCGCA 246
 DB 219 CCGTCAAGCAAGGAGCGCATGAGCTTTTGAAGAGCAAGCAAGATGAGATGCGCA 278
 QY 247 GTTGTGCTACATCTGCTGTGTATGCAATCTGCGCGAACTGTGCGCTGTGATGA 306
 DB 279 GTTGTGCTACATCTGCTGTGTATGCAATCTGCGCGAACTGTGCGCTGTGATGA 338

Qy	307	GTACATGAGAGCGGGCTCTCCCTGGAAAAGCTGCTGGCTTCGAGACCATTTGGCATGGGATCT	366
Db	339	GTACATGAGAGAGGGGCTCTCTGGAAAAGCTGCTGGCTTCGAGACCATTTGGCATGGGATCT	398
Qy	367	CCGGTTCGCAATCATCATCAGAGCGGGCGGTGGGCATGAACTTCCCTGCACCTGCATGGACCC	426
Db	399	CCGGTTCGCAATCATCATCAGAGCGGGCGGTGGGCATGAACTTCCCTGCACCTGCATGGACCC	458
Qy	427	GCCACTCTGCACCTTGGACCTTCAGAGCCCGAGAACATCTCTGCTGAGTGCCTACCTACAGT	486
Db	459	GCCACTCTGCACCTTGGACCTTCAGAGCCCGAGAACATCTCTGCTGAGTGCCTACCTACAGT	518
Qy	487	CAGAATTTCTGATTTTGTGTCTGGCCAAATGCAACGGGCTGTCCCATCTGGCATGACCTCAG	546
Db	519	CAGAATTTCTGATTTTGTGTCTGGCCAAATGCAACGGGCTGTCCCATCTGGCATGACCTCAG	578
Qy	547	CATGATTTGGCTGTTTGTGGACAATGGCCCTACCTCCCTCAGAGCGCATCAGAGGAGAGAG	606
Db	579	CATGATTTGGCTGTTTGTGGACAATGGCCCTACCTCCCTCAGAGCGCATCAGAGGAGAGAG	638
Qy	607	CCGGCTCTTTCAGACCCAGAACAGATGTATACACTTTTGCGATTCGTCATCTGGGGGTGTCT	666
Db	639	CCGGCTCTTTCAGACCCAGAACAGATGTATACACTTTTGCGATTCGTCATCTGGGGGTGTCT	698
Qy	667	CACACAGAAAGAGCCGTTTTCAGATGAGAGAAACATCTTCGACATCATGTGTGAAGTGTGT	726
Db	699	CACACAGAAAGAGCCGTTTTCAGATGAGAGAAACATCTTCGACATCATGTGTGAAGTGTGT	758
Qy	727	GAAAGGCGACCGGCGCGAGCTGGCGCGGTGGAGAGCGCGGCGCGCGCGCGCTGAGCGCA	786
Db	759	GAAAGGCGACCGGCGCGAGCTGGCGCGGTGGAGAGCGCGGCGCGCGCGCGCTGAGCGCA	818
Qy	787	CCGTATACGCTTCATGACAGCGGTGTCTGGCAGGGGGGATCCGCGATTTAGGCCCATCTTCCA	846
Db	819	CCGTATACGCTTCATGACAGCGGTGTCTGGCAGGGGGGATCCGCGATTTAGGCCCATCTTCCA	878
Qy	847	AGAAATTACTTCTGAAACCGAGAGACTGTGTGTAAAGCTGTATGACGAATGTAAAGAAAC	906
Db	879	AGAAATTACTTCTGAAACCGAGAGACTGTGTGTAAAGCTGTATGACGAATGTAAAGAAAC	938
Qy	907	TGCTCATGATCTTGAAGGTGAAGAAAGCCCGCGGAGCCAGAGACGAGGTGTGTGCTGCGAG	966
Db	939	TGCTCATGATCTTGAAGGTGAAGAAAGCCCGCGGAGCCAGAGACGAGGTGTGTGCTGCGAG	998
Qy	967	GCTCAAGCGGGCTCTGCGGCCCATCTTCGATTAACGATACAGCTCTCCGAGTCTCTC	1026
Db	999	GCTCAAGCGGGCTCTGCGGCCCATCTTCGATTAACGATACAGCTCTCCGAGTCTCTC	1058
Qy	1027	ACAGCTTGAATCTTGAAGTTTCCAGAGCTGTCCAGGGCCCGAGAGCTCAGCCGAGCTC	1086
Db	1059	ACAGCTTGAATCTTGAAGTTTCCAGAGCTGTCCAGGGCCCGAGAGCTCAGCCGAGCTC	1118
Qy	1087	CTCTGATGCCAAGCTGCATCGTCGGGCGAGTGGGAAAGAGGCTCTGCGGGGTGTCTCGGT	1146
Db	1119	CTCTGATGCCAAGCTGCATCGTCGGGCGAGTGGGAAAGAGGCTCTGCGGGGTGTCTCGGT	1178
Qy	1147	GGACTCCGCTTCTCTTCAGAGGATCATCTGTCCGCTGTCTCTTTGAGCGGGAACTTTCAAC	1206
Db	1179	GGACTCCGCTTCTCTTCAGAGGATCATCTGTCCGCTGTCTCTTTGAGCGGGAACTTTCAAC	1238
Qy	1207	CAGCGATCTTGGGTACCAACAAGAGCTCCAGAGGAGAGAGCTTGTGATGTCATCGTGTCC	1266
Db	1239	CAGCGATCTTGGGTACAC-AGAAGTCCAAAGAGAGAGCTTGTGATGTCATCGTGTCCG	1297
Qy	1266	GGGACACACAGCAACTGATGGAAGATCTCTGACCGCAGACGTTGACCTTGGGACCTGGACA	1325
Db	1298	GGGACACACAACTGATGGAAGATCTCTGACCGCAGACGTTGACCTTGGGACCTGGACA	1357
Qy	1326	GCGGTGCAAGCTGTGTCAGCTTGGCGGTGAGAGCGCGGCAAGAGAGTGTGCGCAAGTGGC	1385
Db	1358	GCGGTGCAAGCTGTGTCAGCTTGGCGGTGAGAGCGCGGCAAGAGAGTGTGCGCAAGTGGC	1417
Qy	1386	TGCTGTCAACAAATGCCAACCCCAACTGAGCAACCTGTAAGGGGCTTCAACCCGTTTGACA	1445

Db	1418	TGCTGCTTACAAATGCCAACCCCAACTTGAGCAACCGTAGGGCTCCACCCCTGTGCACA	1477
QY	1446	TGGCGGTGAGAGAGAGGTGCGGGGTGTCTGAGACTCTTGTCGACGGAAATCACTG	1505
Db	1478	TGGCGGTGAGAGAGGGGTGCGGGGTGTCTGAGAGCTCTGTGTCGACGGAAATCACTG	1537
QY	1506	TCAAGCCCAAGAGATGAGAGACCAATGAGACAGGCTCTCCACTTTGACGCCCAACGGGGATG	1565
Db	1538	TCAAGCCCAAGAGATGAGAGACCAATGAGACAGGCTCTCCACTTTGACGCCCAACGGGGATG	1597
QY	1566	AGTCTAGACACAGGCTGTGTTTGGAGAGAACGCTCGATCAACGAGGTGGACTTTGAGG	1625
Db	1598	AGTCTAGACACAGGCTGTGTTTGGAGAGAACGCTCGATCAACGAGGTGGACTTTGAGG	1657
QY	1626	GCCGAGCGCCCATGCAAGTGGCGCTTGACAGCACGGGACAGAGAAATATGTGCGCATCTGC	1685
Db	1658	GCCGAGCGCCCATGCAAGTGGCGCTTGACAGCACGGGACAGAGAAATATGTGCGCATCTGC	1717
QY	1686	TGCGCCGAGCGGTGAGACTGAGGCTTGACAGGGCAAGATGCTTGCTGGCTGCATGACATACG	1745
Db	1718	TGCGCCGAGCGGTGAGACTGAGGCTTGACAGGGCAAGATGCTTGCTGGCTGCATGACATACG	1777
QY	1746	CTGCGCTGGCAGGGGCACTTGCCCATTCGTCAAGCTGTGGCCCAACAGCGGGGGGTGAGTG	1805
Db	1778	CTGCGCTGGCAGGGGCACTTGCCCATTCGTCAAGCTGTGGCCCAACAGCGGGGGGTGAGTG	1837
QY	1806	TGAAGCCGCAGACGCTGTAGTGGAGAGACGCCATTGCACTTGCGCGCAACGCGCGGGCACT	1865
Db	1838	TGAAGCCGCAGACGCTGTAGTGGAGAGACGCCATTGCACTTGCGCGCAACGCGCGGGCACT	1897
QY	1866	ACCGGTGTGGCCCGCATCTCATTCGACTGTGTCTCCGAGTCAACGTCTGCAGGCTGTCTGG	1925
Db	1898	ACCGGTGTGGCCCGCATCTCATTCGACTGTGTCTCCGAGTCAACGTCTGCAGGCTGTCTGG	1957
QY	1926	CACAGACACCCCTGACGTTGGCGCGGGAGACGGGGCACACGAGCACTGGCAGGCTGCTCC	1985
Db	1958	CACAGACACCCCTGACGTTGGCGCGGGAGACGGGGCACACGAGCACTGGCAGGCTGCTCC	2017
QY	1986	TGCATCGGGGCGCTTGACAGAGAGGCGGTGACCTTCAACGCGTACACGCTCTGCACTTGG	2045
Db	2018	TGCATCGGGGCGCTTGACAGAGAGGCGGTGACCTTCAACGCGTACACGCTCTGCACTTGG	2077
QY	2046	CTGCCCGCAACGAGACCTTGCGCACTGTGCAAGCTGTGTGTGAGAGAGAGGCCGATGTGC	2105
Db	2078	CTGCCCGCAACGAGACCTTGCGCACTGTGCAAGCTGTGTGTGAGAGAGAGGCCGATGTGC	2137
QY	2106	TGGCCCGGGGACCCCTGAAACAGACGGGCGCTGACCTTGCGCTGCGGCCACGGGCACTCGG	2165
Db	2138	TGGCCCGGGGACCCCTGAAACAGAGGCGCTGACCTTGCGCTGCGGCCACGGGCACTCGG	2197
QY	2166	AGGTGTGAGAGAGTTGGTTCAGCGCCGATGTCAATTGACCTGTTTGCACGAGCAGGGGCTCA	2225
Db	2198	AGGTGTGAGAGAGTTGGTTCAGCGCCGATGTCAATTGACCTGTTTGCACGAGCAGGGGCTCA	2257
QY	2226	GCGCGCTGCACCTGGCGCGCCACGGGCGGGCACGCAACGATGTGAGACTTGTCTCAAGC	2285
Db	2258	GCGCGCTGCACCTGGCGCGCCACGGGCGGGCACGCAACGATGTGAGACTTGTCTCAAGC	2317
QY	2286	ATGGGGGCCCAATCAACTGCAAGGCGTCAAGTTTCCAGGGGGGGCATGAGCCCGCGCGCA	2345
Db	2318	ATGGGGGCCCAATCAACTGCAAGGCGTCAAGTTTCCAGGGGGGGCATGAGCCCGCGCGCA	2377
QY	2346	CACCTCTCGCGGAGCAAGACTTGAAGCTGAGCTGCTGCGGAGACCGGGGGTCTCAAGTGGG	2405
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QY	2406	GCTCTTGTCTGTCTGTGTTCTTGTGGGGATGGAAGCATCTTGCGTGGGGCCCGCTTG	2465
Db	2438	GCTCTTGTCTGTCTGTGTTCTTGTGGGGATGGAAGCATCTTGCGTGGGGCCCGCTTG	2497
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Db      2498 TGGCTTACCTAAATGTTAAACGAAGAGAGTGAATGTCATGTCATGACGAGGCGCTGCTG 2557
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Db      2558 CTGACCGGAGTGTCCCTCCAGGTGAAGCTGCTCAGTGCACATGCCGCTCCATCATC 2617
Qy      2586 GATCTTAGGCACTGCTGCTGTAAGGGAACGCTGGCTCAGAAATCATTTCCCTGGCTCCAA 2645
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Qy      2646 TGGGTGCTGAGAGCTGTCTCTCAGTATGAAGCCCAAGCGCTGGAAGCATCACTCT 2705
Db      2678 TGGGTGCTGAGAGCTGTCTCTCAGTATGAAGCCCAAGCGCTGGAAGCATCACTCT 2737
Qy      2706 CCTGAGGCGAGCCACTTGGGTTGCTGAGCTCAACAGTCTTGAAGGAGTGCAGGGGAA 2765
Db      2738 CCTGAGGCGAGCCACTTGGGTTGCTGAGCTCAACAGTCTTGAAGGAGTGCAGGGGAA 2797
Qy      2766 ACTGCTGTTTTTATCTTCAATACATGACGCTGGGCGAAGAGGCGCTGCTTAAAGTTCCAT 2825
Db      2798 ACTGCTGTTTTTATCTTCAATACATGACGCTGGGCGAAGAGGCGCTGCTTAAAGTTCCAT 2857
Qy      2826 GGAATGTTTTTATTAATATCTTAAGAGATGAATACCTTATCAGCTGTGCTTGAACCT 2885
Db      2858 GGAATGTTTTTATTAATATCTTAAGAGATGAATACCTTATCAGCTGTGCTTGAACCT 2917
Qy      2886 GTTAAATATGTTTCAATACATTTGATAGTCTAGTCTTAAATGATGCTTAAAGTGGGT 2945
Db      2918 GTTAAATATGTTTCAATACATTTGATAGTCTAGTCTTAAATGATGCTTAAAGTGGGT 2977
Qy      2946 TGGCTTGAAGAACATGTTTTTATGCAACAAGAAAGAAATGATGAGCCAGCTTTGGCGG 3005
Db      2978 TGGCTTGAAGAACATGTTTTTATGCAACAAGAAAGAAATGATGAGCCAGCTTTGGCGG 3037
Qy      3006 GGGTATGTTGGGCACTCTTAAACATTCAGTCACTTAACTTGGGAGTCTTGTGAC 3065
Db      3038 GGGTATGTTGGGCACTCTTAAACATTCAGTCACTTAACTTGGGAGTCTTGTGAC 3097
Qy      3066 AACCAACAACGCTGCCAATGATGTAATGCTGCGCTGCTTCTGCTTGCCTAAGATGT 3125
Db      3098 AACCAACAACGCTGCCAATGATGTAATGCTGCGCTGCTTCTGCTTGCCTAAGATGT 3157
Qy      3126 TTTGGCACTCTTAGAGCCCAAGGCTTAAAGATCATTTAAATTTCCCTTGTATACCTC 3185
Db      3158 TTTGGCACTCTTAGAGCCCAAGGCTTAAAGATCATTTAAATTTCCCTTGTATACCTC 3217
Qy      3186 AGTGTGGGGAAGTGAAGGCGAGCCCTCAGGTGCTGAGTGCACAGTCTTGGGGAAGA 3245
Db      3218 AGTGTGGGGAAGTGAAGGCGAGCCCTCAGGTGCTGAGTGCACAGTCTTGGGGAAGA 3277
Qy      3246 GGTGCAAGAGAAGCTGTGTTTTTATCTCCACAGCAAGATGAAATTAATCAATAGT 3305
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Qy      3306 ATTAACCTAAGACATAGACATTAATTAAGTATGATCACTGCTCACTGCAACCTTCCCA 3365
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Db      3458 TTTCTGACCTGCTTGGCAAGTGCCTCCGACCTCAGCAAGTTTGGGATGAGGCCCAAG 3517
Qy      3486 GCGGTTCTTGGATGATAAAGATGAGCATCTAGCCCTGTAACCTTCACTGCTGCTGT 3545
Db      3518 GCGGTTCTTGGATGATAAAGATGAGCATCTAGCCCTGTAACCTTCACTGCTGCTGT 3577
Qy      3546 CCCATAGAGGCTCTTGAATACGTATTAAGATAAGTTGTTGGCAAGCTGACCTG 3605
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Qy      3606 CGTGCAACATGTAACCGGAGCTGTATATGATGATGATTAATATGATACCATGTAT 3665
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Qy      3726 ACTGCTATGTTTTTAAATATGCTTCAATGCTTATCTGTTGATGATGCTGAGGGA 3785
Db      3758 ACTGCTATGTTTTTAAATATGCTTCAATGCTTATCTGTTGATGATGCTGAGGGA 3817
Qy      3786 CAAGAGTTCATTTGATGATGATTAAGCAAGTACTGCTTATTTTGAANCTGAA 3845
Db      3818 CAAGAGTTCATTTGATGATGATTAAGCAAGTACTGCTTATTTTGAANCTGAA 3877
Qy      3846 AA 3847
Db      3878 AA 3879

RESULT 3
US-09-949-016-5205
; Sequence 5205, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5205
; LENGTH: 3868
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5205

Query Match          97.9%; Score 3777.4; DB 4; Length 3868;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3818; Conservative 0; Mismatches 11; Indels 4; Gaps 3;

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Db 339 GTACATGAGACGGGCTCCCTGGAAAGCTGTGGCTCGAGGCATTGGCATGGGATCT 398
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Db 399 CCGGTTCCGCAATCATCCAGAGACGGCGGTGGGCAATGAACCTTCTGCACTGCAATGGCCCC 458
Qy 427 GCCACTCTCGACCTGAGACCTTCAAGCCCGGAAACATCTCGGTGAGATGCGCACTACACAGT 486
Db 459 GGCACCTCTCGACCTGAGACCTTCAAGCCCGGAAACATCTCGGTGAGATGCGCACTACACAGT 518
Qy 487 CAAGATTTCTGATTTTGGTCTGGCCAAAGTGCACACGGGCTGTCCCATCTGCATGACCTGAG 546
Db 519 CAAGATTTCTGATTTTGGTCTGGCCAAAGTGCACACGGGCTGTCCCATCTGCATGACCTGAG 578
Qy 547 CATGATGGCTGTTTGGCACAATGGCTTACTCTCTTCAGAGCCCATTCAGGAGAAAGAG 606
Db 579 CATGATGGCTGTTTGGCACAATGGCTTACTCTCTTCAGAGCCCATTCAGGAGAAAGAG 638
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Db 699 CACACAGAAAGACGGTTTGCAGATGAGAAACAATCTGCAATCATATGTTGAAGTGTGT 758
Qy 727 GAAGGGCCACCGGCCCCGAGCTGCGGCGGTGTGCAGAGCCCGGCGCGCTGCAACCCA 786
Db 759 GAAGGGCCACCGGCCCCGAGCTGCGGCGGTGTGCAGAGCCCGGCGCGCTGCAACCCA 818
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Db 819 CCGTATACGCTCATGACAGCGGTGTGCGAGGGGGATCCGAGGTTAAGGCCACCTTCCA 878
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Qy 1147 GGAATCCGGCTTCTCTTCAGAGGATCACTGTGCTGCTTCTTGAAGCGGAACTTTCAAC 1206
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Db 1298 GGGACACCAAGCAATGATGAAGATCTGCAAGCCGAGAGAGCTTGTGCACTGTGACA 1357
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Db 1358 GCGGTGACAGCTGTGCACTGTGCGGTGAGAGCCGGGCAAGAGAGTGCAGAAAGTGC 1417
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Db 1958 CACAGACACCCCTTGCAGTGGCCCGGAGAGGGGGCAACAGAGACTGTCCAGGCTTCTCC 2017
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Db 2018 TGCAATCCGGGGGCTGTGAGAGAGGCGGTGACCTGACCTGACAGCGCTTGTGACCTTG 2077
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QY 2526 CTGACCGGAGTGTCCCTCCAGGTGAAGTGGCTCAGGTCACATGCCGCTCATCATC 2585
DB 2558 CTGACCGGAGTGTCCCTCCAGGTGAAGTGGCTCAGGTCACATGCCGCTCATCATC 2617
QY 2586 GATCTAGGCACTGTGTCTGAAGGAGCCGTGGGTCAAGATCATTTCCGTGTCTCTAA 2645
DB 2618 GATCTAGGCACTGTGTCTGAAGGAGCCGTGGGTCAAGATCATTTCCGTGTCTCTAA 2677
QY 2646 TGGGTCTGAGAGGTGTCTCTCAGTGATGAAGCCCGAGGCTGAGAGCATCTCTCT 2705
DB 2678 TGGGTCTGAGAGGTGTCTCTCAGTGATGAAGCCCGAGGCTGAGAGCATCTCTCT 2737
QY 2706 CTTGAGGAGGACCACTTGGGGTTCGTGAGCTCAACAAGCTTGAAGGAGGTGCAAGGGA 2765
DB 2738 CTTGAGGAGGACCACTTGGGGTTCGTGAGCTCAACAAGCTTGAAGGAGGTGCAAGGGA 2797
QY 2766 ACTGATTTTTTATCTTCATATCATGACGGTGGGCAAGAGGCGCTGCTTAAAGTTTCCAT 2825
DB 2798 ACTGATTTTTTATCTTCATATCATGACGGTGGGCAAGAGGCGCTGCTTAAAGTTTCCAT 2857
QY 2826 GGAATTTGTTTTTAAATATCTTAAAGATGAATACCTTATCAGCTGTGCTTGAACCT 2885
DB 2858 GGAATTTGTTTTTAAATATCTTAAAGATGAATACCTTATCAGCTGTGCTTGAACCT 2917
QY 2886 GTTAAATATGTTTCATTAACATTTGATAGTCTTACTTCTTAAATGATGGCTTAAGTGGGT 2945
DB 2918 GTTAAATATGTTTCATTAACATTTGATAGTCTTACTTCTTAAATGATGAAGTGGGT 2977
QY 2946 TGGCTTTGAAAACAATGTTTTATGCAACAAGAAACAATGATGAGCAGGCTTTGGCGG 3005
DB 2978 TGGCTTTGAAAACAATGTTTTATGCAACAAGAAACAATGATGAGCAGGCTTTGGCGG 3037
QY 3006 GGGTATGTGTGGCCAGCTCTTAAACAATTCAGTCTATTTACTTGGGTAGTCTTGTGAC 3065
DB 3038 GGGTATGTGTGGCCAGCTCTTAAACAATTCAGTCTATTTACTTGGGTAGTCTTGTGAC 3097
QY 3066 AACCAACAACAGTGGCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 3125
DB 3098 AACCAACAACAGTGGCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 3157
QY 3126 TTTGGCACTCTAGAGCCACAGGCTTAAGATCATTTAAATATTCCTTTGTAACTTC 3185
DB 3158 TTTGGCACTCTAGAGCCACAGGCTTAAGATCATTTAAATATTCCTTTGTAACTTC 3215
QY 3186 AGTGTGGGAGCTGAGGCGAGCCCTCAGTGTGCTGAGTGCACCAAGTCTTGGGAGAGA 3245
DB 3216 AGTGTGGGAGCTGAGGCGAGCCCTCAGTGTGCTGAGTGCACCAAGTCTTGGGAGAGA 3275
QY 3246 GGTGCAAGAAAGCTGTGTTTTTATCTCAACGAGATGAAATTAATTAACATAGT 3305
DB 3276 GGTGCAAGAAAGCTGTGTTTTTATCTCAACGAGATGAAATTAATTAACATAGT 3335
QY 3306 ATTTACTTACATAGACAGTATTAAGTATGATGATGATGATGATGATGATGATGATGAT 3365
DB 3336 ATTTACTTACATAGACAGTATTAAGTATGATGATGATGATGATGATGATGATGATGAT 3395
QY 3366 GCTCTCATTTTTTTGATGATGATTTGGGATGAGGATGATGATGATGATGATGATGATGAT 3425
DB 3396 GCTCTCATTTTTTTGATGATGATTTGGGATGAGGATGATGATGATGATGATGATGATGAT 3455
QY 3426 TTTTCTGACCTGTTTGAACGTCCTCCGACCTCAAGCATTTTGGGGTGTGGCCCCAAG 3485
DB 3456 TTTTCTGACCTGTTTGAACGTCCTCCGACCTCAAGCATTTTGGGGTGTGGCCCCAAG 3515
QY 3486 GGGGTTCTTGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3545
DB 3516 GGGGTTCTTGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3575
QY 3546 CCCATAGGGTCTTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3605
DB 3576 CCCATAGGGTCTTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3635
QY 3606 CCGCAAAATGATCCGTGCTGTATATGATGATGATGATGATGATGATGATGATGATGAT 3665

DB 3636 CGTGCAAAACATGATCCGTGGCTGTATATGATGATGATGATGATGATGATGATGATGAT 3695
QY 3666 GTTATATGATCTGTGGGAGAGATFACCTTTTCCATGCGAAGAAATATCCAGCTGTGAA 3725
DB 3696 GTTATATGATCTGTGGGAGAGATFACCTTTTCCATGCGAAGAAATATCCAGCTGTGAA 3755
QY 3726 ACTGCTATGTTTTTAAATATGCTCATTTGTGCTTACTGTTGTGTGAGACTGCGTAGGGA 3785
DB 3756 ACTGCTATGTTTTTAAATATGCTCATTTGTGCTTACTGTTGTGTGAGACTGCGTAGGGA 3815
QY 3786 CAAGAAGTTCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3838
DB 3816 CAAGAAGTTCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3868

RESULT 4
US-09-799-451-905
; Sequence 905, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feijian
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799, 451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 905
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2496)
US-09-799-451-905

Query Match 94.4%; Score 3643; DB 4; Length 3981;
Best Local Similarity 96.1%; Pred. No. 0; Mismatches 11; Indels 146; Gaps 3;
Matches 3825; Conservative 0;

QY 17 ATGAGGCGGAGCGGCGGAGCCCATGAGGCTGTGCGTGTGCGACCTTGCACGCGGAGC 76
DB 1 ATGAGGCGGAGCGGCGGAGCCCATGAGGCTGTGCGTGTGCGACCTTGCACGCGGAGC 60
QY 77 GAGTTACGGGCTGGAGAAAGTGGGCTCGGGCGGCTTGGGCAAGTGTACAAAGTGGGC 136
DB 61 GAGTTACGGGCTGGAGAAAGTGGGCTCGGGCGGCTTGGGCAAGTGTGTGCGG 120
QY 137 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGGCTGACAGTGCAGAC 196
DB 121 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGGCTGACAGTGCAGAC 180
QY 197 AGGAGCCCATGAGACTTTTGAAGAAAGCAAGAAATGAGATGAGATGAGATGAGATGAGATGAGAT 256

Dh 181 AGGAGCCCATGAGACTTTTGGAAAGAACCAAGATGAGATGGCCAGTTTCGCTAC 240
Qy 257 ATCTGCTGTGTATGCGATCTGCCGAACCTGTGGCTGTGTATGAGATCATGGAG 316
Dh 241 ATCCGCTGTGTATGCGATCTGCCGAACCTGTGGCTGTGTATGAGATCATGGAG 300
Qy 317 ACCGCTCCCTGGAAAGCTGTGGCTTCCGAGCAATGGACATGGGATCTCGGTTCCGA 376
Dh 301 ACCGCTCCCTGGAAAGCTGTGGCTTCCGAGCAATGGACATGGGATCTCGGTTCCGA 360
Qy 377 ATCATCGAAGACGCGGTGGGCAATGAACTTCTGCACTGATGAGCCCGCACTCTG 436
Dh 361 ATCATCGAAGACGCGGTGGGCAATGAACTTCTGCACTGATGAGCCCGCACTCTG 420
Qy 437 CACCTGACCTCAACCCCGCAACATCTGTGTGATGCCCCACTACCAAGTCAAGTTTCT 496
Dh 421 CACCTGACCTCAACCCCGCAACATCTGTGTGATGCCCCACTACCAAGTCAAGTTTCT 480
Qy 497 GATTTGTGTGGCAAGTGCAGCGGGCTGTCCCACTGGCATGACCTGAGCATGGATGAC 556
Dh 481 GATTTGTGTGGCAAGTGCAGCGGGCTGTCCCACTGGCATGACCTGAGCATGGATGAC 540
Qy 557 CTGTTGGCACAATGCGCTTACTCTCTCCAGACGCAATCAGGAGAAAGCGGCTCTTC 616
Dh 541 CTGTTGGCACAATGCGCTTACTCTCTCCAGACGCAATCAGGAGAAAGCGGCTCTTC 600
Qy 617 GACACCAAGCAGATGTATACAGCTTTGCGATGTATCTGGGGCTGTCAACAGAG 676
Dh 601 GACACCAAGCAGATGTATACAGCTTTGCGATGTATCTGGGGCTGTCAACAGAG 660
Qy 677 AAGCGTTTGCAGATGAGAAAGATCTGCAATCATGTGTGAGTGTGAGAGGCGAC 736
Dh 661 AAGCGTTTGCAGATGAGAAAGATCTGCAATCATGTGTGAGTGTGAGAGGCGAC 720
Qy 737 CGCCCGAGCTGCGCCGCTGTGAGAGCGCCGCGCGCTGAGCCACTGTATGCG 796
Dh 721 CGCCCGAGCTGCGCCGCTGTGAGAGCGCCGCGCGCTGAGCCACTGTATGCG 780
Qy 797 CTCAATGACCGGTGTGGGAGGGGATCCGCGAGTTAAGGCCCACTTC----- 844
Dh 781 CTCAATGACCGGTGTGGGAGGGGATCCGCGAGTTAAGGCCCACTTC----- 840
Qy 845 ----- 844
Dh 841 CTGAATGGGAGCTCATCCGCCAGGTGTGGGAGCTGTCTCCCTGTGACTGGCAGTGG 900
Qy 845 ----- 844
Dh 901 CGCTCCCCGGGAAAGCTTCCGCTTGAAGTCTGAAGTCAATCATCGAGTGCATGTCCC 960
Qy 845 -----CAAGAAATTACTTCTGAACCGAGAGACTGTGTGAAGAGCTGTATGAC 892
Dh 961 CTTTCTTCCCAACAAGAAATTACTTCTGAACCGAGAGACTGTGTGAAGAGCTGTATGAC 1020
Qy 893 GAAGTGAAGAAAGTGTATGATCTGAGCTGGAAGAGCCCGGAGGCCAGAGCGAG 952
Dh 1021 GAAGTGAAGAAAGTGTATGATCTGAGCTGGAAGAGCCCGGAGGCCAGAGCGAG 1080
Qy 953 GTGTGTGCTGCGAGGCTCAAGCGGGCTGTGCCCCCACTTTGATTAAGACTACGCTC 1012
Dh 1081 GTGTGTGCTGCGAGGCTCAAGCGGGCTGTGCCCCCACTTTGATTAAGACTACGCTC 1140
Qy 1013 TCCGAGCTTCTCTCAAGCTGAGCTCTGGAAGTTTCCGAGGCTGTGAGAGGCCAGAG 1072
Dh 1141 TCCGAGCTTCTCTCAAGCTGAGCTCTGGAAGTTTCCGAGGCTGTGAGAGGCCAGAG 1200
Qy 1073 CTCAAGCGGAGCTCTCTGAGTCAAGCTGCAATGCTCGGAGAGTGGAGAGGCTCTCG 1132
Dh 1201 CTCAAGCGGAGCTCTCTGAGTCAAGCTGCAATGCTCGGAGAGTGGAGAGGCTCTCG 1260
Qy 1133 GGGGTGTCTCTCGGTGAGCTCGGCTTCTCTTCAAGAGATCACTGTGCTCTTTGAG 1192
Dh 1261 GGGGTGTCTCTCGGTGAGCTCGGCTTCTCTTCAAGAGATCACTGTGCTCTTTGAG 1320

Qy 1193 CGGGAACCTTCAACCAAGCATCTGGGGTACCAAGAAGTCCAGAGAAAGAGCTTGTGGA 1252
Dh 1321 CGGGAACCTTCAACCAAGCATCTGGGGTACCAAGAGTCCAGAGAAAGAGCTTGTGGA 1379
Qy 1253 TGCATCGTGTCC-GGGACACCAAGCAAACTGATGAAGATCTGTGAGCCGAGAGCGTGA 1311
Dh 1380 TGCATCGTGTCCGGGGACACCAAGCAAACTGATGAAGATCTGTGAGCCGAGAGCGTGA 1439
Qy 1312 CTGTGACCTGAGACAGCGGTGCGAGCTGTGTGCACTGTGGCGGTGAGAGCCGGGAAAGGA 1371
Dh 1440 CTGTGACCTGAGACAGCGGTGCGAGCTGTGTGCACTGTGGCGGTGAGAGCCGGGAAAGGA 1499
Qy 1372 GTGGCCAAAGTGTGTGCTCAACAAATGCAACCCCAACTGAGCAACGTAGAGGCTC 1431
Dh 1500 GTGGCCAAAGTGTGTGCTGTGTCAACAAATGCAACCCCAACTGAGCAACGTAGAGGCTC 1559
Qy 1432 CACCCGTTGCAATGAGCCGTGAGAGAGAGGTGCGGGGTGTGTGTGAGCTCTGTGCG 1491
Dh 1560 CACCCGTTGCAATGAGCCGTGAGAGAGAGGTGCGGGGTGTGTGTGAGCTCTGTGCG 1619
Qy 1492 ACGAAGATCAGTGTCAACGCGCAAGATGAGAACCAAGTGCAGAGCTTCACTTTGAGC 1551
Dh 1620 GCGAAGATCAGTGTCAACGCGCAAGATGAGAACCAAGTGCAGAGCTTCACTTTGAGC 1679
Qy 1552 CCAAGACGGGGATGAGTCTAGCAACGCGCTGTGTGAGAGAGAGCGCTCGGTCAACGA 1611
Dh 1680 CCAAGACGGGGATGAGTCTAGCAACGCGCTGTGTGAGAGAGAGCGCTCGGTCAACGA 1739
Qy 1612 GGTGACCTTTGAGAGGCGGAGCGCCCATGACGTTGAGCTTCCAGCAGGCGAGAGATAT 1671
Dh 1740 GGTGACCTTTGAGAGGCGGAGCGCCCATGACGTTGAGCTTCCAGCAGGCGAGAGATAT 1799
Qy 1672 GTGTGCACTCTGTGTGGCGGAGCGGTGTGAGAGCTGTGAGAGGCAAGATGCTGTGCT 1731
Dh 1800 GTGTGCACTCTGTGTGGCGGAGCGGTGTGAGAGCTGTGAGAGGCAAGATGCTGTGCT 1859
Qy 1732 GCACTGACATTAAGCTGTGTGAGAGGCGCACTGCGCATGCTCAAGCTGTGTGAGAGCA 1791
Dh 1860 GCACTGACATTAAGCTGTGTGAGAGGCGCACTGCGCATGCTCAAGCTGTGTGAGAGCA 1919
Qy 1792 GCGGGGGGTGAGTGTGAACGCGCCAGACGCTGTGATGAGAGAGCGCATTTGCACTGGCCGC 1851
Dh 1920 GCGGGGGGTGAGTGTGAACGCGCCAGACGCTGTGATGAGAGAGCGCATTTGCACTGGCCGC 1979
Qy 1852 ACAAGCGGGGACATTAAGCGGTGTGAGAGCGGTGTGAGAGCGGTGTGAGAGCGGTGTGAG 1911
Dh 1980 ACAAGCGGGGACATTAAGCGGTGTGAGAGCGGTGTGAGAGCGGTGTGAGAGCGGTGTGAG 2039
Qy 1912 CTGAGAGCTGTGTGACAGACACCCCTGTGACGTTGAGAGAGCGGTGTGAGAGCGGTGTGAG 1971
Dh 2040 CTGAGAGCTGTGTGACAGACACCCCTGTGACGTTGAGAGAGCGGTGTGAGAGCGGTGTGAG 2099
Qy 1972 TGCAGAGCTGTCTGTGATCGGGGCGCTGTGAGAGAGCGGTGTGAGAGCGGTGTGAG 2031
Dh 2100 TGCAGAGCTGTCTGTGATCGGGGCGCTGTGAGAGAGCGGTGTGAGAGCGGTGTGAG 2159
Qy 2032 CGCTGTGACCTGTGTGCGCGCAACGACACTGTGGCCACTGTCAAGCTGTGTGTGAGAG 2091
Dh 2160 CGCTGTGACCTGTGTGCGCGCAACGACACTGTGGCCACTGTGTCAAGCTGTGTGTGAGAG 2219
Qy 2092 GAAGGCGGATGTGTGTGCGCGGAGACCCCTGAACCAAGCGGCGGTGTGACCTGTGTGCGC 2151
Dh 2220 GAAGGCGGATGTGTGTGCGCGGAGACCCCTGAACCAAGCGGCGGTGTGACCTGTGTGCGC 2279
Qy 2152 CCAAGGCGACTCGAGAGGTGTGAGAGAGTGTGAGAGCGCGGATGTCAATGACTGTGTGGA 2211
Dh 2280 CCAAGGCGACTCGAGAGGTGTGAGAGAGTGTGAGAGCGCGGATGTCAATGACTGTGTGGA 2339
Qy 2212 CGAGCAGGGGCTCAAGCGGTGTGACCTGTGCGGCCAGAGGCGGTGTGAGAGCGAGGTGGA 2271
Dh 2340 CGAGCAGGGGCTCAAGCGGTGTGACCTGTGCGGCCAGAGGCGGTGTGAGAGCGAGGTGGA 2399

OY	2272	GACTCTGTCAAGCATATGGGCGCCACATCAACCTGCAGAAGCCTCAAATTCCAAGGGCGGCCA	2331
Dp	2400	GACTCTGTCAAGCATATGGGCGCCACATCAACCTGCAGAAGCCTCAAAGTTTCCAGGGCGGCCA	2459
OY	2332	TGGCCCCCGCCACACAATCTCTGCGGGCGAAAGAACCTAGCTGTGCTGCTTCGAGACCG	2391
Dp	2460	TGGCCCCCGCCACAGCTCTCTGCGCGGAAGAACCTAGCTGTGCTGCTGCGAGACCG	2519
OY	2392	GGGGTCAACGTGGGGCTCTTGTCCTGTCTGTGTCTCTGTGGGAGTAGAACATCTCTGC	2451
Dp	2520	GGGGTCAACGTGGGGCTCTTGTCCTGTCTGTGTCTCTGTGGGAGTAGAACATCTCTGC	2579
OY	2452	GTCGGGAGCCCGTGTGTGTCTTAACCTTAAGTTTAACCAAGCAGAAGGTGACATGTGCTCATCA	2511
Dp	2580	GTCGGGAGCCCGTGTGTGTCTTAACCTTAAGTTTAACCAAGCAGAAGGTGATGTGTCTCATCA	2639
OY	2512	GGAAGCGGCTCTGTCTGAACCGGAGGTGTCCTCCCTCAGAGTGAAAGCTGTGCTCAAGTGCACATG	2571
Dp	2640	GGAAGCGGCTCTGTCTGAACCGGAGGTGTCCTCCCTCAGAGTGAAAGCTGTGCTCAAGTGCACATG	2699
OY	2572	CCCGCTCCATCATGCATCTAGGCAACTGCTGTCTGAAGGAAACCGTGAGTCAGAATCAATT	2631
Dp	2700	CCCGCTCCATCATGCATCTAGGCAACTGCTGTCTGAAGGAAACCGTGAGTCAGAATCAATT	2759
OY	2632	CCTTGTGTCTCTTAATAGSGTCCCTGAAGGTGTGTCTCTCAATGATATAAGCCCAGGCGTGTGA	2691
Dp	2760	CCTTGTGTGTCTCTTAATAGSGTCCCTGAAGGTGTGTCTCTCAATGATATAAGCCCAGGCGTGTGA	2819
OY	2692	AGCATCACTCTCTCTGAGGGCGAGCACCTTGGGTGTCTGGAAGTCAACAGTCTTGAAG	2751
Dp	2820	AGCATCACTCTCTCTGAGGGCGAGCACCTTGGGTGTCTGGAAGTCAACAGTCTTGAAG	2879
OY	2752	GAGGTGACAGGGGAAACTGTGTTTTTTATCTTATATCATGACGGTGTGGCAGAGAGGCTGT	2811
Dp	2880	GAGGTGACAGGGGAAACTGTGTTTTTTATCTTATATCATGACGGTGTGGCAGAGAGGCTGT	2939
OY	2812	CTTAAAGTTTCAATGGAATGTTTATATATAATCTTAAAGATGATAAACCCTTAATCAAGT	2871
Dp	2940	CTTAAAGTTTCAATGGAATGTTTATATATAATCTTAAAGATGATAAACCCTTAATCAAGT	2999
OY	2872	GTTGTCTTGAACCTGTATAAAAAATGTTCTATAACAATGGATGTCTAGTCTCTAAATGATGG	2931
Dp	3000	GTTGTCTTGAACCTGTATAAAAAATGTTCTATAACAATGGATGTCTAGTCTCTAAATGATGA	3059
OY	2932	CTAAGTAGTGGGGTGTGGCTTTGAAAAACAATGTTTATCAACAAGAACGAAATGGTAGCA	2991
Dp	3060	CTAAGTAGTGGGGTGTGGCTTTGAAAAACAATGTTTATCAACAAGAACGAAATGGTAGCA	3119
OY	2992	GCCAGCTTTGCGGGCGGTAATGTGTGGCCAGAGCTCTTAACAATCCAGTCTAATTACTTGGGT	3051
Dp	3120	GCCAGCTTTGCGGGCGGTAATGTGTGGCCAGAGCTCTTAACAATCCAGTCTAATTACTTGGGT	3179
OY	3052	GAGTCTTGTGGACAAACACACACAGTGCCACATGGTACTAGCTGCGCTTGTGTTCTC	3111
Dp	3180	GAGTCTTGTGGACAAACACACACAGTGCCACATGGTACTAGCTGCGCTTGTGTTCTC	3239
OY	3112	GTTGTCTAAGATGTTTGTGGCAACTCTAAGACCAAGGCTAAGATCATTAATAAAATTTCT	3171
Dp	3240	GTTGTCTAAGATGTTTGTGGCAACTCTAAGACCAAGGCTAAGATCATTAATAAAATTTCT	3299
OY	3172	CCCTTTGTACCTCAAGTGTGGGGACTGAAGGAGACCCCTCAAGTCCGTGTGAAGTGCAC	3231
Dp	3300	CCCTTTGTACCTCAAGTGTGGGGACTGAAGGAGACCCCTCAAGTCCGTGTGAAGTGCAC	3359
OY	3232	AGCTTGGGGAAGAGGTGACAGAGAAGCTGTTTTTTATCTCCACAAGCAGATGAGAAGA	3291
Dp	3360	AGCTTGGGGAAGAGGTGACAGAGAAGCTGTTTTTTATCTCCACAAGCAGATGAGAAGA	3419
OY	3292	TAAAAATTACATATGATTACCTTAGACATACAGATATTACCTAGTAGATGACCTGTCAAC	3351
Dp	3420	TAAAAATTACATATGATTACCTTAGACATACAGATATTACCTAGTAGATGACCTGTCAAC	3479
OY	3352	CTGCACCCCTTCCCAAGCTCTCAATTTTGTGTAAGGTATGTGGATATAGGAATAGTGTTTGGG	3411

Db	3480	CTGGGCCCTTCCAGCTCTATTTTGTAGTGATTTGGGATAGGAAATAGTGTTTGGG	3539
Qy	3412	GTATGGGGGGAGTGTTCGACCTGCTTTGGCAGACGTGCTCCGCACCTCAGACAGTTTGG	3471
Db	3540	GTATGGGGGGAGTGTTCGACCTGCTTTGGCAGACGTGCTCCGCACCTCAGCAGTTTGG	3599
Qy	3472	GGTGTGGCCCCCAGGGGGGTTCTTGAGTGTAAAGATGTGGCCACTAGCCTCGTAACCTC	3531
Db	3600	GGTGTGGCCCCCAGGGGGGTTCTTGAGTGTAAAGATGTGGCCACTAGCCTCGTAACCTC	3659
Qy	3532	ACTGTCACTGTGTCCCATAGGGGTCCTCTGAATACTGTATTAGAAATAGTTTGTGC	3591
Db	3660	ACTGTCACTGTGTCCCATAGGGTGCCTCTGAATACTGTATTAGAAATAGTTTGTGC	3719
Qy	3592	AGAACTGACCCCTGCGTGCAACATGTACCGTGGCCTGTGTATGTATAGAGATTGATATT	3651
Db	3720	AGAACTGACCCCTGCGTGCAACATGTACCGTGGCCTGTGTATGTATAGAGATTGATATT	3779
Qy	3652	AATGTACATGTATGTATATGTAAATCTGTGGGACAGATACCTTTTGCATGGCAGAAATA	3711
Db	3780	AATGTACATGTATGTATATGTAAATCTGTGGGACAGATACCTTTTGCATGGCAGAAATA	3839
Qy	3712	TCCAAAGCTGTGGAACCTGCTATATGTATATATGCTCATATGTGACCTTATCTGTGTGTG	3771
Db	3840	TCCAAAGCTGTGGAACCTGCTATATGTATATATGCTCATATGTGACCTTATCTGTGTGTG	3899
Qy	3772	GACTGCGTGAAGGACAAAGATTCATTTGATGTCAATTAAGCAAAAGTACTTGCTTACTT	3831
Db	3900	GACTGCGTGAAGGACAAAGATTCATTTGATGTCAATTAAGCAAAAGTACTTGCTTACTT	3959
Qy	3832	TTTTGAATCGTGAAGGAAAAA 3853	
Db	3960	TTTTGAAGAAAAA 3981	

RESULT 5

US-09-949-016-12845
; Sequence 12845, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307

;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

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; ERROR FEEING DATE: 2008-02-06
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

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/ SOFWAKE. F88C8E9 101 WINDOWS 101
; SEQ ID NO 12845
. LENGTH. 31718

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1  LENGTH: 31/18
2  TYPE: DNA
3  ORGANISM: Human

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US-09-949-016-12845

Query Match	Score	2586
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Best Local Similarity 99.6%; Pred. NO.
Matches 2623; Conservative 0; Mismatch

1211 GATCTGGTACCACAAGACGTCAGAAGAA

Db 27095 GATCTGGGCACCAC-AGACGTCAGAAGAA

1270 CACCAGCAACTGATGAAGATCCTGCAGCC

Db 27154 CACCAGCAACTGATGAAGATCCTGCAGCC

Db	3480	CTGGGCCCTTCCAGCTCTCATTTTGTAGTGATTTGGGATAGGAAATAGTGTTCGGG	3539
Qy	3412	GTATGGGGGGAGTGTTCGACCTGCTTTGGCAGACGTGCTCCGCACTTCAGACATTTGG	3471
Db	3540	GTATGGGGGGAGTGTTCGACCTGCTTTGGCAGACGTGCTCCGCACTTCAGACATTTGG	3599
Qy	3472	GGTGTGCCCCCAGGGGGGTTCTTGGATGTAAAGATGTGGCCATTCAGCTCGTAACCTTC	3531
Db	3600	GGTGTGCCCCCAGGGGGGTTCTTGGATGTAAAGATGTGGCCATTCAGCTCGTAACCTTC	3659
Qy	3532	ACTGTCACTGTGTCCCATATGAGGTGCTTCGTAATACTGTATTAGAAATAGTTTGTGC	3591
Db	3660	ACTGTCACTGTGTCCCATATGAGGTGCTTCGTAATACTGTATTAGAAATAGTTTGTGC	3719
Qy	3592	AGAACGTGACCTTCGCTGCAACATGTACCTGTGCTCTGTATATGTATAGATTTGATATT	3651
Db	3720	AGAACGTGACCTTCGCTGCAACATGTACCTGTGCTCTGTATATGTATAGATTTGATATT	3779
Qy	3652	AATGTATCATGTATGTATATGTATATCTGTGTGGCAGAGATCTTTTCCATGGCAGAAATA	3711
Db	3780	AATGTATCATGTATGTATATGTATATCTGTGTGGCAGAGATCTTTTCCATGGCAGAAATA	3839
Qy	3712	TCCAGCTGTGTGAACCTGCTATGTATTTATATATGCTCATTTGTGCTTAACTGTGTGTG	3771
Db	3840	TCCAGCTGTGTGAACCTGCTATGTATTTATATATGCTCATTTGTGCTTAACTGTGTGTG	3899
Qy	3772	GACTGCGTGAAGGACAAAGATTCATTTGATGTCAATTAAGCAAGTACTTGTGCTTACTT	3831
Db	3900	GACTGCGTGAAGGACAAAGATTCATTTGATGTCAATTAAGCAAGTACTTGTGCTTACTT	3959
Qy	3832	TTTTGAATCTGAAAAAATAAATAA 3853	
Db	3960	TTTTGAATCTGAAAAAATAAATAA 3981	
RESULT 5			
US-09-949-016-12845			
; Sequence 12845, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERE			
; FILE REFERENCE: C1001307			
; CURRENT APPLICATION NUMBER: US/09/949, 016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: PasteSeq for Windows Version 4.0			
; SEQ ID NO 12845			
; LENGTH: 31718			
; TYPE: DNA			
; ORGANISM: Human			
US-09-949-016-12845			
Query Match 67.0%; Score 2586; DB 4; Length 31718;			
Best Local Similarity 99.6%; Pred. No. 0;			
Matches 2623; Conservative 0; Mismatches 6; Indels 4; Gaps 3;			
Qy	1211	GATCTGGGTACCAACAGCTCCAGAGAAGAACTTGTGATGTCATCGTGTCC-GGGA	1269
Db	27095	GATCTGGGACACAC-ACACCTCCAGAGAAGAACTTGTGATGTCATCGTGTCCGGGGA	2715
Qy	1270	CACCAAGCAACTGATGAAATCTCTGACGCCGACAGACGTGACCTGCGCACTGCACAGCG	1329
Db	27154	CACCAAGCAACTGATGAAATCTCTGACGCCGACAGACGTGACCTGCGCACTGCACAGCG	2721

QY	1330	TCGCACGCTGCTGCACTCTGCGCGTGTGAGAGCGCGGCACAGAGAGTGGCCCAAGTGGCTGCT	1389
Db	27214	TGCACAGCTGTGTGCACTCTGGCGGTGAGAGCGCGGCACAGAGAGTGGCCCAAGTGGCTGCT	27273
QY	1390	GCTCAACATATGCACAACTCCAACTGAGCAACCGTAGGGGGCTCCACCCTGTTGCAATATGGC	1449
Db	27274	GCTCAACATATCCCAACCTCCAACTGAGCAACCGTAGGGGGCTCCACCCTGTTGCAATATGGC	27333
QY	1450	CGTGGAGAGAGGGGTGCGGGGTGTCTGTGAGACTCTGCTGGCAAGAGATCAGTGTCAA	1509
Db	27334	CGTGGAGAGAGGGGTGCGGGGTGTCTGTGAGACTCTGCTGGCAAGAGATCAGTGTCAA	27393
QY	1510	CGCCACGAGATGAGGACCACTGTGAGACAGCGCTTCACTTTTGACGCCCAAGACGGGGCATGAGTTC	1569
Db	27394	CGCCACGAGATGAGGACCACTGTGAGACAGCGCTTCACTTTTGACGCCCAAGACGGGGCATGAGTTC	27453
QY	1570	TAGCAACAGCGGTGCTGTGGAGAGAAAGCCTCGGTCAACAGAGGTGACCTTTTAGAGGGCCG	1629
Db	27454	TAGCAACAGCGGTGCTGTGGAGAGAAAGCCTCGGTCAACAGAGGTGACCTTTTAGAGGGCCG	27513
QY	1630	GACGCCCATGCACTGTGCGCTTGCACGACAGGGCAGAGAAATATCGTGGCAATCCTGTGTGCG	1689
Db	27514	GACGCCCATGCACTGTGCGCTTGCACGACAGGGCAGAGAAATATCGTGGCAATCCTGTGTGCG	27572
QY	1690	CCGAGGCGTGGACGTGAGCTTGCAGGGGCAGAGAGATGCTGGCTGCACACTGCATACGCTGC	1749
Db	27574	CCGAGGCGTGGACGTGAGCTTGCAGGGGCAGAGAGATGCTGGCTGCACACTGCATACGCTGC	27633
QY	1750	CTGGCAGGGGCCACCTGGCCCATCGTCAAGCTGTGGCCAAACAGCGCGGGGGGTGAGTGTGAA	1809
Db	27634	CTGGCAGGGGCCACCTGGCCCATCGTCAAGCTGTGGCCAAACAGCGCGGGGGGTGAGTGTGAA	27693
QY	1810	CGCCCAAGCGCTGAGATGGAGAGAGCGCAATTGCACTTGGCCGACAGCGCGGGGCATTAACG	1869
Db	27694	CGCCCAAGCGCTGAGATGGAGAGAGCGCAATTGCACTTGGCCGACAGCGCGGGGCATTAACG	27753
QY	1870	CGTGGCCCGCATCTCTCATCGACTGTGTGCTCCGACGTCAAGTGTGACAGCTTGTGGCACT	1929
Db	27754	CGTGGCCCGCATCTCTCATCGACTGTGTGCTCCGACGTCAAGTGTGACAGCTTGTGGCACT	27813
QY	1930	GACACCCCTGACGCTGGCGCGCGGAGAGCGGGGCACAGAGGACTGGCAGCTGCTCCGTGCA	1989
Db	27814	GACACCCCTGACGCTGGCGCGCGGAGAGCGGGGCACAGAGGACTGGCAGCTGCTCCGTGCA	27873
QY	1990	TGCGGGGCGCTGGCAGAGAGGCGCTGAGCCTCAAGACGAGCTAACCGCTCTTGCACTGTGCTCG	2049
Db	27874	TGCGGGGCGCTGGCAGAGAGGCGCTGAGCCTCAAGACGAGCTAACCGCTCTTGCACTGTGCTCG	27933
QY	2050	CCGCACAGGACACTCTGGCTCATTTGTCAAGCTGTCTGTGAGAGAGAGGCGATGTGCTGGC	2109
Db	27934	CCGCACAGGACACTCTGGCTCATTTGTCAAGCTGTCTGTGAGAGAGAGGCGATGTGCTGGC	27993
QY	2110	CGGGGGAACCCCTGAAACAGAGCGGGGCTGACCTGGCTGCGGGCCACGGGGCACTCGAGAGT	2169
Db	27994	CGGGGGAACCCCTGAAACAGAGCGGGGCTGACCTGGCTGCGGGCCACGGGGCACTCGAGAGT	28053
QY	2170	GGTGAGGAGTGTGTCAAGCGCGCATTTGACTTGTGACGAGCAGGCGGGCTCAGCGC	2229
Db	28054	GGTGAGGAGTGTGTGTCAAGCGCGCATTTGACTTGTGACGAGCAGGCGGGCTCAGCGC	28113
QY	2230	GCTGCACCTTGGCGCGCCAGGGCCGGGCACGACAGAGCGGTGAGACTTGTCTCAGGCAATGG	2289
Db	28114	GCTGCACCTTGGCGCGCCAGGGCCGGGCACGACAGAGCGGTGAGACTTGTCTCAGGCAATGG	28173
QY	2290	GGCCCAATTCAACTGTGAGAGGCTCAAGTTCAGAGGGGGGCAATGAGCCCGCGGCCCAACT	2349
Db	28174	GGCCCAATTCAACTGTGAGAGGCTCAAGTTCAGAGGGGGGCAATGAGCCCGCGGCCCAACT	28233
QY	2350	CCTGGCGGGAAGCAAGACCTTAGCTGAGCTGCTGTGGAGAGACGGGGGGGTCAACGTGTGGGGCTC	2409
Db	28234	CCTGGCGGGAAGCAAGACCTTAGCTGAGCTGCTGTGGAGAGACGGGGGGGTCAACGTGTGGGGCTC	28293
QY	2410	TTGTCTGTCTGTGTGTCTCTGTGTGGGATGAGAGATCTTGCTGTGGGGCCCGTGTGTGC	2469

[illegible]

Db	28474	TAAGCACTGCTGCTCTAAGAGGACCGTGGGTCAAGAAATCAATTCCTGTGTGCTCTTAATGGG	28553
Qy	2650	TCGCTGAGGGCTGAGTCTCTCAAGTAATGAAGCCCAAGCGTGGAGACATCCATCTCTCTCG	2709
Db	28534	TCGCTGAGGGCTGAGTCTCTCAAGTAATGAAGCCCAAGCGTGGAGACATCCATCTCTCTCG	28593
Qy	2710	AGGCGAGCCACCTTGGGTTGCTGGAAGTCAACAAGCTTTGAGGGAGAGGTGACAGGGGAAACTGG	2769
Db	28594	AGGCGAGCCACCTTGGGTTGCTGGAAGTCAACAAGCTTTGAGGGAGAGGTGACAGGGGAAACTGG	28653
Qy	2770	TGTTTTTATCTTCATACATGACGAGTGGGAGAGAGGCGCTGTCTTAAAGTTTCAATGAA	2829
Db	28654	TGTTTTTATCTTCATACATGACGAGTGGGAGAGAGGCGCTGTCTTAAAGTTTCAATGAA	28713
Qy	2830	TTGTTTTATAAATATCTTAAGAGATGAATCCTTATCAAGCTGTGCTTGAAACTGTTA	2889
Db	28714	TTGTTTTATAAATATCTTAAGAGATGAATCCTTATCAAGCTGTGCTTGAAACTGTTA	28773
Qy	2880	AAAAATGTTCAATACATTTGGATAGTCTAGTCTCTTAATGATGGCTAAGTAGTGGGTTGGC	2949
Db	28774	AAAAATGTTCAATACATTTGGATAGTCTAGTCTCTTAATGATGGCTAAGTAGTGGGTTGGC	28833
Qy	2950	TTTGAAGAACATGTTTTATATGCAACAGAGAACATATGTTAGCAGCCAGCTTTGCGGGGCGT	3009
Db	28834	TTTGAAGAACATGTTTTATATGCAACAGAGAACATATGTTAGCAGCCAGCTTTGCGGGGCGT	28893
Qy	3010	ATGTGTGGCCAGCTCTTAAACCATTCAGAGCTAATTACTTGGGATAGTCTTGTGGACAAAC	3069
Db	28894	ATGTGTGGCCAGCTCTTAAACCATTCAGAGCTAATTACTTGGGATAGTCTTGTGGACAAAC	28953
Qy	3070	ACACACACGTGCCCAATGTAATCTAGCTGCCGTTCCGTTCTCGTGGCTTAAGATGTTTTG	3129
Db	28954	ACACACACGTGCCCAATGTAATCTAGCTGCCGTTCCGTTCTCGTGGCTTAAGATGTTTTG	29013
Qy	3130	GCAACTCTAAGAGCACAAGGCGCTAAGAGCTAATAAAATCTGCCCTTGTAACTCAAGT	3189
Db	29014	GCAACTCTAAGAGCACAAGGCGCTAATAAAATCTGCCCTTGTAACTCAAGT	29071
Qy	3190	CTGGGGACTGAGGGGAGGCCCTTCAGAGTGGCTGAGTGCACAAGTCTTGGGGAAGAAGTG	3249
Db	29072	CTGGGGACTGAGGGGAGGCCCTTCAGAGTGGCTGAGTGCACAAGTCTTGGGGAAGAAGTG	29133
Qy	3250	CAGAGAAAGCTGTGTTTTTATCTCCACAAGCAGTATGAAGATPAAATTCATATGATTA	3309
Db	29132	CAGAGAAAGCTGTGTTTTTATCTCCACAAGCAGTATGAAGATPAAATTCATATGATTA	29191
Qy	3310	CCTAGACATPACACAGTATTAATCTAAGAGTAAAGTCAACCTGCAACCCCTCCAGAGTC	3369
Db	29192	CCTAGACATPACACAGTATTAATCTAAGAGTAAAGTCAACCTGCAACCCCTCCAGAGTC	29251
Qy	3370	TCAATTTTGTAGAGGATTTTGGATPAGGAGTATGTTTGGGATATGGGGAGAGTGTTC	3429
Db	29252	TCAATTTTGTAGAGGATTTTGGATPAGGAGTATGTTTGGGATATGGGGAGAGTGTTC	29311
Qy	3430	TGACCTGCTTGCAGACGTCGCTCCGACCTCAGACAGTTTGGGATGTGGCCCGGACGAGCG	3489
Db	29312	TGACCTGCTTGCAGACGTCGCTCCGACCTCAGACAGTTTGGGATGTGGCCCGGACGAGCG	29371
Qy	3490	TTCTTTGATATGTAAGAATGTGGCCATCTAGCTGTGTAATCTTCACTGACATCTGTGCCCA	3549
Db	29372	TTCTTTGATATGTAAGAATGTGGCCATCTAGCTGTGTAATCTTCACTGACATCTGTGCCCA	29431
Qy	3550	TAGGGTGGCCTTCTGAATACTGTTATTAAGAAATATGTTGTGGAGAAAGTACCTGCGTG	3609
Db	29432	TAGGGTGGCCTTCTGAATACTGTTATTAAGAAATATGTTGTGGAGAAAGTACCTGCGTG	29491
Qy	3610	CAAAATGTACCGTGGCCCTGTGTATATGATAGAGATTGATATTAATGTACATGTATGTTA	3669
Db	29492	CAAAATGTACCGTGGCCCTGTGTATATGATAGAGATTGATATTAATGTACATGTATGTTA	29551
Qy	3670	ATGTGAATCTGTGGGACAGATATCTTTTTCATGTGACAGAAATATTCAAAGCTGTGGAACGTG	3729
Db	29552	ATGTGAATCTGTGGGACAGATATCTTTTTCATGTGACAGAAATATTCAAAGCTGTGGAACGTG	29611

Qy	3730	GCATGTTTAAATATGCTCATTTGTGCTTACTGTTGTGTGTGAGCATGCGTGAAGGACAAAG	3789
Db	29612	GCATGTTTAAATATGCTCATTTGTGCTTACTGTTGTGTGTGAGCATGCGTGAAGGACAAAG	29657
Qy	3790	AAGTTCATTTGATGATGCAATTAAGCAAGTACTTGCCACTTTTGTGANAATG	3842
Db	29672	AAGTTCATTTGATGATGCAATTAAGCAAGTACTTGCCACTTTTGTGAGCTG	29724

RESULT 7
US-09-781-882-3
; Sequence 3, Application US/09781882
; Patent No. 6630335
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 14171 Protein Kinase, a No. 6630335el Human
; TITLE OF INVENTION: Protein Kinase and Uses Thereof
; FILE REFERENCE: 035800-209014(5800-6
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: U.S. 60/182,096
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-781-882-3

Query Match	61.0%; Score 2355; DB 4; Length 2355;
Best Local Similarity	100.0%; Prod. No. 0;
Matches 2355; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy	17	ATGAGAGGCGACGCGCGGAGCCCATGGGCGCTGCGCTGCGCACCTTGACGCGGCG	76
Db	1	ATGAGAGGCGACGCGCGGAGCCCATGGGCGCTGCGCTGCGCACCTTGACGCGGCG	60
Qy	77	GAGTTCAAGCGGCTGGGAGAAAGTGGGCTCGGCGCGGCTTCGGGAGAGTGAACAAGTGGCG	136
Db	61	GAGTTCAAGCGGCTGGGAGAAAGTGGGCTCGGCGCGGCTTCGGGAGAGTGAACAAGTGGCG	120
Qy	137	CATGTCACCTGGAAGAAGCTGGCTGGCCATCAAGTGTGCGCCAGCTTGCAAGTGCAGCAG	196
Db	121	CATGTCACCTGGAAGAAGCTGGCTGGCCATCAAGTGTGCGCCAGCTTGCAAGTGCAGCAG	180
Qy	197	AAGGAGCGCATGAGACTTTTGGAGAGAGCCCAAGAGATGAGATGGCCAATTTCGTAC	256
Db	181	AAGGAGCGCATGAGACTTTTGGAGAGAGCCCAAGAGATGAGATGGCCAATTTCGTAC	240
Qy	257	ATCCGCTGCTGTATGATGATGATGATGCGCGGACCTGTGCGGCGGTGATGATGATGATGAG	316
Db	241	ATCCGCTGCTGTATGATGATGATGATGCGCGGACCTGTGCGGCGGTGATGATGATGATGAG	300
Qy	317	ACGGGCTCCCTGGAAAAAGCTGCTGGCTTCGGAGGCATTTGCCATGGGATCTTCGGTTCGA	376
Db	301	ACGGGCTCCCTGGAAAAAGCTGCTGGCTTCGGAGGCATTTGCCATGGGATCTTCGGTTCGA	360
Qy	377	ATCATCCACGAGACGCGCGGTGGGATGAACCTTCTGCACTGATGAGCCCGGCACTCTGT	436
Db	361	ATCATCCACGAGACGCGCGGTGGGATGAACCTTCTGCACTGATGAGCCCGGCACTCTGT	420
Qy	437	CACCTGGGACCTCAAGCCCGCGCAACCTCGCTGGATGCGCACTACAGCTCAAGATTTCT	496
Db	421	CACCTGGGACCTCAAGCCCGCGCAACCTCGCTGGATGCGCACTACAGCTCAAGATTTCT	480
Qy	497	GATTTTGGTCTGGCCAGTGCACGCGGCTGTCCACTTCGATGATGACCTTCAGATGGATGGC	556
Db	481	GATTTTGGTCTGGCCAGTGCACGCGGCTGTCCACTTCGATGATGACCTTCAGATGGATGGC	540
Qy	557	CTGTTTGGACAAATGCGCTACTCTCCTTCAAGAGGCGATCAGAGGAAAGACCGGCTCTTC	616

Query Match		45.6%	Score 1760.8	DB 3	Length 3516
Best Local Similarity		83.7%	Pred. No. 0		
Matches 2044		Conservative	0	Mismatches 387	Indels 11
				Gaps	4
QY	18	TGAGAGCGACGCGCGGAGACCCCATGAGGCGCTGCGCTGCGACCTTCGACGCGGCG	77		
DB	5	TGAGAGCGAGGCGCGGCGCGGCGCTGCGCTGCGCTGCGCTGCGCTTCGACGCGGCG	64		
QY	78	AGTTACCGGGCTGGGAGAAAGTGGGCTGGGCGGCTTGGGCGAGGTTGACAAAGTGGCGC	137		
DB	65	AATTGCGAGGCTGGGAGAAAGTGGGCTGGGCGGCTTGGGCGAGGTTGACAAAGTGGCGC	124		
QY	138	ATGTCCATGGAAGACTGCTGCGCATCAAGTGTCCGCCAGCTGACGTGACGACCA	197		
DB	125	ATGTGCATGGAAGAGTGGCTGCGCATCAAGTGTCCGCCAGCTGACGTGACGACCA	184		
QY	198	GGAGCGCATGAGGCTTTTGGAAAGCCAGAGAGTGAAGTGGCCAAAGTTGCTACA	257		
DB	185	GGAGCGCATGAGGCTTCCTGGAGAAAGCTTAAGAGATGAAGATGGCCAAAGTTCCGATACA	244		
QY	258	TCCTGCTGTGTATGGCATCTGCGCGGAACTGTGCGGCTGTGATGAGATGACATGAGA	317		
DB	245	TTCTACCTGTGTATCGGCATATGCGCAGAACTGTGCGGCTGTGATGAGATGACATGAGA	304		
QY	318	CGGCTCCCTGGAAAGCTGCTGCGCTTGGAGCCATTGCGCATGGGATCTCCGGTTCCGAA	377		
DB	305	CAGGCTCCCTGGAGAAAGCTGCTGCGCTTGGAGCCATTGCGCATGGGATCTCCGGTTCCGCA	364		
QY	378	TCATCCACGAGACGCGCGTGGGATGAATCTTCTGCACTGCAATGAGCCCGCCACTTCCTGC	437		
DB	365	TCGTCACGAGACACCCGCGGCGCATGAACTTCTGCAATGCAATGCTCCGCGCATGCTGCG	424		
QY	438	ACCTGACCTCAAGCCCGCGGAACTCTGCTGGAAGGCCCATCAACAGTCAAGATTTCTG	497		
DB	425	ACCTGACCTCAAGCCCGCGGAACTCTGCTGGAAGGCCCATCAACAGTCAAGATTTCTG	484		
QY	498	ATTTTGTCTGCGCAAGTGCACACGCGCTGTCCCATCTGCATGACCTTCAGCATGATGAGCC	557		
DB	485	ACTTTGGGCTGGCCAGTGCATATGCAATGTCCCATCTTCATGACCTTCAGCATGATGAGCC	544		
QY	558	TGTTTGGCAATGCGCTCACTTCCCTCCAGAGCGCATCAAGGAGAAAGCCGCTTCTCG	617		
DB	545	TGTTTGGTATCATTCCTTACCTCCCTCCAGAGCGAATTCGTGAAGAGCCGCTTGTGTTG	604		
QY	618	ACAACGAGACGATGTATACAGCTTTGCGATGCTGATCTGCGGCGCTGCTCAACAGAGA	677		
DB	605	ACAACGAGACGATGTATACAGCTTTGCGATGCTGATCTGCGGCGCTGCTCAACAGAGA	664		
QY	678	AGCCGTTTGCATGATGAAGAACATCTGTCACATCATGTGTAAGGTGTAAGGCGCAC	737		
DB	665	AGCCATTTTGCATATGAAGAACATCTTCATCATATGATGAAGGTGTAAGGCGCAC	724		
QY	738	GCCCGAGCTGCGCGCGTGTGCAGAGCCCGGCGCGCTGCGACGCACTGATAGCGC	797		
DB	725	GCCCGAGGCTGCGCACCATCTGCAGACCCCGGCGCGCTGCTGTCAGACCTGATAGGCGC	784		
QY	798	TCATCAGCGGTGCTGCGCGAGGGAGTCCGCGAGTTAGCGCCCACTTCCAGAAATTAATCT	857		
DB	785	TCATCAGCGGTGCTGCGCGATGACCCACAGGTGCGGCCCACTTCCAGAAATTAATCT	844		
QY	858	CTGAACCGAGAGACCTGTGTGAAGAACCTGATGACGAAGTGAAGAAATGCTCATGATC	917		
DB	845	CTGAACCGAGAAACCTTTGTGTGAAGAACCTGATGAGAGGTGAAGAACTGCGCTCATGAGC	904		
QY	918	TGAGCGTGAAGAGCCCGCGAGCCCGAGAGCGAGGTGTGCTG-----CGAGGCTCA	971		
DB	905	CAGGCGAGAAAGCTCTCTTAGAGTCCAAAGTGAAGGCGCAGGCGCGAGTCTCACGCTCA	964		
QY	972	AGCGGCGCTTGGCCCCCACTTTCGATTAAGATTAAGACCTTCGAGCTTCTTCAAGC	1031		
DB	965	AGCGGCGCTTGTCTCCCTTCGATTAAGATTAAGACCTTCGAGCTTCTTCAAGCT	1024		
QY	1032	TGAGACTGTGAAGTTTCCAGGCTGTGAGAGGCCCGAGAGAGCTCAGCGCAGCTCTCTG	1091		

DB	1025	TGAGACTGTGAAGTTTCCAGGCTCTTGAAGGCCCGGAAAGCTCAGCGCAAGTTCTCTG	1084		
QY	1092	AGTCCAAAGCTCCATCTGTCCGCGAGTGGGAAAGAGCTCTGGGGGTGTCTCCGTTGAC	1151		
DB	1085	AATCCAAAGCTCCATCTGTCCAGAGTGGGAAAGAGCTCTGGGGGTGTCTCCGTTGAC	1144		
QY	1152	CGGCTTCTCTTCCAGAGGATCACTGTGCTGTCTTGTGAAGCGGAACTTCAACAGCG	1211		
DB	1145	CAGCTTTTCTCTCCAGAGGATCTGTGATCTGTCTTGTGAAGCGGAAAGCTTCAACAGCG	1204		
QY	1212	ATCTGGGTACCAAGACGTTCCAGAGAAAGAGCTTGTGAATGTCATGTGTCTC- CGGAC	1270		
DB	1205	ACTTGGGCGCCAC-AGACATCCAGAAAGAGCTAGTGAATGCATATCATAGGCGAC	1263		
QY	1271	ACGACCAATGTAAGATCTGTCACACCGAGGACGTCGACCTGGACATGAGGAGT	1330		
DB	1264	ACGACGAGCTGAAGAAATCTTACAGCCCGCAAGATGTGACTTGTGTTTAGACAGAGT	1323		
QY	1331	GCAAGCTGCTGACCTGCGGCTGAGAGCGCGGCAAGAGAGTGCACCAAGTGGCTG	1390		
DB	1324	GCAAGCTGCTGACCTGCGGCTGAGAGCGCGGCAAGAGAGTGTCAAGTGGCTG	1383		
QY	1391	CTCAACAAATGCAACCCCAACTGAGCAACCGTAGGGGCTTCAACCCGTTGCAATGAGCC	1450		
DB	1384	CTTAACAAATGCAACCCCAACTGACCAACAGAAAGGCTTCAACCACTGCATATGAGCT	1443		
QY	1451	GTGAGAGAGAGGTGGGGGTGTGTGAGAGTCTGTGTCGAGAGGAAAGATGAGTCAAC	1510		
DB	1444	GTGAGAGGAGAGAGCGTGAAGTTGTGAGTCTGTGTCGAGAGGAAAGATGAGTCAAT	1503		
QY	1511	GCAAGAGTGAAGACCAAGTGAACAGCCCTCCACTTTCAGCGCCAGAAACGAGGATGAGTCT	1570		
DB	1504	GCAAGAGTGAAGACCAAGTGAACAGCCCTCCACTTTCAGCGCCAGAAAGTGAAGGCGC	1563		
QY	1571	AGCAACGAGCTGTGTGAGAGAAAGCGCTCGGTCAACGAGGTGAACCTTTGAGGCGCG	1630		
DB	1564	AGCAACAGGCTGTGTGAGAGAAAGTCTTCTGATGAGGTGAGCTTTGAGGCGCGA	1623		
QY	1631	ACGCCCATGCACTGTGGCTGCGACACGCGAGAGAAATTCGCGCATCTGCTGCGC	1690		
DB	1624	ACGCCCATGCACTGTGGCTGCGACACGCGAGAGAAATTCGCGCATCTGCTGCGC	1683		
QY	1691	CGAGCGTGAAGTGAAGCTGTCAGAGGCAAGGATCTGTGCTGACATGACATGACGCTGCC	1750		
DB	1684	CTGTGTGTGAATGTGTGGCTGTGACAGGAAAGGATGCTGTGTGCTGTGACATGAGTGGC	1743		
QY	1751	TGGAGGGCGACCTGCCATCTGCAAGCTGTGCGCAAGCAGCGGGGTGAAGTGTGAAC	1810		
DB	1744	TGGAGGGCGACCTTCCATTTGTTAAGCTGTGACCAAGCAGCGGTGAGTGTGAAT	1803		
QY	1811	GCCAGAGCTGTGAATGAGAGAGCGCATTTGCACTGCGCGGCGACAGCGCGGCACTACCGC	1870		
DB	1804	GCCAGAGCTGTGAAGAGAGAGCGCATTTGCACTGCGCGGCGACAGCGCGGCACTTACCGT	1863		
QY	1871	GTCGCGCATCTCATCTGATGACTGTGCTCCGACGTCAACGTCTGACGCTGTGCGACAG	1930		
DB	1864	GTCGCTGCGCATCTCATCTGATGACTGTGCTCTGATGTTAACATCTGACGCTTACAGGCAAG	1923		
QY	1931	ACACCTTGCAGCTGTGGCGCGAGAGCGGGCAACAGACCTGCGCAGGCTGCTCTGAT	1990		
DB	1924	ACACCTTGCAGTGTGCTGCGAGAGCTGGAACACTGTGATGCTGCGCAGGCTACTCTTGAT	1983		
QY	1991	CGGGCGCTGGCAAGAGAGCGGTGACCTCAACCGGCTTACACCGCTTGCACCTGGCGGCGC	2050		
DB	1984	CGGTGTGTGCAAGAGAGGCTTTTGACTCAAGAGGCTTATATCTTGCACCTGGCAGGCC	2043		
QY	2051	CGCAACGAGACCTTGGCACTGTCAAGCTGTGTGAGAGAGAGCGAGATGTGCTGCC	2110		
DB	2044	CAGAAATGACACTGTGCTACTGTCAAGCTGTCTCATTAAGAGAGAGGCTGATGTATGCT	2103		
QY	2111	CGGGAGCCCTGAACCAAGCGGCGTGTGCACTGTGCTGCGGCCACGCGGCACTCGAGGTG	2170		

Db 2104 CGGGGTCCTGTAATCAGACAGACTGCACCTGCTGCTGCCCTGGAACATCAGAGGTG 2163
Qy 2171 GTGAGAGATTGGTCAAGCCGCGATGTCATTGACCTGTTTCAGACAGAGGCTCAGCGG 2230
Db 2164 GTAGAGAGCTGGTCAAGTCTGACCTCATTTGACTGTCTGATGAGACAGAGGCTCAGCGCA 2223
Qy 2231 CTGACACTGCGCCGCGGCGGCGGACGACAGAGAGTGAAGATCTGCTCAGGATGGG 2290
Db 2224 CTGACACTGCGCTGCTCAGAGGCGAGGATTCACAGACTGTGAGAGACCTGCTCAACATGGA 2283
Qy 2291 GCCCATCACTCACTGACAGAGCTCAAGTTCCAGGGCGGCGCATGGCCCGCGCCACATCTC 2350
Db 2284 GCACACATCACTTTCAGAGTCTCAAGTTCCAGAGAGGCGCAGAGCTCTGCTCCAGTTGG 2343
Qy 2351 CTGCGCGAGAGCAGACCTTCAAGTGTGCTGCTGCGAGACCGGGGGTCCAGTGGGGCTCT 2410
Db 2344 CTCGACGCGAGAGCAGACTAGCT--TGCACCAACAACAGAGGCTCGTGTAGGCTTCC 2400
Qy 2411 TGTCTGTCTGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2452
Db 2401 TGACCATCTCTGTCTCTCTCATGAGGAGAGAAATGCTCTGGG 2442

RESULT 9
US-09-312-283C-257
Sequence 257, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murlson, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 257
LENGTH: 3516
TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-257

Query Match 45.6%; Score 1760.8; DB 4; Length 3516;
Best Local Similarity 83.7%; Pzed. No. 0;
Matches 2044; Conservative 0; Mismatches 387; Indels 11; Gaps 4;

Qy 18 TGGAGGCGGACGCGGCGGACCCCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 77
Db 5 TGGAGGCGGACGCGGCGGACCCCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 64
Qy 78 AGTTCAAGGCTGAGAGAGAGTGGCTCGGCGGCTTTCGAGAGTGTACAAAGTTCGCC 137
Db 65 AATTCGCAAGGCTGAGAGAGTGGCTCGGCGGCTTTCGAGAGTGTACAAAGTTCGCC 124
Qy 138 ATGTCACTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 197
Db 125 ATGTCACTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
Qy 198 GGGAGCGCATGAGCTTTTGGAGAGAGCCAAAGAGATGAGATGGCCAAAGTTTCGTAC 257
Db 185 GGGAGCGCATGAGCTTCTTGGAGAGAGCTTAAAGATGAGATGGCCAAAGTTTCGTAC 244
Qy 258 TCTGCTGTGTATGAGATTCGCGGAGACCTTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
Db 245 TTCTACTGTGTATGAGATTCGCGGAGACCTTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
Qy 318 CGGGCTCCCTGAGAGAGCTGCTGCTTTCGAGGCAATTCGAGGATTCCTCGGTTCCGAA 377

Db 305 CAGGCTCCCTGAGAGAGCTGTGCTCTCAGAGCCATTGCTTTGGAGACTGTGCTTTCGCA 364
Qy 378 TCAATCCAGAGACGCGGCTGAGAGTAACTTCCGCACTGACAGGCGCGGCACTCTGCTG 437
Db 365 TCGGACAGAGACGCGGCTGAGAGTAACTTCCGCACTGAGATGTCTCCGCACTGCTGCTG 424
Qy 438 ACTGAGACTCAACCCGCGAGACATCTGCTGAGTGGCCATCAAGTCAAGATTTCTG 497
Db 425 ACTGAGACTCAACCCGCGAGACATCTGCTGAGTGGCCATCAAGTCAAGATTTCTG 484
Qy 498 AATTTGCTGCGCAAGTGCACAGGCGCTGTCCACTGCGATGACTCAGCATGAGATGGCC 557
Db 485 ACTTTGGCTGGCCAAAGTGCATGATGTCCACTCTCATGAGCTCAGCATGAGATGGCC 544
Qy 558 TGTTTGGCAATAGGCTCACTCTCCCTCAGAGGCGCATCAGGAGAGAGCGGCTTTCG 617
Db 545 TGTTTGGCAATAGGCTCACTCTCCCTCAGAGGCGCATCAGGAGAGAGCGGCTTTCG 604
Qy 618 ACACCAAGCAGATGATATCAGCTTTGCGATGCTCATCTGAGGCGGTCTCACAAGAGA 677
Db 605 ACACCAAGCAGATGATATCAGCTTTGCGATGCTCATCTGAGGCGGTCTTACAGAGAGA 664
Qy 678 AGCGTTTGAGATGAGAGAACTCTGCACTCATGCTGAGAGTGTGAGAGGCGCAC 737
Db 665 AGCGTTTGAGATGAGAGAACTCTGCACTCATGATGATGATGATGATGATGATGATGATGATG 724
Qy 738 GCGCGAGCTGCGCGCGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 797
Db 725 GCGCGAGCTGCGCGCGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 784
Qy 798 TCATGACAGGCTGCGAGGAGATCCGAGTTTGAAGCCACCTTCCAGAAATTAATCT 857
Db 785 TCATGACAGGCTGCGAGATCCGAGTTTGAAGCCACCTTCCAGAAATTAATCT 844
Qy 858 CTGAAACGAGAGCTGTGTGAGAAAGCTGATGAGAGTGAAGAAAGAACTGCTCATGATC 917
Db 845 CTGAAACGAGAGCTGTGTGAGAAAGCTGATGAGAGTGAAGAAAGCTGCTCATGATGAGC 904
Qy 918 TGAAGTGAAGAGCG 971
Db 905 CAGGCGAGAGAGAGCTCTTGAAGTCCAGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 964
Qy 972 AGCGGCGCTGCG 1031
Db 965 AGCGGCGCTGCG 1024
Qy 1032 TGAAGTGAAGTTCAGAGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1091
Db 1025 TGAAGTGAAGTTCAGAGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1084
Qy 1092 AGTCAAGCTGATGCTGCGCGAGTGGAGAGAGGCTCTCGGGGGTGTCTCGTGGAGCT 1151
Db 1085 AATGCAAGCTGATGCTGCGCGAGTGGAGAGAGGCTCTCGGGGGTGTCTCGTGGAGCT 1144
Qy 1152 CGGCTTCTTCCAGAGATCACTGCTGTCTTTCGAGGCGGAGACCTTCAACAGCG 1211
Db 1145 CAGCTTCTTCTCAGAGATGCTGTCTGTCTTTCGAGGCGGAGACCTTCAACAGCG 1204
Qy 1212 ATCTGAGTACAGAGAGTTCAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGATG 1270
Db 1205 ACTTGGGCGCGAC-AGATTCAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGATG 1263
Qy 1271 ACCAGGAACTGATGAGATCTGTGAGCGCGAGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 1330
Db 1264 ACCAGGAACTGATGAGATCTGTGAGCGCGAGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 1323
Qy 1331 GCGAGCTGCTGCACTGCGGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1390
Db 1324 GCGAGCTGCTGCACTGCGGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1383
Qy 1391 CTCAACAAATGCGCAACCTGAGCAACGCTGAGAGCGCTGCAACCTGAGCAATGAGC 1450
Db 1384 CTCAACAAATGCGCAACCTGAGCAACGCTGAGAGCGCTGCAACCTGAGCAATGAGC 1443

QY 1451 GTGAGAGAGGGGTCCGGGGTGTCTGTGAAGCTCTGCTGGCA CGGAAGATCACTGTCAAC 1510
Db GTGGAGCGGAAGGGGAGCTGGAAATTTGTGAGGTACTAGACCCGGAGACCAAGCTGTCAAT 1503
QY 1511 GCCAAGATGAGGACCACTGGGACAGCCCTCCACTTTGGAGCCCAAGAGGGGATGAGCT 1570
Db 1504 GCGAAGATGAGGACCACTGGGACAGCCCTCCACTTTGGAGCCCAAGAGGGGATGAGCT 1563
QY 1571 AGCACAAGGCTGCTGTGGAGAGAACGCTTCGCTCAACGAGGTGAGCTTTGAGGGCCGG 1630
Db 1564 AGCACAAGGCTGCTGTGGAGAGAACGCTTCGCTCAACGAGGTGAGCTTTGAGGGCCGA 1623
QY 1631 AGCCCAATGCACTGAGCTGCTGGCAAGCAGGACAGGAATATGTGCGCATCTGCTGGCC 1690
Db 1624 ACACCAATGCACTGAGCTGCTGGCAAGCAGGACAGGAATATGTGCGCATCTGCTGGCC 1683
QY 1691 CGAAGCGTGGACGTAGAGCTGCAAGGCAAGATGCTGGCTGGCACTGCACTAGCGTGGC 1750
Db 1684 CGTGTGTGGATGTGGGCTGCAAGGAGAGATGCTGGTGGCTGCTGCACTAGCTGGCC 1743
QY 1751 TGGCAGGGCCACTGCTCCCATCTGTCAAGCTGTGCGCAAGCAGCGGGGTGAGTGTGAAC 1810
Db 1744 TGGCAGGGCCACTCTCCCATCTGTTAAGCTGTGCAAGCAGCCTGGGGTGAAGTGTGAAT 1803
QY 1811 GCCCAGAGCGCTGAGTGGAGAGACGCCATTGCACTGCGCGCAAGCCGGGCACTAACGCC 1870
Db 1804 GCCCAGAGCACTTAGCGGGAGGACACCCCTGCACTGGCTGTCAAGAGGGGGCACTTAACGGT 1863
QY 1871 GTGGCCCGCATCTCATGCAAGCTGTGCTCGAGCTCAAGCTGTGAGCGCTGTGGCAAG 1930
Db 1864 GTGGCTCGCATCTCATTTGACCTGTGCTGTGATGTTAACATCTTGACCTTAAGGCAAG 1923
QY 1931 ACACCCCTGCAAGCTGGCCGCGGAGACAGGGGCAACAGAGCACTGCAAGCTGTCTGTCAAT 1990
Db 1924 ACACCTGCTCATGTTGCTGCAAGACTGAGACACTAGTACTGCAAGGCTTACTTTGCAAT 1983
QY 1991 CGGGGCGCTGGCAAGAGAGCCGCTGACCTGACAGCGCTTACACCGCTCTGCACTTGGCTGCC 2050
Db 1984 CGTGTGTGGAGAGAGAGGCTTTGACCTTCAAGAGGGCTTATCTGCTGCACTGGCAAGCC 2043
QY 2051 CGCAACGAGCACTGGCCCACTGTCAAGCTGTGTGTGAGAGAGAGGCGAGTGTGCTGGCC 2110
Db 2044 CAGAAATGAGCACTGTGCTACTGTCAAGCTGTCTCAAGAGAGAGAGGCTGATGTGCTGT 2103
QY 2111 CGGGGACCCCTGAAACCAAGACAGCGCGCTGCACTGTGCTGCGCCCAAGGCACTCGAAGGTG 2170
Db 2104 CGGGGGTCCCTGAAATCAAGACAGCACTGCACTGGCTGCTGCGCGTGGACACTCAAGAGGTG 2163
QY 2171 GTGAGAGAGTGTGTCAAGCCGCAATGTCAATTGACCTGTGTGACAGAGAGAGGGCTCAAGCCGG 2230
Db 2164 GTAGAGAGAGCTGTGTGCTGACTGTCACTTGTGATGTGAGAGAGGGCTTCAAGCCGA 2223
QY 2231 CTGCACTGTGGCGCCCAAGGGGCGGCAAGCAGAGACGATGAGAGACTTGTGCTCAGGACATGGG 2290
Db 2224 CTGCACTGTGGCTGTCAAGGAGAGGCAATTCAAGAGCTGTGAGAGCACTGTCTCAAAATGGA 2283
QY 2291 GCCCAATCAACCTGCAAGAGCTTCAAGTTCAAGGGGAGCCATGAGCCCGCGCCCACTC 2350
Db 2284 GCACACATCAACTGTGAGAGGTCTCAAGTTCCAAAGAGGCGCAGAGGCTGTCTGCAAGTGG 2343
QY 2351 CTGCGCGCAAGAGCAAGCTTAACTGTGCTGCTGAGAGACCGGGGGTTCACAGTGGGGCTCT 2410
Db 2344 CTCCCAAGAGAGCAAGCTTAACT--TGCACCACAAAAACAGAGGCTTCGTGTAGGCTTTC 2400
QY 2411 TGTCTGTCTGTGTCTCTGTGTGGAGATGAAAGATCTGTGGC 2452
Db 2401 TGGACCATCTTGTCTTCTCAAGGAGCAAGAAATGTCTGTGG 2442

RESULT 10
us-09-509-802-1
; Sequence 1, Application US/09509802

; Patent No. 6489130
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virca, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/09/509,802
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Mus sp.
us-09-509-802-1

Query Match 45.2%; Score 1745.4; DB 4; Length 2370;
Best Local Similarity 84.6%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 356; Indels 8; Gaps 3;

QY 18 TGAAGGCGACGAGGAGGCCCATGGGCGCTGCGCTGCGCACTTGGACGCGGCG 77
Db 11 TGAAGGCGAGGCGCGGCGCGGTGGCTGTGGGCTGTGCGCACCCTTGCAGCCGCGCG 70
QY 78 AGTTCAAGGCTGGAGAGAGGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAAGTGGGCC 137
Db 71 AATTCAAGGCTGGAGAGAGGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAAGTGGGCC 130
QY 138 ATGTCACTGGAAGACCTGTGCTGCAATCAAGTGTGCGCCAGCTGCACTGCAAGCA 197
Db 131 ATGTCACTGGAAGACGTGTGCTGCAATCAAGTGTGCGCCAGTGTGCAAGTGTGCAAGCA 190
QY 198 GGAAGCGATGAGAGCTTTTGAAGAGCAAGAGAGAGAGATGAGATGGCCAAAGTTTGTGCA 257
Db 191 GGAAGCGATGAGAGCTTCTGAGAGAGAGTAAAGAGAGAGAGAGAGTGGCAAGTTTGTGCA 250
QY 258 TCCGCGCTGTATGAGATCTGCGCGGCAAGCTGTGCGGCTGTGATGAGATGAGAGAG 317
Db 251 TTCTACCTGTATGAGATGAGATGAGAGAGCTGTGCGGCTGTGATGAGATGAGAGAG 310
QY 318 CGGGCTCCCTGGAAGAGCTGTGCTGCGAGCCATTGCAATGGAGATCTCCGATTCGGA 377
Db 311 CAGGCTCCCTGGAAGAGCTGTGCTGCGAGCCATTGCAATGGAGATCTGCGAGCTTTCGCA 370
QY 378 TCATTCACAGAGAGCGCGGTGGCAATGAATCTTCTGCACTGTGATGAGCCCGGCACTCTGCG 437
Db 371 TCGTGCAGAGAGAGCGCGGTGGCAATGAATCTTCTGCAATGATGTCTCCGCACTGCTGC 430
QY 438 ACCTGGAAGCTGAAGCGCGGCAAGATCTGCTGAGATGAGCCATACAGAGTCAAGATTTCTG 497
Db 431 ACCTGGAAGCTGAAGCGCGGCAAGATCTGCTGAGATGAGCCATACAGAGTCAAGATTTCTG 490
QY 498 ATTTGTGTCTGCGCAAGTGAAGCGGCTGTGCTCACTGCGATGAGCTTCAAGATGAGGCC 557
Db 491 ACTTTGGGCTGCGCAAGTGAAGCGGCTGTGCTCACTGCGATGAGCTTCAAGATGAGGCC 550
QY 558 TGTTTGGCAATGAGCTTCTCTCTGAGGCGCATGAGGAGAGAGAGCGGCTCTTTCG 617
Db 551 TGTTTGGCAATGAGCTTCTCTCTGAGGCGCATGAGGAGAGAGAGCGGCTCTTTCG 610
QY 618 ACACCAAGCAGAGATGATACAGCTTTGCGATGCTCATGTGGGGGTGTGCAAGAGAGA 677
Db 611 ACACCAAGCAGAGATGATACAGCTTTGCGATGCTCATGTGGGGGTGTGCAAGAGAGA 670
QY 678 AGCCGTTTGCAGATGAGAGAGATCTGCAATCATGTGTAAGGTGTGAAGGCCCAAC 737
Db 671 AGCCATTTGCAGATGAGAGAGATCTTCAACATCATATGATGAAGTGTGAAGGCCCAAC 730
QY 738 GCCCGAGCTGCGCGCTGTGCAAGAGCGCGCGCGCGCTGCAAGCCACTGATAGGCC 797
Db 731 GCCCGAGCTGCGCGCTGTGCAAGAGCGCGCGCGCGCGCTGCTGCGAGCTGATAGGCC 790

[illegible]

Db	1207	ACCTGGGGCCCCAC - AGCATTCCAGGAAGAAGACTGATGATGCATCATATCAGGGAGC	1265
QY	1271	ACGACGAAACTGATGAAAGATCTTCGACACCCGACAGGACTGTGAACCTGGGACATCGACAGGGGT	1330
Db	1266	ACGACGAGCGCTGAAGAAAGATCTTCACAGCCCCCAATGTGACCTTGATTCAGACAGCAGT	1325
QY	1331	GCAGCGCTGCTGCACCTGGGCGGTGGAGGACCGGGCCAAAGAGAGTGCAGCAAGTGGCTCTGTG	1390
Db	1326	GCCAGCCTGCTGCACCTGGCTGTGGAGGACCGGACAGAGAGTGTGTCTAGTGGCTGCTG	1385
QY	1391	CTCAACAATGCGCAACCCCAACTTGAGCAACGTAGGGGCTTCACCCCGTTGCAATGGCC	1450
Db	1386	CTTAACAATGCGCAACCCCAACTTCACCAAGAGAGGGCTCTTAACACCATGCAATAGGCT	1445
QY	1451	GTGAGAGAGAGGGGTGGCGGGGTGTCTGTGAGGCTCTGCTGGCACGGAAGATCATGTCTAAC	1510
Db	1446	GTGAGAGCGGAAGGGGACGTGGAAATGTGTGAGACTTACTGTAGCCCGGAAGACCATGTCTAAT	1505
QY	1511	GCCAAAGATGATGAGACCAAGTGGACAGCCCTCACCTTTCAGACCCAGAAACGGGGAATGAGCT	1570
Db	1506	GCCAAAGATGGAAGACCAAGTGGACAGCCCTTCGACTTTCAGACCCAGAAATGGGGAATGAGGCC	1565
QY	1571	AGCAACAGCGCTGCTGTTTGGAGAGAACAAGCCTCGGTCAACGAGGTGGACTTTTGAAGGGCGG	1630
Db	1566	AGCAACAGCGCTGCTGCTGATGAGAGAACAATCTTCTGTCAATGAGGTGGAATTTTGAAGGCCGA	1625
QY	1631	ACGCCCATGCAAGTGGGCTGTCCAGCACGGGACGAGAGAATATCGTGGCATCTCTGCTGCGC	1690
Db	1626	ACACCCCAATGCAATGATAGCTGTCCAGCATGAGACAGGAACAATGTGGCCACCTGTCTCGC	1685
QY	1691	CGAGGCGTGGACGTGAGGCTTCGACAGGGCAAGGATGCCCTGGCTGCCCATCTGCACTACGCTGGCC	1750
Db	1686	CGTGGTGTGGATGTGGGCGCTTCGACAGGAAAGGATCCGTGGTTCCTTCGCACTATGACTGGCC	1745
QY	1751	TGGCAGGGGCGCACTGCCCATGTCAGGCT	1779
Db	1746	TGGCAGGGGCGCACTTCCCATGTGTAGCT	1774

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RESULT 12
US-09-188-930-66
/ Sequence 66, Application US/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Muirson, James Greg
/ TITLE OF INVENTION: Compositions Isolated From Skin Cells
/ TITLE OF INVENTION: and Methods For Their Use
/ FILE REFERENCE: 11000.1011c1
/ CURRENT APPLICATION NUMBER: US/09/188.930A
/ CURRENT FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 66
/ LENGTH: 1888
/ TYPE: DNA
/ ORGANISM: mouse
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1690)...(1690)
/ NAME/KEY: unsure
/ LOCATION: (1755)...(1755)
/ NAME/KEY: unsure
/ LOCATION: (1864)...(1864)
US-09-188-930-66

Query Match      33.3%,      Score 1284; DB 3, Length 1888;
Best Local Similarity 83.1%,      Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 299; Indels 21; Gaps 9;

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QY 18 TGGAGGCGACCGCGGACCCCATGAGCCCTGCGCTGCGCACTTTGACCGCGGCG 77
 DB 5 TGGAGGCGACCGCGGACCCCGGCGCTGCGGCTGCGCACTTTGACCGCGGCG 64
 QY 78 AGTTTCCGAGGCTGGAGAGAGTGGGCTCGGCGCGCTTTGGGAGAGTGTACAGAGTGGCG 137
 DB 65 AATTGCGCAGGCTGGAGAGAGTGGGCTCGGCGCGCTTTGGGAGAGTGTACAGAGTGGCG 124
 QY 138 ATGTCCATGGAAGACCTGGCTGGCATCAAGTGTCTGCCAGCTGCACTGTGACGACA 197
 DB 125 ATGTGACATGGAAGACGTGGCTGGCATCAAGTGTCTGCCAGCTGCACTGTGACGACA 184
 QY 198 GGGAGGCGATGAGAGCTTTTGGAGAGCCAGAGAGATGAGATGGCGAAGTTTCTGTACA 257
 DB 185 GGGAGAGATGAGAGCTCTGAGAGAGCTTAAAGAGATGAGATGGCGAAGTTTCTGTACA 244
 QY 258 TCCGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGATGAGATGATGAGAGA 317
 DB 245 TTCTACTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGATGAGATGATGAGAGA 304
 QY 318 CGGAGCTCCCTGAGAAAGCTGCTGCTTGGAGCCATTTGCCATGGATCTTCGGTTCCGA 377
 DB 305 CAGGCTCCCTGAGAGAGCTGCTGCTGCTGAGAGCCATTTGCCATGGATCTTCGGTTCCGA 364
 QY 378 TCATCCAGAGAGCGGCTGGGAGATGAATCTTCTGTGACATGAGCGCGGCACTCTGCG 437
 DB 365 TCGTGACAGAGAGCGGCTGGGAGATGAATCTTCTGTGACATGAGCGCGGCACTCTGCG 424
 QY 438 ACCTGAGCCCTCAGAGCCCGGAGACATCTGCTGAGATGCCCATAC--AGCTCAAGATTTC 495
 DB 425 ACCTGAGCCCTCAGAGCCCGGAGACATCTTGTGTGATGCTGCACTACCAATGTCAAGATTTC 484
 QY 496 -TGATTTGTGTGCGCAAGTGTGCAAGGCTGTCCCATCTGCAATGACTTCAGATGATG 554
 DB 485 TTGACCTTTGGGCTGGCGCAAGTGTGCAATGATGCTCCCATCTGCAATGACTTCAGATG 544
 QY 555 GCTGTTTGGCAATATGCTTACCTCTTCAAGAGGCACTCAGGAGAGAGAGCGGCTCT 614
 DB 545 GCTGTTTGGTACATATGCTTACCTCTTCAAGAGGCAATCTGTGAGAGAGCGGCTCTG 604
 QY 615 TCGACCAAGACAGATGTATACAGCTTTGCGATCTGCTGAGGCGTGTGACACAGA 674
 DB 605 TTGACCAAGACAGATGTATACAGCTTTGCGATCTGCTGAGGCGTGTGACACAGA 664
 QY 675 AGAAGCGTTTGGAGATGAGAGAGACATCTGCAATCATGTGAGAGTGTGAGAGGCGC 734
 DB 665 ATATATCATTTTGGAGATGAGAGAGACATCTTACATCATGATGAGAGTGTAAAGGCGC 724
 QY 735 ACCGCGCGAGCTGCGCGCTGTGTGACAGACCGCGCGCGCGCTGTGACAGCATGTATAC 794
 DB 725 ACCGCGCGAGCTGCGCGCATCTGCAAGACCGCGCGCGCGCTGTGCGAGCTGTATAG 784
 QY 795 GCGTCAATGACAGGCTGTGCGAGGAGATCCGCGAGTGTAGAGCCCATCTTCAAGAAATTA 854
 DB 785 GCGTCAATGACAGGCTGTGCGAGATCCGCGAGTGTAGAGCCCATCTTCAAGAAATTA 844
 QY 855 CTTCAGAACCGAGACCTGTGTGAAAAGCTGTATGACAGAGTGTGAAAAGAACTGTATG 914
 DB 845 CCGTGTGAAAAGAGACCTTTGTGAGAGAGCTGTATGAGAGTGTGAAAAGAGCTGTATG 904
 QY 915 ATCTGACGTGAAAAG 968
 DB 905 AGCGAGCGGAGAAAGCTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964
 QY 969 TCAAGCGGCGCTGCGCGCGCATTTGATACAGACCTCTCCAGAGCTTCTGTAC 1028
 DB 965 TCAAGCGGCGCTGCGCGCGCATTTGATACAGAGCTCTCTCCAGAGTGTCTGTAC 1024
 QY 1029 AGCTGACCTGTGAGATTTCAGAGCTGTG---GAGGCGCGCGAGAGAGCTCAGCGCAGCT 1085
 DB 1025 AGTTGAGCTCTGGGATCTTCCAGAGACTTTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1084
 QY 1086 CCGTGTGAGTCCAGAGCTGCGCATCTGCGCGAGTGTGAGAGAGAGAGCTCTCGGCGG 1145

DB 1085 CCTGTGATGAGAGTGTCCATCTGTGACAGACATGTGCGAGAGGCTCTCGGAGGCTGTCTCAG 1144
 QY 1146 TGAAGTCCGCTTCTCTTCCAGAGATCATCTGTGCTGTCTCTTGAAGGAGAGACCTTCAA 1205
 DB 1145 TGAAGTCCGCTTCTCTTCCAGAGATCATCTGTGCTGTCTCTTGAAGGAGAGCTTCAA 1204
 QY 1206 CAGGAGCTGTGGATCCAGAGAGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
 DB 1205 CAGGAGCTGTGGAG 1263
 QY 1265 CAGGAGCTGTGGAG 1324
 DB 1264 CAGGAGCTGTGGAG 1323
 QY 1325 AGGAGTCCAGCTGTGCTGACCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1384
 DB 1324 AGGAGTCCAGCTGTGCTGACCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
 QY 1385 CCGCTGTCCAAATATGCAACCCCACTGAGCAACCGTAGAGGCTCCACCCGTTGAC 1444
 DB 1384 CCGCTGTCCAAATATGCAACCCCACTGAGCAACCGTAGAGGCTCCACCCGTTGAC 1443
 QY 1445 ATGAGCTGTGAG 1504
 DB 1444 ATGAGCTGTGAG 1503
 QY 1505 GTCAAGCCAGAGATGAGAGACATGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
 DB 1504 GTCAAGCCAGAGATGAGAGACATGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1563
 QY 1565 G-AGCTTGTGACAG 1623
 DB 1564 G-AGCTTGTGACAG 1623
 QY 1624 GGGCGGAG 1683
 DB 1624 GGGCGGAG 1683
 QY 1684 GCTGCGCGAG 1743
 DB 1684 GCTGCGCGAG 1743
 QY 1744 CGCTGCGCGAG 1803
 DB 1744 CGCTGCGCGAG 1803
 QY 1804 TGTGAAGCCAG 1863
 DB 1803 TGTGAAGCCAG 1863
 QY 1864 CTACCGGCTGTGCGCGAG 1894
 DB 1858 TTTACGAGGCTGTGCGAG 1888
 RESULT 13
 US-09-312-283C-66
 ; Sequence 66, Application US/09312283C
 ; Patent No. 6573095
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Muriel, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011C2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425

Search completed: September 16, 2005, 07:15:47
Job time : 1884.6 secs

US-10-658-904-1

Query Match 100.0%; Score 3859; DB 18; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACGGCTCCGGCGGATGAGAGGCGAGCGGCGGACCCCATGAGGCGCTGCGGCTGCGG 60
DB 1 CCACGGCTCCGGCGGATGAGAGGCGAGCGGCGGACCCCATGAGGCGCTGCGGCTGCGG 60
QY 61 CACCTTGCACGCGGCGCAGATTCAAGGCTGGAGAGAGTGGGCTCGGCGGCTTGGGCA 120
DB 61 CACCTTGCACGCGGCGCAGATTCAAGGCTGGAGAGAGTGGGCTCGGCGGCTTGGGCA 120
QY 121 GGTGTACAAAGTGGCGCCATGTCTCACTGGAAAGCTGGCTGGCCATCAAGTGTCTGGCCAG 180
DB 121 GGTGTACAAAGTGGCGCCATGTCTCACTGGAAAGCTGGCTGGCCATCAAGTGTCTGGCCAG 180
QY 181 CCTGCAGCTGCACGACGAGGAGCGCATGAGCTTTTGGAAAGAGCCAAAGATGAGAGT 240
DB 181 CCTGCAGCTGCACGAGAGGAGCGCATGAGCTTTTGGAAAGAGCCAAAGATGAGAGT 240
QY 241 GGCCTAAGTTTGCCTACATCTGCTGTGTATGGCATCTGCGCGAACCCTGTGCGCTGAT 300
DB 241 GGCCTAAGTTTGCCTACATCTGCTGTGTATGGCATCTGCGCGAACCCTGTGCGCTGAT 300
QY 301 CATGAGATACATGAGAGAGCGGCTCCCTGGAAAAGCTGCTGGCTTGGAGCCATTGGCATTG 360
DB 301 CATGAGATACATGAGAGAGCGGCTCCCTGGAAAAGCTGCTGGCTTGGAGCCATTGGCATTG 360
QY 361 GGAATCCGCGGTTCCGAAATCATCCAGAGAGCGGCGGATGAACTTCTGSCATCTGAT 420
DB 361 GGAATCCGCGGTTCCGAAATCATCCAGAGAGCGGCGGATGAACTTCTGSCATCTGAT 420
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DB 421 GGCCTCCGCGCATCTCTGCACTTGAACCTCAAGCCCGGAAATCATCTGCTGATGCGCACATA 480
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DB 481 CCAAGTCAAGATTTTCTGATTTTGTGTGCGCAAGTGCACAGCGGCTGTCCCATCTCCATGTA 540
QY 541 CCTCAGCATGATGAGCTGTTTGGCAAAATGCGCTACCTCCCTCCAGAGCGCATGAGGTA 600
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DB 661 CGTGTCTCACAGAAAGAGCGTTTGGCATATGAGAAAGCATCTCTGCAATATGATGTA 720
QY 721 GGTGTGAAAGGCGCACCGGCCCGAGCTGCGCCCGTGTGACAGAGCCGCGCGCGCTG 780
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QY 1021 TCTCTCAAGCTGGAATCTTGAGATTTCACAGGCTGTGAGGAGCCCGAGAGAGCTCAGCCG 1080
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QY 1141 CTGGTGGACTCCGCTTCTTCTTCAAGAGATCACTGTCCGTCTCTTTGAGCGGAAAC 1200
DB 1141 CTGGTGGACTCCGCTTCTTCTTCAAGAGATCACTGTCCGTCTCTTTGAGCGGAAAC 1200
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DB 1561 GGAATGATCTAGCAACAGGCTGTGTTGAGAGAAAGCGCTCGGTCAACGAGTGGACTT 1620
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DB 1621 TGAAGGCGGAGCGCCATGACAGTGGCGCTGACAGCAGGAGAGAAATATGTCGAT 1680
QY 1681 CCTGCTGGCGGAGCGGTGACATGAGCTTGCAGAGGCAAGATCCCTGCGCTGCCACTGCA 1740
DB 1681 CCTGCTGGCGGAGCGGTGACATGAGCTTGCAGAGGCAAGATCCCTGCGCTGCCACTGCA 1740
QY 1741 CTAAGCTGCTGGAGAGGCGCACTGCGCATATGTCAGAGCTGTGCAAGCAGCGGAGGT 1800
DB 1741 CTAAGCTGCTGGAGAGGCGCACTGCGCATATGTCAGAGCTGTGCAAGCAGCGGAGGT 1800
QY 1801 GAGTGTGAACGCCAGAGCGTGAATGAGAGAGCCCATTTGACCTTGGCGCGACAGCGCG 1860
DB 1801 GAGTGTGAACGCCAGAGCGTGAATGAGAGAGCCCATTTGACCTTGGCGCGACAGCGCG 1860
QY 1861 GCACTACCGGCTGGCGGCTCTCATATGACCTGTGTCCGACGTCAACGCTCTGACGCT 1920
DB 1861 GCACTACCGGCTGGCGGCTCTCATATGACCTGTGTGTCCGACGTCTGACGCT 1920
QY 1921 GGTGGCAGACACCCCTGACAGTGGCGCGGAGAGACGAGGAGCACTGCGAGGCT 1980
DB 1921 GGTGGCAGACACCCCTGACAGTGGCGCGGAGAGACGAGGAGCACTGCGAGGCT 1980
QY 1981 GCTCTGATGAGGAGCGCTGAGAGAGGCGGTGACCTCAAGCGCTACACCGCTCTGCA 2040
DB 1981 GCTCTGATGAGGAGCGCTGAGAGAGGCGGTGACCTCAAGCGCTACACCGCTCTGCA 2040
QY 2041 CTTGGCTGCGGCAACGAGCACTTGGCGCATCTGTCAAGTGTCTTGTGAGAGAGGCGCA 2100
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;; PRIOR APPLICATION NUMBER: US 60/364,517
;; PRIOR FILING DATE: 2002-03-15
;; PRIOR APPLICATION NUMBER: US 60/371,075
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: US 60/371,507
;; PRIOR FILING DATE: 2002-04-10
;; PRIOR APPLICATION NUMBER: US 60/372,984
;; PRIOR FILING DATE: 2002-04-16
;; PRIOR APPLICATION NUMBER: US 60/374,194
;; PRIOR FILING DATE: 2002-04-19
;; PRIOR APPLICATION NUMBER: US 60/382,995
;; PRIOR FILING DATE: 2002-05-24
;; PRIOR APPLICATION NUMBER: US 60/385,023
;; PRIOR FILING DATE: 2002-05-31
;; PRIOR APPLICATION NUMBER: US 60/388,853
;; PRIOR FILING DATE: 2002-06-14
;; PRIOR APPLICATION NUMBER: US 60/389,395
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: FastSeq For Windows Version 4.0
;; SEQ ID NO: 37
;; LENGTH: 3860
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (17) ... (2371)
US-10-354-358-37
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Query Match 99.4%; Score 3836; DB 16; Length 3860;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 2; Gaps 2;

Matches 3858; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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DB 61 CACCTTCCAGCGGCGGCGAGCTTCA CGGCGCTGGAGAAAGTGCGGCGCTTGCGGCGCA 120
QY 121 GGTGACAAAGGCGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GGTGACAAAGGCGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CTTGCACTGCAAGCAAGGAGCGGATGAGCTTTTGAAGAAAGCCAAAGATGAGAT 240
DB 181 CTTGCACTGCAAGCAAGGAGCGGATGAGCTTTTGAAGAAAGCCAAAGATGAGAT 240
QY 241 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CATGAGATGATGAGAGCGGCGCTCCCTGAGAAAGCTGCGGCTTGAGGCAATGCGCATG 360
DB 301 CATGAGATGATGAGAGCGGCGCTCCCTGAGAAAGCTGCGGCTTGAGGCAATGCGCATG 360
QY 361 GGAATCTCCGCTTCCGATCATCTCAAGAGCGGCGTGGGCAATGAACTTCTGCTGCTGAT 420
DB 361 GGAATCTCCGCTTCCGATCATCTCAAGAGCGGCGTGGGCAATGAACTTCTGCTGCTGAT 420
QY 421 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CCAAGTCAAGATTTCTGATTTTGTCTGCGCAAGTGAAGCAAGCGGCTGCTGCTGCTGCTG 540
DB 481 CCAAGTCAAGATTTCTGATTTTGTCTGCGCAAGTGAAGCAAGCGGCTGCTGCTGCTGCTG 540
QY 541 CTTGAGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 CTTGAGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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DB 541 CTTGAGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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QY 661 CGTCTCAACAGAAAGCGGCTTGGAGATGAGAAAGCAATCTGTCATCATGATGATGATGATG 720
DB 661 CGTCTCAACAGAAAGCGGCTTGGAGATGAGAAAGCAATCTGTCATCATGATGATGATGATG 720
QY 721 GGTGTGAAGGCGCACCGCCCGAGCTGCGCGCGCTGTGCAAGAGCCCGCGCGCGCTG 780
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DB 841 CTTCCAGAAATTTCTTCTGAAACCGAGACCTGTGTGAAAGGCTGATGACGAAGTGA 900
QY 901 AGAAATGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
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QY 1261 TGTCTC- GAGACCAAGCAAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1319
DB 1261 TGTCTC- GAGACCAAGCAAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1319
QY 1320 TGTGAGGCGGAGCAAGCAAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1379
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QY 1380 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
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QY 1440 TGCATATGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499
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QY 1560 GGGATGAGTCTGAGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1619
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QY	1680	TCCTGCTGCGCCGAGGCGCTGACCTGAGCCCTGCAAGGCGCAAGAGTACCTGCTGCGCACTGCG	1739
Db	1680	TCCTGCTGCTGCGCGAGGCGCTGAGCCTGACCTGCAAGGCGCAAGAGTACCTGCTGCGCACTGCG	1739
QY	1740	ACTAGCGCTGCGGCGAGGCGCAACCTGCGCCATCTGTCATCAACTCTGCGCAAGCAGCGCGGCG	1799
Db	1740	ACTAGCGCTGCGGCGAGGCGCAACCTGCGCCATCTGTCATCAACTCTGCGCAAGCAGCGCGGCG	1799
QY	1800	TGAGGTGAAACGCCCAACCGCTGAGATGGAGAGACGCCATTTGCACTTGGCCGCAACGCCGCG	1859
Db	1800	TGAGGTGAAACGCCCAACCGCTGAGATGGAGAGACGCCATTTGCACTTGGCCGCAACGCCGCG	1859
QY	1860	GCGACTACCGCGGTGGCCCGCGCACTCTCATGACCTGTGCTCGAGCGTCAACGCTGCGCAACC	1919
Db	1860	GCGACTACCGCGGTGGCCCGCGCACTCTCATGACCTGTGCTCGAGCGTCAACGCTGCGCAACC	1919
QY	1920	TGCTTGCGCAACAGCACCCCTGACAGTGAGCGCGGAGACCGGCGCAACAGCACCTGCGCAACC	1979
Db	1920	TGCTTGCGCAACAGCACCCCTGACAGTGAGCGCGGAGACCGGCGCAACAGCACCTGCGCAACC	1979
QY	1980	TGCTTCTGCAATCGGGGCGCTGGCAAGAGGCGGTGACCTCAAGCGGCTTACACCGCTCTGCG	2039
Db	1980	TGCTTCTGCAATCGGGGCGCTGGCAAGAGGCGGTGACCTCAAGCGGCTTACACCGCTCTGCG	2039
QY	2040	ACCTGGCTGCGCGGCAACGGACACCTGGGCGCACTGTCAACTCTGTTCCAGAGAGAGGCGCG	2099
Db	2040	ACCTGGCTGCGCGGCAACGGACACCTGGGCGCACTGTCAACTCTGTTCCAGAGAGAGGCGCG	2099
QY	2100	ATGTGCTGAGCCCGGGAGACCCCTTGAACAGACCGGCGCTGACCTGCTGCGCGCCCAACGGGCG	2159
Db	2100	ATGTGCTGAGCCCGGGAGACCCCTTGAACAGACCGGCGCTGACCTGCTGCGCGCCCAACGGGCG	2159
QY	2160	ACTGCGAAGTGTGTGAGAGATTTGTGTACCGCGAGTCAATTGACCTGTTCCAGACAGACGAG	2219
Db	2160	ACTGCGAAGTGTGTGAGAGATTTGTGTACCGCGAGTCAATTGACCTGTTCCAGACAGACGAG	2219
QY	2220	GCGTCAAGCGCGGTGACCTTGGCGCGGCCAGGCGCGGCAACAGACGCTGAGACCTTGGCG	2279
Db	2220	GCGTCAAGCGCGGTGACCTTGGCGCGGCCAGGCGCGGCAACAGACGCTGAGACCTTGGCG	2279
QY	2280	TCAGGCATGAGGGCGCCACATCAACTGACAGCCTTAAGTTCCAGGCGCGCCATGCGCCCGCG	2339
Db	2280	TCAGGCATGAGGGCGCCACATCAACTGACAGCCTTAAGTTCCAGGCGCGCCATGCGCCCGCG	2339
QY	2340	CGGCAACACTCCTGCGGGGAGAACAGACCTTAAGTGGCGCTGCGCGAGACCGGCGGGTCTCA	2399
Db	2340	CGGCAACACTCCTGCGGGGAGAACAGACCTTAAGTGGCGCTGCGCGAGACCGGCGGGTCTCA	2399
QY	2400	CGTGGGGGCTCTTGTCTGTCTGTGTCTCGTGGGAGATGAAACGATCTTGCGTGGGGCGC	2459
Db	2400	CGTGGGGGCTCTTGTCTGTCTGTGTCTCGTGGGAGATGAAACGATCTTGCGTGGGGCGC	2459
QY	2460	CGGTGTGCGCTTAACTTAAATGTTAACAGAGCAGAGTCAATGTGGCCATCAGAGAGGCGCG	2519
Db	2460	CGGTGTGCGCTTAACTTAAATGTTAACAGAGCAGAGTCAATGTGGCCATCAGAGAGGCGCG	2519
QY	2520	CTGCTGCTGACCGGAGTGTCCCTCAAGGTGAAGCTGCGTCAAGTGTGACATGCGCCGCTCC	2579
Db	2520	CTGCTGCTGACCGGAGTGTCCCTCAAGGTGAAGCTGCGTCAAGTGTGACATGCGCCGCTCC	2579
QY	2580	ATCATCATGATCTTAAAGCACCTGCTGTCTGAAAGGACCGTGGGTCTGAATCATTTCTGTTGGC	2639
Db	2580	ATCATCATGATCTTAAAGCACCTGCTGTCTGAAAGGACCGTGGGTCTGAATCATTTCTGTTGGC	2639
QY	2640	TCCTTAATGGGTGCGTGAAGCTGTCTCTCAAGATGAAGACCCCAAGCGCTGAAAGATCA	2699
Db	2640	TCCTTAATGGGTGCGTGAAGCTGTCTCTCAAGATGAAGACCCCAAGCGCTGAAAGATCA	2699
QY	2700	CTCTCTCTGAGGCGAGCCACTTGTGGGTGTCTGAGCTTCCAGCTCTTGAAGGAGTGTCA	2755
Db	2700	CTCTCTCTGAGGCGAGCCACTTGTGGGTGTCTGAGCTTCCAGCTCTTGAAGGAGTGTCA	2755

OY	2760	GGGGAAACGTGTTTTTTTATCTTCATCATGAAGTGCGGCAGAGAAGCCCTGTCTTAAGT	2819
Db	2760	GGGGAAACGTGTTTTTTTATCTTCATCATGAAGTGCGGCAGAGAAGCCCTGTCTTAAGT	2819
OY	2820	TTCCAATGGAATTGTTTTTAAATAATCTTAAAGAGTAGAATATACCCTTACAGCTGTGCTTG	2879
Db	2820	TTCCAATGGAATTGTTTTTAAATAATCTTAAAGAGTAGAATATACCCTTACAGCTGTGCTTG	2879
OY	2880	AAACCTGTAAAAAANGTTCATPAACAATGGATAGCTATGCTCTAAATGATGCTTAAGTAG	2939
Db	2880	AAACCTGTAAAAAANGTTCATPAACAATGGATAGCTATGCTCTAAATGATGCTTAAGTAG	2939
OY	2940	TGGGTTGGCTTTGAAAACAATGTTTTATGCAACAAGAACGAATGCTAGCAGCTT	2999
Db	2940	TGGGTTGGCTTTGAAAACAATGTTTTATGCAACAAGAACGAATGCTAGCAGCTT	2999
OY	3000	TGCGGGGGGTATNGTGTGCCAGCTCTTAACATTCAGCTATACTTGGGTAGTCTT	3059
Db	3000	TGCGGGGGGTATNGTGTGCCAGCTCTTAACATTCAGCTATACTTGGGTAGTCTT	3059
OY	3060	GTGACAAACCAACAACAAGTCCCAACATNGTACTAGTGCCTGTGTTCTCGTTGCTA	3119
Db	3060	GTGACAAACCAACAACAAGTCCCAACATNGTACTAGTGCCTGTGTTCTCGTTGCTA	3119
OY	3120	AGATGTTTTGCAACTTAAAGCCAAGGCTTAAGATCATTTAAAAAATCTCCCTTGT	3179
Db	3120	AGATGTTTTGCAACTTAAAGCCAAGGCTTAAGATCATTTAAAAAATCTCCCTTGT	3179
OY	3180	AACCTCATGCTGTGGGACCTAAGGGAGCCCCCTAGGTCGTGGAAGCACACACTTGG	3239
Db	3180	AACCTCATGCTGTGGGACCTAAGGGAGCCCCCTAGGTCGTGGAAGCACACACTTGG	3239
OY	3240	GGAAGAGGTGACGAGAGAGCTGTGTTTTTTATCTCCAACGCAAGTATGAAGATAAAAATTA	3299
Db	3240	GGAAGAGGTGACGAGAGAGCTGTGTTTTTTATCTCCAACGCAAGTATGAAGATAAAAATTA	3299
OY	3300	CATAGTATTAACCTAACAATPACAGATTAACCTAAGTATGCACTGCTCACCTGCACCC	3359
Db	3300	CATAGTATTAACCTAACAATPACAGATTAACCTAAGTATGCACTGCTCACCTGCACCC	3359
OY	3360	TTCCCAAGCTCTCATTTTTTGTTAGGTGATTTGGGATAGGGAATAGTTTTGGGGTATGGGG	3419
Db	3360	TTCCCAAGCTCTCATTTTTTGTTAGGTGATTTGGGATAGGGAATAGTTTTGGGGTATGGGG	3419
OY	3420	GGAAGTTTTGCAACTGCTTTGCAACAAGTGCCTCCGACCTCACAGATTTGGGGTGTGGC	3479
Db	3420	GGAAGTTTTGCAACTGCTTTGCAACAAGTGCCTCCGACCTCACAGATTTGGGGTGTGGC	3479
OY	3480	CCCAAGGGCGGTTCTTGATGTAAAAAGATGTGGCACTAAGCTCGTAACTTCACTGTCAAC	3539
Db	3480	CCCAAGGGCGGTTCTTGATGTAAAAAGATGTGGCACTAAGCTCGTAACTTCACTGTCAAC	3539
OY	3540	CTGTGTCCCATAGGGTGCCTTCTGAATATCTGTATTTAGAAATAAAGTTTTGTTCGAACGTG	3599
Db	3540	CTGTGTCCCATAGGGTGCCTTCTGAATATCTGTATTTAGAAATAAAGTTTTGTTCGAACGTG	3599
OY	3600	ACCCTGCGTGAACAACATGATACCGTGGCTGGTATATGATAGAGATTTGAATTTAATGTACC	3659
Db	3600	ACCCTGCGTGAACAACATGATACCGTGGCTGGTATATGATAGAGATTTGAATTTAATGTACC	3659
OY	3660	ATGATATGTTAATGTGAATCTGTGGCAGAGATACTTTTCATGGAAGAAATATCCAAAGCT	3719
Db	3660	ATGATATGTTAATGTGAATCTGTGGCAGAGATACTTTTCATGGAAGAAATATCCAAAGCT	3719
OY	3720	GTTGAAACTGGCTATGTTTTTAAATATGCTCATATGTCCTTTAATCTGTGTGTGGAAGTGGT	3779
Db	3720	GTTGAAACTGGCTATGTTTTTAAATATGCTCATATGTCCTTTAATCTGTGTGTGGAAGTGGT	3779
OY	3780	GAGGAGCAAGAAGTTCATTTGATGTCAATATGAAGAAAGTACTTGCTCACTTTTGTGAN	3839
Db	3780	GAGGAGCAAGAAGTTCATTTGATGTCAATATGAAGAAAGTACTTGCTCACTTTTGTGAAG	3839
OY	3840	CTGAAAAAAAAAAAAAAAAAGG	3860

Db 3840 CTGAAAAAAAAAAAAAG 3860

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; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1840
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_020639
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1840

Query Match 98.6%; Score 3804.2; DB 17; Length 3879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

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Db 279 GTTTCGCTACATCTGCTGTGTATGCACTGCGGAACTGTTCGCTGTGATGGA 338
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Db 459 GCCACTCTGCACTTGACCTTCAAGCCCGGAACTCTGCTGATGCGCACTACAGT 518
QY 487 CAAGATTTTGATTTTGTGCTGCGCAAGTGCACCGGCTGTCCACTCGCATGACCTCAG 546
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QY 547 CATGATGCGCTGTTGGCAATCGCTTACCTCCCTCAGAGCGCATCAGAGAAAG 606
Db 579 CATGATGCGCTGTTGGCAATCGCTTACCTCCCTCAGAGCGCATCAGAGAAAG 638
QY 607 CCGGCTCTTGCAACCAAGCAGATGTATACGTTTGGATGCTCATCTGGGGCGTCT 666
Db 639 CCGGCTCTTGCAACCAAGCAGATGTATACGTTTGGATGCTCATCTGGGGCGTCT 698
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Db 699 CACACAGAGAGCGGCTTGGATGAGAAAGATCTCTGCACTCATGAGGAGTGT 758
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 Db 1718 TCGCGCGAGGCGCTGAGACGTGAGCTGCAAGGCGAAGATGCTGAGCTGCCACTGACCTACG 1777
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 Db 1958 CACAGACACCCCTGCACTGCGCGCGAGAGCGGAGCAACGACATGCGACAGGCTGCTGC 2017
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OY      3846 AA 3847
Db      3878 AA 3879

RESULT 4
US-10-342-887-1840
; Sequence 1840, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Lineley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1840
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1840

Query Match      98.6%; Score 3804.2; DB 18; Length 3879;
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Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
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OY      667 CACAGAGAAAGGCGTTTGCAAGATGAGAAACAATCTGCAATCATCTGATGAGTGTGT 726
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Qy 1866 ACCGCGTGGCCCGCATCTCTCATTCGACCTGTGCTCGGACGTCAACGTCTGACAGCTGCTG 1925
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Qy 1926 CACAGACACCCCTGACGTTGAGCGCGAGAGACGAGGCAACAGACACTGCGACAGCTGCTCC 1985
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DB 3818 CAAGAGTTTCATTTGATGCAATTAAGCAAAAGTACTTGCCACTTTTGGAAAGTAAA 3877
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RESULT 5
US-10-648-593-16
; Sequence 16, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 16
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-16

Query Match 98.6%; Score 3804.2; DB 19; Length 3879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
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OY 1626 GCCGAGCGCCCATGACAGTGGCTTGCAGACAGGAGAGAGATATGTGTGCGATCTGTC 1685
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DB 1658 GCCGAGCGCCCATGACAGTGGCTTGCAGACAGGAGAGAGATATGTGTGCGATCTGTC 1717
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 QY 1806 TGAAGCCGAGACGCTGATGAGGAGACGCACTTGCACCTTGGCCGCAACAGCGGGGCACT 1865
 Db 1838 TGAAGCCGAGACGCTGATGAGGAGACGCACTTGCACCTTGGCCGCAACAGCGGGGCACT 1897
 QY 1866 ACCGCGTGGCCCGCATCTCTCATGACCTGTGCTCGACCTTCAACGCTTGCACCTGCTGG 1925
 Db 1898 ACCGCGTGGCCCGCATCTCTCATGACCTGTGCTCGACCTTCAACGCTTGCACCTGCTGG 1957
 QY 1926 CACGACACCCCTGACCGTGGCGCGGAGACGAGGAGCACTGCGCAGGCTGCTGC 1985
 Db 1958 CACGACACCCCTGACCGTGGCGCGGAGACGAGGAGCACTGCGCAGGCTGCTGC 2017
 QY 1986 TGCATGAGGCGGCTGGCAAGAGAGCGCTGACCTCAAGACGCTTACACCGCTTGCACCTGG 2045
 Db 2018 TGCATGAGGCGGCTGGCAAGAGAGCGCTGACCTCAAGACGCTTACACCGCTTGCACCTGG 2077
 QY 2046 CTGCTGAGGCGGCACTGGCCATCTGCAAGCTGCTTGTCAAGAGAGGCGGATGCTGC 2105
 Db 2078 CTGCTGAGGCGGCACTGGCCATCTGCAAGCTGCTTGTCAAGAGAGGCGGATGCTGC 2137
 QY 2106 TGGCCCGGGGAGACCCCTGAAACGAGACGCGCTGCACTGGCTGCGGCCACGCGGCACTCGG 2165
 Db 2138 TGGCCCGGGGAGACCCCTGAAACGAGACGCGCTGCACTGGCTGCGGCCACGCGGCACTCGG 2197
 QY 2166 AGGTGATGAGAGAGTGTGCAAGCGCGATGTCACTTGAACCTGTTCAGACGAGAGGAGCTCA 2225
 Db 2198 AGGTGATGAGAGAGTGTGCAAGCGCGATGTCACTTGAACCTGTTCAGACGAGAGGAGCTCA 2257
 QY 2226 GCGCGCTGACACTGGCCGCGCCAGAGGCGGCAACGACGAGACGAGGAGGAGCTGTGCTCAAGC 2285
 Db 2258 GCGCGCTGACACTGGCCGCGCCAGAGGCGGCAACGACGAGACGAGGAGGAGCTGTGCTCAAGC 2317
 QY 2286 ATGAGGCGCCACATCAACTGCGAGAGGCTCAAGTTCAGAGGCGGCGCAATGCGCGCGGCA 2345
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 Db 2498 TGGCTTAAGTAAATGTTAAACCAAGAGAGTGAATGCTGCGCTCAAGAGGCGGCTGCTGG 2557
 QY 2526 CTGACCGGAGTGCCTCCCTCAGGCTGAGAGCTGCTCAGGCTGCAATGCTCCGCTCATCATC 2585
 Db 2558 CTGACCGGAGTGCCTCCCTCAGGCTGAGAGCTGCTCAGGCTGCAATGCTCCGCTCATCATC 2617
 QY 2586 GATCTAGGCACTGCTGTCTGAAGGACCGTGGGTCAAGATCAATTCCTTGTGCTCTCTAA 2645
 Db 2618 GATCTAGGCACTGCTGTCTGAAGGACCGTGGGTCAAGATCAATTCCTTGTGCTCTCTAA 2677
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 Db 2738 CTTGAGGCGAGCACTTGGGTTGCTGAGCTCAACAGTCTTGAAGGAGGTGACGAGGAGAA 2797

QY 2766 ACTGTGTTTTTATCTTATCATATGACGAGTGGGAGAGAGGCGTGTCTTAAAGTTTCCAT 2825
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 QY 2826 GGAATGTTTTTAAATAATATCTTAAAGATGAATACCTTATCAGCTGTGCTTGAACCT 2885
 Db 2858 GGAATGTTTTTAAATAATATCTTAAAGATGAATACCTTATCAGCTGTGCTTGAACCT 2917
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 Db 2918 GTTAAAAATGTTCAATATGAGATGCTAGTCTTAAATGATGAGGCTTAAATGAGGAGT 2977
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 Db 2978 TGGCTTTGAAAAACAATGTTTTATGCAACAAGAAAGATGATGACAGCCTTTGCGGG 3037
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 Db 3038 GCGTATGTGGCCAGCTCTTAAACATTCAGTCTTATTAATCTTGGGTAGTCTTGTGAC 3097
 QY 3066 AACCAACAACGAGGCCCAATGGATAGAGCTGCGGCTGCTGCTTGAAGATGT 3125
 Db 3098 AACCAACAACGAGGCCCAATGGATAGAGCTGCGGCTGCTGCTTGAAGATGT 3157
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 QY 3246 GGTGAGAGAGAGCTGTGTTTTTATCTCCACAAGCAATTAAGAAATTAATCATAGT 3305
 Db 3278 GGTGAGAGAGAGCTGTGTTTTTATCTCCACAAGCAATTAAGAAATTAATCATAGT 3337
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 QY 3426 TTTCTGACCTGTTTGCAGAGCTGCTCCGACCTCAACAAGTTTGGGGTGGGCGCCAGG 3485
 Db 3458 TTTCTGACCTGTTTGCAGAGCTGCTCCGACCTCAACAAGTTTGGGGTGGGCGCCAGG 3517
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 Db 3518 GCGGTTCTTGAATGTAAGATGTGGCATCTAGGCTGTAACCTTCACTGTCACTGTGT 3577
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 Db 3578 CCCATAGGAGTGCCTTCTGAATACCTGTATTAAGATTAAGTTTGGCAAGACCTGCTG 3637
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 Db 3698 GTTAAATGGAATCTGAGGAGAGATACCTTTTCAATGAGAGAAATATCAAGCTGTTGAA 3757
 QY 3726 ACTGCTATGTTTAAATATGCTCAATGTGCTTTAATGTTGTGAGACTGCTGAGGGA 3785
 Db 3758 ACTGCTATGTTTAAATATGCTCAATGTGCTTTAATGTTGTGAGACTGCTGAGGGA 3817
 QY 3786 CAAGAAGTCCATTTGATATGATCAATTAAGCAAGTACTTGGCTTAATTTTGAANTCTGAA 3845
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 QY 3846 AA 3847

Db 3878 AA 3879

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RESULT 6
US-10-923-035-23
; Sequence 23, Application US/10923035
; Publication No. US20050130189A1
; GENERAL INFORMATION:
; APPLICANT: Pasricha, Pankaj
; APPLICANT: Shenoy, Mohan
; APPLICANT: Winston, John
; TITLE OF INVENTION: Compositions and Methods for Treating and Diagnosing
; TITLE OF INVENTION: Irritable Bowel Syndrome
; FILE REFERENCE: 9511-136-27
; CURRENT APPLICATION NUMBER: US/10/923,035
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/496,716
; PRIOR FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 3890
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-923-035-23

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Query Match	98.3%	Score 3794.8;	DB 22;	Length 3890;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 3836;	Conservative	0;	Mismatches 13;	Indels 4;
				Gaps 3

QY	7	GTTCGGGCGCGAATGGAAGGGGAGACGGCGGGAGACCCCATGGCCCTGGCGCTGTGGGCACTT	66
Db	39	GACGTGCGGAGTGAAGGGGCGACGGCGGGAGCCCATG39CCTGGCGCTGTGGCACTT	98
QY	67	CGACGCGGGCGAGTTTCACCGGGCTGGAGAGAGTGGGCTCGGCGGGCTTCGGGCAAGTGT	126
Db	99	CGACGCGGGCGAGTTTCACCGGGCTGGAGAGAGTGGGCTCGGCGGGCTTCGGGCAAGTGT	158
QY	127	CAAGGTGCGCCATGTTCATCTGGAAAGCTTGGCTGGCCATCAATGCTTCGCCAGCTTGA	186
Db	159	CAAGGTGCGCCATGTTCATCTGGAAAGCTTGGCTGGCCATCAATGCTTCGCCAGCTTGA	218
QY	187	CGTCGACGACAGGAGCGGATGGAGCTTTTGGAAAGCCAAAGATGAGATGGCCAA	246
Db	219	CGTCGACGACAGGAGCGGATGGAGCTTTTGGAAAGCCAAAGATGAGATGGCCAA	278
QY	247	GTTTGGCTACATCTGCGCTGTGTATGGCATCTGCGCGAACTGTGGGCTGGTCATGA	306
Db	279	GTTTGGCTACATCTGCGCTGTGTATGGCATCTGCGCGAACTGTGGGCTGGTCATGA	338
QY	307	GTACATGAGACGGGCGTCCCTGGAAAGCTGTGGCTTCGGAGCCCAATGCGATGGGATCT	366
Db	339	GTACATGAGACGGGCGTCCCTGGAAAGCTGTGGCTTCGGAGCCCAATGCGATGGGATCT	398
QY	367	CCGGTTCGGAATCATCAAGAGACGGCGGTGGGCAATGAATTCCTGTGACCTGCAATGGCCCC	426
Db	399	CCGGTTCGGAATCATCAAGAGACGGCGGTGGGCAATGAATTCCTGTGACCTGCAATGGCCCC	458
QY	427	GGCATTCTGGAACCTTGAAGCCTCAAGCCCGGGAACATCTGCTGGATGSCCACTACCAAGT	486
Db	459	GGCATTCTGGAACCTTGAAGCCTCAAGCCCGGGAACATCTGCTGGATGSCCACTACCAAGT	518
QY	487	CAAGATTCTGATTTTGTGTCTGGCCAAATGCAAGGGCTGTCCCATCTCGATACCTCAG	546
Db	519	CAAGATTCTGATTTTGTGTCTGGCCAAATGCAAGGGCTGTCCCATCTCGATACCTCAG	578
QY	547	CATGATGCGCGTGTGGGCAATGCGCTACCCCTCGAGAGCGGATCGAGGAGAAAG	606
Db	579	CATGATGCGCGTGTGTGGGCAATGCGCTACCCCTCGAGAGCGGATCGAGGAGAAAG	638
QY	607	CCGGCTCTTCGACCAACAGACGATGTATACGCTTTGCGATGTCACTGGGCGGTCT	666

Db	639	CCGGCTCTTCGACACCAAGACACGATGTAATACGCTTTGGCATCTGTCATCTGGGCGGTGCT	698
Qy	667	CACACAGAAAGAGCCGTTTGTGAGATGAGAAAGACATCTCTGCACATCATGTGAAAGTGGT	726
Db	699	CACACAGAAAGAGCCGTTTGTGAGATGAGAAAGACATCTCTGCACATCATGTGAAAGTGGT	758
Qy	727	GAAGGGCCACCGCCGCCGAGCTGGCCGCCCTGTGTGAGAGCCCGGGCCGGCCGCTGCACCA	786
Db	759	GAAGGGCCACCGCCGCCGAGCTGGCCGCCCTGTGTGAGAGCCCGGGCCGGCCGCTGCACCA	818
Qy	787	CCTGATACGCTCTCATGACAGCGGTCTGGCAGAGGGAGATCCCGAGATTAGGCCCACTTCCA	846
Db	819	CCTGATACGCTCTCATGACAGCGGTCTGGCAGAGGGAGATCCCGAGATTAGGCCCACTTCCA	878
Qy	847	AGAAATTACTTCTGAAACCGAGGACTGTGTGTGAAAGCTGTATGACGAAGTGAAAGAAAC	906
Db	879	AGAAATTACTTCTGAAACCGAGGACTGTGTGTGAAAGCTGTATGACGAAGTGAAAGAAAC	938
Qy	907	TGCTCATATATCTGGACCGTAAAGCCCCCGGAGATCCAGAGACGAGGTGTGTGCTTGGAG	966
Db	939	TGCTCATATATCTGGACCGTAAAGCCCCCGGAGATCCAGAGACGAGGTGTGTGCTTGGAG	998
Qy	967	GCTCAAGGGGGCTCTGCGCCCCCACTTTCGATTAAGACTACGCTCTCCAGCTTCTCTC	1026
Db	999	GCTCAAGGGGGCTCTGCGCCCCCACTTTCGATTAAGACTACGCTCTCTCCAGCTTCTCTC	1058
Qy	1027	ACAGCTGAGCTCTGAGAGTTTCCAGAGCTGTGAGAGGCCCCGAGAGCTCAGCCGACGTC	1086
Db	1059	ACAGCTGAGCTCTGAGAGTTTCCAGAGCTGTGAGAGGCCCCGAGAGCTCAGCCGACGTC	1118
Qy	1087	CTCTGAGTCCAAAGCTGCCATGTGTCCGCGAGTGGGAAAGAGGTCTTCGGGGGTGTCTCGGT	1146
Db	1119	CTCTGAGTCCAAAGCTGCCATGTGTCCGCGAGTGGGAAAGAGGTCTTCGGGGGTGTCTCGGT	1178
Qy	1147	GGAAGTCCGAGCTTCTCTTCCAGAGGATCACTGTGCTGTCTCTTTCAGCGGGAACCTTCAAC	1206
Db	1179	GGAAGTCCGAGCTTCTCTTCCAGAGGATCACTGTGCTGTCTCTTTCAGCGGGAACCTTCAAC	1238
Qy	1207	CAGCGATCTGTGATACCAAGACGATCCAGAAAGAAAGCTTGTGATGCCATCGTGTCC	1265
Db	1239	CAGCGATCTGTGATACCAAGACGATCCAGAAAGAAAGCTTGTGATGCCATCGTGTCCG	1297
Qy	1266	GGGACACCAAGCAAACTGATGAAAGATCTGTCAAGCCGCAAGACGTGACCTGGCACTGGACA	1325
Db	1298	GGGACACCAAGCAAACTGATGAAAGATCTGTCAAGCCGCAAGACGTGACCTGGCACTGGACA	1357
Qy	1326	GCGGTGGCAGGCTGTGTGCACTGGCGGTGGAGGCCGGGCAAGAGTGGCGCAAGTGGC	1385
Db	1358	GCGGTGGCAGGCTGTGTGCACTGGCGGTGGAGGCCGGGCAAGAGTGGCGCAAGTGGC	1417
Qy	1386	TGCTGTCAACATATGCCAACCCCAACTGAGCAACCTGTAAGGGGCTTCAACCCCGTTGGACA	1445
Db	1418	TGCTGTCAACATATGCCAACCCCAACTGAGCAACCTGTAAGGGGCTTCAACCCCGTTGGACA	1477
Qy	1446	TGGCCGTGGAAGAGAGGTGTGGGGGTGTCTGTGAGCTCTCTGTGCACAGGAAGATCAATG	1505
Db	1478	TGGCCGTGGAAGAGAGGTGTGGGGGTGTCTGTGAGCTCTCTGTGCACAGGAAGATCAATG	1537
Qy	1506	TCAAAGCCAAAGATGAGGACCAAGTGGACAGGCCCTCACTTTGACGCCAAGACGGGGATG	1565
Db	1538	TCAAAGCCAAAGATGAGGACCAAGTGGACAGGCCCTCACTTTGACGCCAAGACGGGGATG	1597
Qy	1566	AGTCTAGACACAGGCTGTGTGTGGAAGAAAGCCTCGATCAACGAGGTGACCTTTGAGG	1625
Db	1598	AGTCTAGACACAGGCTGTGTGTGGAAGAAAGCCTCGATCAACGAGGTGACCTTTGAGG	1657
Qy	1626	GCCGAGCCCATATGACATGTGCTGTGCGACACCGGCAAGAGATATGTGTCGCAATCTTGC	1685
Db	1658	GCCGAGCCCATATGACATGTGCTGTGCGACACCGGCAAGAGATATGTGTCGCAATCTTGC	1717
Qy	1686	TGCGCCGAGGCGGTGACGTGAGCCTGTGACGGGCAAGATATGCTGTGCTGCACTTGACATAG	1745
Db	1718	TGCGCCGAGGCGGTGACGTGAGCCTGTGACGGGCAAGATATGCTGTGCTGCACTTGACATAG	1777

QY 1746 CTGCTGGAGGGCCACTGCTCCATCTGTAAGCTGCTGGCCAAAGCAGCCGGGGGTGAAGT 1805
 Db 1778 CTGCTGGAGGGCCACTGCTCCATCTGTAAGCTGCTGGCCAAAGCAGCCGGGGGTGAAGT 1837
 QY 1806 TGAAGCCCGAAGCGCTGGAATGGAGGAGCGCAATTGCACTGGCCGCAAGCGGGGCACT 1865
 Db 1838 TGAAGCCCGAAGCGCTGGAATGGAGGAGCGCAATTGCACTGGCCGCAAGCGGGGCACT 1897
 QY 1866 ACCGCTGGCCCGCATCTCATCGACTGTGCTCCAGCTCAACGTCGTCAGCTGCTG 1925
 Db 1898 ACCGCTGGCCCGCATCTCATCGACTGTGCTCCAGCTCAACGTCGTCAGCTGCTG 1957
 QY 1926 CACAGACATCCCTGCACTGTGGCCCGGAGACGGGGGCAACAGACATGCGCAAGCTGCTC 1985
 Db 1958 CACAGACATCCCTGCACTGTGGCCCGGAGACGGGGGCAACAGACATGCGCAAGCTGCTC 2017
 QY 1986 TGCATCGGGGCGCTGGCAAGAGGCGGTGACCTCAAGCGCTTACACCGCTTGGACCTG 2045
 Db 2018 TGCATCGGGGCGCTGGCAAGAGGCGGTGACCTCAAGCGCTTACACCGCTTGGACCTG 2077
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 Db 2558 CTGAACGAGAGTCCCTCCAGGATGAAGCTGCTCAGGTGCAATGCGCGCTCATCATC 2617
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 Db 3098 AACCAACAACGTGCCCAATGATCTAGCTGCGTGTGTTCTGTTGCTTAAGATGT 3157
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 Db 3816 CAAGAAGTTCAATTTGATGTCAATTAAGCAAGTACTTGTCTTTTGAAGCTGAAA 3875
 QY 3846 AAAAAAAAAA 3858
 Db 3876 AAAAAAAAAA 3888

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RESULT 7
US-10-302-172-905
; Sequence 905, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids an
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 1CNP
; CURRENT APPLICATION NUMBER: US/10/302,172
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pc_fl_genes Version 2.0
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2496)
US-10-302-172-905

Query Match      94.4%; Score 3643; DB 18; Length 3981;
Beet Local Similarity 96.1%; Pred. No. 0;
Matches 3825; Conservative 0; Mismatches 11; Indels 146; Gaps 3;

QY 17 ATGAGAGGCGAAGCGGAGAGCCCATGAGGCTGAGGCTGCTGCGACCTTCGACCGGAGC 76
DB 1 ATGAGAGGCGAAGCGGAGAGCCCATGAGGCTGAGGCTGCTGCGACCTTCGACCGGAGC 60
QY 77 GAGTTCAAGGCTGAGAGAGGTGGCTTGGGCGGCTTGGGCAAGTGTACAGAGTGGG 136
DB 61 GAGTTCAAGGCTGAGAGAGGTGGCTTGGGCGGCTTGGGCAAGTGTACAGAGTGGG 120
QY 137 CATGTCACCTGAGAGCCTGCTGAGCATCAAGTGTGAGCCGAGCTGACAGTGCAGCAG 196
DB 121 CATGTCACCTGAGAGCCTGCTGAGCATCAAGTGTGAGCCGAGCTGACAGTGCAGCAG 180
QY 197 AGGAGCGCATGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAGTTTGGCTAC 256
DB 181 AGGAGCGCATGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAGTTTGGCTAC 240
QY 257 ATCTGCTGTGTATGAGCATCTGCGCGCAACTGTGCGCTGTGATGAGAGTACATGAG 316
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGCAACTGTGCGCTGTGATGAGAGTACATGAG 300
QY 317 AGGAGCTGCTGAGAGAGCTGCTGAGCTTGGAGCCATTGAGGAGTCTCGGTTCCGA 376
DB 301 AGGAGCTGCTGAGAGAGCTGCTGAGCTTGGAGCCATTGAGGAGTCTCGGTTCCGA 360
QY 377 ATCATCAAGAGAGCGGCTGAGCATGAGCTTCTGCACTGATGAGCCCGGCACTCTG 436
DB 361 ATCATCAAGAGAGCGGCTGAGCATGAGCTTCTGCACTGATGAGCCCGGCACTCTG 420
QY 437 CACCTGAGCTTCAAGCCCGGAGACATCTGCTGAGATGCCACTACAGATCAAGATTTT 496
DB 421 CACCTGAGCTTCAAGCCCGGAGACATCTGCTGAGATGCCACTACAGATCAAGATTTT 480
QY 497 GATTTGATCTGGCCAAAGTGAACCGGGCTGCCACTGATGAGCCTCGAGATGAGTGC 556
DB 481 GATTTGATCTGGCCAAAGTGAACCGGGCTGCCACTGATGAGCCTCGAGATGAGTGC 540
QY 557 CTGTTTGGAGCAATCGCTTACCTCTCGAGAGCGCATGAGGAGAGAGCGGCTTTC 616
DB 541 CTGTTTGGAGCAATCGCTTACCTCTCGAGAGCGCATGAGGAGAGAGCGGCTTTC 600

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QY 617 GACACCAAGACCATGATATACGCTTTGGAGTGTGATCTGAGGCGGTCTCACAGAG 676
DB 601 GACACCAAGACCATGATATACGCTTTGGAGTGTGATCTGAGGCGGTCTCACAGAG 660
QY 677 AAGCGTTTGCAGATGAGAGAAATCTCTGCAATCATGATGAGAGTGTGAGAGGCGCAC 736
DB 661 AAGCGTTTGCAGATGAGAGAAATCTCTGCAATCATGATGAGAGTGTGAGAGGCGCAC 720
QY 737 CGCCCCGAGCTGCGCGCGGTGTGAGAGCGCGCGCGCGCTTGCAGACCTGATACGC 796
DB 721 CGCCCCGAGCTGCGCGCGGTGTGAGAGCGCGCGCGCGCTTGCAGACCTGATACGC 780
QY 797 CTGATGAGAGGCTGAGAGAGGAGATCCGAGATTAGGCGCACCTTC----- 844
DB 781 CTGATGAGAGGCTGAGAGAGGAGATCCGAGATTAGGCGCACCTTC----- 840
QY 845 ----- 844
DB 841 CTGATGAGAGGAGCTCATCCGCAAGTGTGAGCTGCTGCCCTGATGATGAGAGTGG 900
QY 845 ----- 844
DB 901 CGCTCCCGGAGAGGCTTCCGCTTGAATCTGAGTCAATCCAGTGAATGTCCC 960
QY 845 -----CAAGAAATTACTTTCTGAAACCGAGGACCTGTGTGAAAGCTGATGAC 892
DB 961 CTTTCTTCCCAAGAGAAATTACTTTCTGAAACCGAGGACCTGTGTGAAAGCTGATGAC 1020
QY 893 GAGTGAAGAGAACTGCTCATGATCTGAGAGTGAAGAGCCCGGAGCCCGAGAGCGAG 952
DB 1021 GAGTGAAGAGAACTGCTCATGATCTGAGAGTGAAGAGCCCGGAGCCCGAGAGCGAG 1080
QY 953 GTGTGCTGTGAGAGCTCAAGCGGCGCTGCGCGCGCACTTTCAGTAACGTAAGCTC 1012
DB 1081 GTGTGCTGTGAGAGCTCAAGCGGCGCTGCGCGCGCACTTTCAGTAACGTAAGCTC 1140
QY 1013 TCCGAGCTTCTCAAGCTGAGCTGAGAGTTCCTGAGGCTGTGAGAGGCGCGAGAG 1072
DB 1141 TCCGAGCTTCTCAAGCTGAGCTGAGAGTTCCTGAGGCTGTGAGAGGCGCGAGAG 1200
QY 1073 CTCAGCGCAGCTCTCTGAGTCCAGCTGCAATGTTCGAGAGTGAAGAGGCTCTCG 1132
DB 1201 CTCAGCGCAGCTCTCTGAGTCCAGCTGCAATGTTCGAGAGTGAAGAGGCTCTCG 1260
QY 1133 GGGGTGTCTGTGTGAGCTCGGCTTCTTTCAGAGAGTCACTGTGCTCTTGGAG 1192
DB 1261 GGGGTGTCTGTGTGAGCTCGGCTTCTTTCAGAGAGTCACTGTGCTCTTGGAG 1320
QY 1193 CGGGAACCTTCAACGAGGATCTGAGTACCAAGAGCTGCAGAGAGAGAGTTGTGGA 1252
DB 1321 CGGGAACCTTCAACGAGGATCTGAGTACCAAGAGCTGCAGAGAGAGAGTTGTGGA 1379
QY 1253 TGCATCTGTCTC--GGGACACAGCAAACTGATGAGATCTGCAAGCGGAGAGTGA 1311
DB 1380 TGCATCTGTCTC--GGGAGACACAGCAAACTGATGAGATCTGCAAGCGGAGAGTGA 1439
QY 1312 CTTGCACTGAGACAGGCTGCAAGCTGCTGCACTTGGCGGTGAGAGCGGCGAGAGGA 1371
DB 1440 CTTGCACTGAGACAGGCTGCAAGCTGCTGCACTTGGCGGTGAGAGCGGCGAGAGGA 1499
QY 1372 GTGCGCCAAAGTGGCTGCTCAACAAATGCAACCCCACTGAGCAACCTGAGGAGTGC 1431
DB 1500 GTGCGCCAAAGTGGCTGCTCAACAAATGCAACCCCACTGAGCAACCTGAGGAGTGC 1559
QY 1432 CACCCGTTTGCATATGCGCGTGAAGAGAGGAGTGTGAGAGCTTCTGCTGCGC 1491
DB 1560 CACCCGTTTGCATATGCGCGTGAAGAGAGGAGTGTGAGAGCTTCTGCTGCGC 1619
QY 1492 ACGAGAGATCATGTGCAACGCGAAGATGAGAGCAAGTGAACACCTTCACTTTGAGC 1551
DB 1620 ACGAGAGATCATGTGCAACGCGAAGATGAGAGCAAGTGAACACCTTCACTTTGAGC 1679

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[illegible]

Db	2760	CGTGTGCTCTTAAAGGGTCGCTGAGGCGTGGTCTCTCAAGTATGAAGCCCAAGGCTGGAA	2819
Qy	2692	AGCATCCACTCTCTCTCTAGAGGAGACCAACTTGGGGTGTGTGAGCTCACAGTCTTGAGG	2751
Db	2820	AGCATCCACTCTCTCTCTAGAGGAGACCAACTTGGGGTGTGTGAGCTCACAGTCTTGAGG	2879
Qy	2752	GAGGTGACAGGGGAACTGTGTGTTTTTATCTTTCATACATGACGGTGGGACAGAGGCTGT	2811
Db	2880	GAGGTGACAGGGGAACTGTGTGTTTTTATCTTTCATACATGACGGTGGGACAGAGGCTGT	2939
Qy	2812	CTTAAAGTTTCCATGAAATGTTTTATATAAATATCTTAAAGATGAATACCTTATCAAGCT	2871
Db	2940	CTTAAAGTTTCCATGAAATGTTTTATATAAATATCTTAAAGATGAATACCTTATCAAGCT	2999
Qy	2872	GTTGTCTTAAACCTCTTAAATATGTCATPAACATGGATAGTCTAGTCTCTTAAATGATGG	2931
Db	3000	GTTGTCTTAAACCTCTTAAATATGTCATPAACATGGATAGTCTAGTCTCTTAAATGATGA	3059
Qy	2932	CTAAGTAGTGGGGTGGCTTTTGAAACCATGTGTTTATGCAACAGGACGAATGGTAGCA	2991
Db	3060	CTAAGTAGTGGGGTGGCTTTTGAAACCATGTGTTTATGCAACAGGACGAATGGTAGCA	3119
Qy	2992	GCCAGCTTTGGCGGGCGTATGTGTGGCCAGCTCTTAACATTCAGTCTTATCTTGGGT	3051
Db	3120	GCCAGCTTTGGCGGGCGTATGTGTGGCCAGCTCTTAACATTCAGTCTTATCTTGGGT	3179
Qy	3052	GAGTCCCTTGTGGACAAACCAACAACAGTGGCCACATGATCTAGTGGCGCTTGTTCTC	3111
Db	3180	GAGTCCCTTGTGGACAAACCAACAACAGTGGCCACATGATCTAGTGGCGCTTGTTCTC	3239
Qy	3112	GTTGCGCTAAGATGTTTGTGGCACTCTAGAGCCAAGGCGCTAAGAGTCAATTAAAAATCT	3171
Db	3240	GTTGCGCTAAGATGTTTGTGGCACTCTAGAGCCAAGGCGCTAAGAGTCAATTAAAAATCT	3299
Qy	3172	CCCTTTGTAACTCAGTGTGGGGAACTGAAGGAGCCCTCTCAGGTGTGCTGAGTGCACC	3231
Db	3300	CCCTTTGTAACTCAGTGTGGGGAACTGAAGGAGCCCTCTCAGGTGTGCTGAGTGCACC	3359
Qy	3232	AGTCTTGGGGAAGAGTGCAGAGAGAAAGCTGTGTTTTTATCTCAACAGCAGATGAAGA	3291
Db	3360	AGTCTTGGGGAAGAGTGCAGAGAGAAAGCTGTGTTTTTATCTCAACAGCAGATGAAGA	3419
Qy	3292	TAAATTTACATAGTATTAACCTAGACATAGACATATTAACCTAGTAGATGCACTGCAC	3351
Db	3420	TAAATTTACATAGTATTAACCTAGACATAGACATATTAACCTAGTAGATGCACTGCAC	3479
Qy	3352	CTGCACCCCTTCCAGCTCTCATTTTGTGTAAGTGAATTTGGGATAGGGATATGTGTTTTGGG	3411
Db	3480	CTGCACCCCTTCCAGCTCTCATTTTGTGTAAGTGAATTTGGGATAGGGATATGTGTTTTGGG	3539
Qy	3412	GTAATGGGGGGAAGTGTTCGACCTGTCTTGGACAGCGCTCCGACCTCAGACAGTTTGG	3471
Db	3540	GTAATGGGGGGAAGTGTTCGACCTGTCTTGGACAGCGCTCCGACCTCAGACAGTTTGG	3599
Qy	3472	GGGTGTGGCCCAAGGGGCGTCTTGGAATGAATGAATGTGGCCATCTAGCTCGTAATCTC	3531
Db	3600	GGGTGTGGCCCAAGGGGCGTCTTGGAATGAATGAATGTGGCCATCTAGCTCGTAATCTC	3659
Qy	3532	ACTGTCACTGTGTGCCATATAGGGTGCCTTCTGAATATCTGTTATTAAGATTAAGTTGTGTC	3591
Db	3660	ACTGTCACTGTGTGCCATATAGGGTGCCTTCTGAATATCTGTTATTAAGATTAAGTTGTGTC	3719
Qy	3592	AGAACTGACCTGTGCGCGTGAACATATGACCGTGGCCGATATATGAATGAAGATGATATT	3651
Db	3720	AGAACTGACCTGTGCGCGTGAACATATGACCGTGGCCGATATATGAATGAAGATGATATT	3779
Qy	3652	AATGTACATATATGTTAATGTGAATCTGTGGCAGAGATCTTTTCCATGCGCAGGAATA	3711
Db	3780	AATGTACATATATGTTAATGTGAATCTGTGGCAGAGATCTTTTCCATGCGCAGGAATA	3839
Qy	3712	TCCAACTGTGAAACCTGCTATGTTTAAATATGCTCATGTGCTTATCTGTGTGTG	3771

Db 3840 TCACAGCTGTGAACCTGGCTATGTTTAAATATGCTCATGTCCTTTACTGTGTG 3899
Qy 3772 GACTGCGTGAAGGACAAAGATTCCATTTGATGTCAATTAAGCAAGTACTTCTACTT 3831
Db 3900 GACTGCGTGAAGGACAAAGATTCCATTTGATGTCAATTAAGCAAGTACTTCTACTT 3959
Qy 3832 TTTTGAANCTGAAAAAAAAAAAA 3853
Db 3960 TTTTGAANCTGAAAAAAAAAAAA 3981

RESULT 8
US-10-172-118-324
; Sequence 324, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Lineley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 324
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: AL137448
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-324

Query Match 67.5%; Score 2606.4; DB 17; Length 2691;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2635; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

Qy 1211 GATCTGGGTACCAAGAGTGCAGAAAGAGTGTGATGTCATCTGCTCC-GGGA 1269
Db 36 GATCTGGGTACCAAGAGTGCAGAAAGAGTGTGATGTCATCTGCTCC-GGGA 94
Qy 1270 CACCAAGAACTGATGAAGATCTGCAAGCCGAGGACGTGACCTGCACTGGAAGCGG 1329
Db 95 CACCAAGAACTGATGAAGATCTGCAAGCCGAGGACGTGACCTGGAAGCGG 154
Qy 1330 TCCAGCTGTGCACTGCGGTGAGAGCGGGCAAGAGTGGCCAACTGCTCT 1389
Db 155 TCCAGCTGTGCACTGCGGTGAGAGCGGGCAAGAGTGGCCAACTGCTCT 214
Qy 1390 GGTCAACATGCAACCCCAACCTGAGCAACCGTGGGGCTCCACCCGTTGCAATGGC 1449
Db 215 GGTCAACATGCAACCCCAACCTGAGCAACCGTGGGGCTCCACCCGTTGCAATGGC 274
Qy 1450 CTTGAGAGAGAGGTGCGGGGTGTGCTGAGAGTCTCTGCTGAGCAGGAAGATCAATGTC 1509
Db 275 CTTGAGAGAGAGGTGCGGGGTGTGCTGAGAGTCTCTGCTGAGCAGGAAGATCAATGTC 334
Qy 1510 CGCCAAAGATGAGACCACTGAGCAGCCCTCACTTTGAGCCCAAGACGGGATGAGTC 1569
Db 335 CGCCAAAGATGAGACCACTGAGCAGCCCTCACTTTGAGCCCAAGACGGGATGAGTC 394
Qy 1570 TTGCAACAGGCTGTGTTGGAAGAAAGCCCTCGGTCACGAGGTGGAATTTGAGGGCGG 1629
Db 395 TTGCAACAGGCTGTGTTGGAAGAAAGCCCTCGGTCACGAGGTGGAATTTGAGGGCGG 454
Qy 1630 GAGCCCAATGACGTGGCTGCGCAGCAGGGCAGGAATATCTGTCGATCTGCTGG 1689

Db 455 GAGCCCAATGACGTGGCTGCGCAGCAGGGCAGGAATATCTGTCGATCTGCTGG 514
Qy 1690 CCGAGGCTGAGACGTGAGCTGCAAGGCAAGAGTCTGTGCTGCACTGCACTAGCTGC 1749
Db 515 CCGAGGCTGAGACGTGAGCTGCAAGGCAAGAGTCTGTGCTGCACTGCACTAGCTGC 574
Qy 1750 CTTGCAAGGACCACTGCACTGCTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 1809
Db 575 CTTGCAAGGACCACTGCACTGCTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 634
Qy 1810 CGCCCAAGCCTGATGAG 1869
Db 635 CGCCCAAGCCTGATGAG 694
Qy 1870 CTTGAGGCTGATCTGCACTGCACTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 1929
Db 695 CTTGAGGCTGATCTGCACTGCACTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 754
Qy 1930 GACACCCCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 1989
Db 755 GACACCCCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 814
Qy 1990 TCGGGGCGCTGCAAG 2049
Db 815 TCGGGGCGCTGCAAG 874
Qy 2050 CCGCAACGAGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 2109
Db 875 CCGCAACGAGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 934
Qy 2110 CCGGGGACCCCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 2169
Db 935 CCGGGGACCCCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 994
Qy 2170 GGTGAGAGAGTGTGATGAG 2229
Db 995 GGTGAGAGAGTGTGATGAG 1054
Qy 2230 GGTGACCTGAG 2289
Db 1055 GGTGACCTGAG 1114
Qy 2290 GGGCCACATCAACCTGCAAG 2349
Db 1115 GGGCCACATCAACCTGCAAG 1174
Qy 2350 CTTGAGGAG 2409
Db 1175 CTTGAGGAG 1234
Qy 2410 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2469
Db 1235 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1294
Qy 2470 TTAACCTAAATTTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2529
Db 1295 TTAACCTAAATTTTAAACCAAG 1354
Qy 2530 CCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2589
Db 1355 CCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1414
Qy 2590 TTAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2649
Db 1415 TTAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1474
Qy 2650 TCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2709
Db 1475 TCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1534
Qy 2710 AGGCGAGCACCTTGGGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2769

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Db 1535 AGGCGAGCCACCTTGCGGTTGCTGAGCTCACCAAGTCTTGAAGGAGTGCAGGGGAAACTG 1594
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Db 1595 TGTCTTTTATCTTACATACGACGCTGGGACAGAGAGCCCTGTCTTAAAGTTCCATGGA 1654
Qy 2830 TGTCTTTTATCTTACATACGACGCTGGGACAGAGAGCCCTGTCTTAAAGTTCCATGGA 2889
Db 1655 TGTCTTTTATCTTACATACGACGCTGGGACAGAGAGCCCTGTCTTAAAGTTCCATGGA 1714
Qy 2890 AAAATGTCATTAACATGATAGTCTAGCTCTTAATGATGAGTAAAGTGGGTTGAC 2949
Db 1715 AAAATGTCATTAACATGATAGTCTAGCTCTTAATGATGAGTAAAGTGGGTTGAC 1774
Qy 2950 TTTGAAAAAATGTTTATGCAACAAGAACAAATGTTAGCAGCCATTTGCGGGGCGT 3009
Db 1775 TTTGAAAAAATGTTTATGCAACAAGAACAAATGTTAGCAGCCATTTGCGGGGCGT 1834
Qy 3010 ATGTGTGCGCAGCTCTTAACATCTTCACTTATCTTGGGAGTCCCTGTGGAACAAC 3069
Db 1835 ATGTGTGCGCAGCTCTTAACATCTTCACTTATCTTGGGAGTCCCTGTGGAACAAC 1894
Qy 3070 AACACAGGTGCGCCACATGCTAGTCTGCTGCGGTTCTGCTGCTGCTGCTGCTGCTGCT 3129
Db 1895 AACACAGGTGCGCCACATGCTAGTCTGCTGCGGTTCTGCTGCTGCTGCTGCTGCTGCT 1954
Qy 3130 GCAACTCTAGAGCCACAGGCTCTAGAGTCTTAAATTTCTCCCTTGTAACTCTCACTG 3189
Db 1955 GCAACTCTAGAGCCACAGGCTCTAGAGTCTTAAATTTCTCCCTTGTAACTCTCACTG 2014
Qy 3190 CTGGGAGCTGAGCGGACGCCCCCTCAGGTGCTGAGTGCACAGTCTTGGGGAAGAGTG 3249
Db 2015 CTGGGAGCTGAGCGGACGCCCCCTCAGGTGCTGAGTGCACAGTCTTGGGGAAGAGTG 2074
Qy 3250 CAGGAGAGCTGCTGTTTATCTCTCACAGCAGTATGAAGATTAATTAATTAATTAATTA 3309
Db 2075 CAGGAGAGCTGCTGTTTATCTCTCACAGCAGTATGAAGATTAATTAATTAATTAATTA 2134
Qy 3310 CCTAGACATAGACATTAATCTAGTAGTACCTGCTCACCTGCACTCTTCCAGCTC 3369
Db 2135 CCTAGACATAGACATTAATCTAGTAGTACCTGCTCACCTGCACTCTTCCAGCTC 2194
Qy 3370 TCAATTTTGTAGTATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTT 3429
Db 2195 TCAATTTTGTAGTATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTT 2254
Qy 3430 TGAACCTGCTTGCAGCGGCTCGGACCTCAGCAGTCTTGGGAGTGGCCCCCAGGAGCG 3489
Db 2255 TGAACCTGCTTGCAGCGGCTCGGACCTCAGCAGTCTTGGGAGTGGCCCCCAGGAGCG 2314
Qy 3490 TTTCTGATGTAAAGATGTGCGCATCTAGCCTCGTAACTTCACTGTCACTGTGTCCCA 3549
Db 2315 TTTCTGATGTAAAGATGTGCGCATCTAGCCTCGTAACTTCACTGTCACTGTGTCCCA 2374
Qy 3550 TAGGGTCTCTTCTGAATCTGTTATTAAGATAATTTGTTGCAAGACCTGCTCGG 3609
Db 2375 TAGGGTCTCTTCTGAATCTGTTATTAAGATAATTTGTTGCAAGACCTGCTCGG 2434
Qy 3610 CAACATGTACCGTGGCTGCTGATATAGATGAATTAATTAATTAATTAATTAATTAATTA 3669
Db 2435 CAACATGTACCGTGGCTGCTGATATAGATGAATTAATTAATTAATTAATTAATTAATTA 2494
Qy 3670 ATGTGAATCTGTGGGAGGATCTTTTCCATGACAGAAATATCCAAAGCTGTGAAACTG 3729
Db 2495 ATGTGAATCTGTGGGAGGATCTTTTCCATGACAGAAATATCCAAAGCTGTGAAACTG 2554
Qy 3730 GCTATGTTTAAATATGCTCATTTGCTTATCTGTTGTGAGTCTGCTGAGGAGCAAG 3789
Db 2555 GCTATGTTTAAATATGCTCATTTGCTTATCTGTTGTGAGTCTGCTGAGGAGCAAG 2614
Qy 3790 AAGTTCATTTGATGTCAATTAAGCAAGTACTGCTACTTTTGAANTGAAATAA 3849
Db 2615 AAGTTCATTTGATGTCAATTAAGCAAGTACTGCTACTTTTGAANTGAAATAA 2674
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Qy 3850 AAAAAAAAA 3858
Db 2675 AAAAAAAAA 2683

RESULT 9
US-10-342-887-324
; Sequence 324, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 324
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-324

Query Match 67.5%; Score 2606.4; DB 18; Length 2691;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2635; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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Qy 1270 CACCAAGCAATGATGAAGATCTTGCACGCCGACAGACCTGGAACCTTGGGACAGAGCG 1329
Db 95 CACCAAGCAATGATGAAGATCTTGCACGCCGACAGACCTGGAACCTTGGGACAGAGCG 154
Qy 1330 TGGCAGCTGTGCGACCTCGGCGGTGAGAGCGGCGCAAGAGAGTGCCTCAAGTGGCTCT 1389
Db 155 TGGCAGCTGTGCGACCTCGGCGGTGAGAGCGGCGCAAGAGAGTGCCTCAAGTGGCTCT 214
Qy 1390 GCTCAACATGCGCAACCCCAACCTTGAAGACCTTGAAGGAGCTTCAACCCGTTGCAATGCG 1449
Db 215 GCTCAACATGCGCAACCCCAACCTTGAAGACCTTGAAGGAGCTTCAACCCGTTGCAATGCG 274
Qy 1450 CGTGAAGAGAGGGTGGCGGGGTGTGTGAGTCTCTGCTGCGACCGAAGATCAAGTGTAA 1509
Db 275 CGTGAAGAGAGGGTGGCGGGGTGTGTGAGTCTCTGCTGCGACCGAAGATCAAGTGTAA 334
Qy 1510 CGCCAAAGATGAGAGCAGTGAACAGCCCTCACTTTCAGAGCCGAAAGCGGAGATGATC 1569
Db 335 CGCCAAAGATGAGAGCAGTGAACAGCCCTCACTTTCAGAGCCGAAAGCGGAGATGATC 394
Qy 1570 TAGCACAAGGCTGCTGTGGAAGAGAGAGCTTGTGCAAGAGTGAATTTGAGAGGCGG 1629
Db 395 TAGCACAAGGCTGCTGTGGAAGAGAGAGCTTGTGCAAGAGTGAATTTGAGAGGCGG 454
Qy 1630 GAGCGCCATGCACTGTGCGCTGCAAGAGGAGAGAGATTCGTGCGCATCTGCTGCG 1689
Db 455 GAGCGCCATGCACTGTGCGCTGCAAGAGGAGAGAGATTCGTGCGCATCTGCTGCG 514
Qy 1690 CCGAGCGGTGAGCGTGAAGCTTGCAGGGCAAGATGCTGCGCTGCACTGCACTACGCTGC 1749
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Qy 1750 CTGGCAGGCGCCACCTGCCATCTGTCAAGCTGTGGCCACGACGCCGGGGGTGAGTGTAA 1809
Db 575 CTGGCAGGCGCCACCTGCCATCTGTCAAGCTGTGGCCACGACGCCGGGGGTGAGTGTAA 634
Qy 1810 CGCCCAAGACGTGTGAATGGGAAGAACGCCCATTTGCACTTGGCCCGCACAAGCGCGGGGCTACTACG 1869
Db 635 CGCCCAAGACGTGTGAATGGGAAGAACGCCCATTTGCACTTGGCCCGCACAAGCGCGGGGCTACTACG 694
Qy 1870 CGTGGCCCGGCATCTCTCATGACCTGTGCTCGACGTCCTCAACGTCCTGCAAGCTGTGGCACA 1929
Db 695 CGTGGCCCGGCATCTCTCATGACCTGTGCTCGACGTCCTCAACGTCCTGCAAGCTGTGGCACA 754
Qy 1930 GACACCCCTGTGCACTGTGCCCGCGGAGACGCGGCGACACGAGCACTGCGACGAGCTGTCTGCA 1989
Db 755 GACACCCCTGTGCACTGTGCCCGCGGAGACGCGGCGACACGAGCACTGCGACGAGCTGTCTGCA 814
Qy 1990 TCGGGGCGCTGGCAAGAGAGCGCGCTGACCTTCAGACCGGCTTACACCGCTTCGACCTGGCTGC 2049
Db 815 TCGGGGCGCTGGCAAGAGAGCGCGCTGACCTTCAGACCGGCTTACACCGCTTCGACCTGGCTGC 874
Qy 2050 CGGCAACGGAACACTGTGCGCACTGTCAAGCTGTGTGCGAGGAGAGAGCGCGATGTGCTGGC 2109
Db 875 CGGCAACGGAACACTGTGCGCACTGTCAAGCTGTGTGCGAGGAGAGAGCGCGATGTGCTGGC 934
Qy 2110 CCGGGAGACCCCTGAAACAGACCGGCGCTGCACTGTGCTGCGCGCCACCGGCGACTCGGAGGT 2169
Db 935 CCGGGAGACCCCTGAAACAGACCGGCGCTGCACTGTGCTGCGCGCCACCGGCGACTCGGAGGT 994
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Db 995 GGTGAGAGAGTGTGTCAAGCGCGAGATGTCAATGACCTGTTCGACGAGCAGGGGCTCAGGCGC 1054
Qy 2230 GCTGCACTGTGCCCGCCAGGGGCGGCGACACGACACGAGCGGTGGAGACTGTGCTCAGGCACTG 2289
Db 1055 GCTGCACTGTGCCCGCCAGGGGCGGCGACACGACACGAGCGGTGGAGACTGTGCTCAGGCACTG 1114
Qy 2290 GGCCCACTCAACCTGTGCAAGAGCTTCAAGTTCAGGGCGGCGCACTGGCCCGCGCCACACT 2349
Db 1115 GGCCCACTCAACCTGTGCAAGAGCTTCAAGTTCAGGGCGGCGCACTGGCCCGCGCCACACT 1174
Qy 2350 CCGTGGGAGAGACCAAGACTAGCTGTGCTGCGCGGAGACCGGGGGTCCAGTGGGGGCTC 2409
Db 1175 CCGTGGGAGAGACCAAGACTAGCTGTGCTGCGCGGAGACCGGGGGTCCAGTGGGGGCTC 1234
Qy 2410 TTGTCTGTCTGTGTCTCTGTGTGGAGATGAAACGATCTGTGCGGGGCGCGGTGTGGC 2469
Db 1235 TTGTCTGTCTGTGTCTCTGTGTGGAGATGAAACGATCTGTGCGGGGCGCGGTGTGTGGC 1294
Qy 2470 TTACTTAAATGTAAACCAAGAGAGTGAATGTGCTTCAAGAGGCGGCTGCTGTGCA 2529
Db 1295 TTACTTAAATGTAAACCAAGAGAGTGAATGTGCTTCAAGAGGCGGCTGCTGTGCA 1354
Qy 2530 CCGAGAGTGTCCCTCAAGGTGAAGCTGTGAGGTGACATGCGCGCTCAATCATCATGATC 2589
Db 1355 CCGAGAGTGTCCCTCAAGGTGAAGCTGTGAGGTGACATGCGCGCTCAATCATCATGATC 1414
Qy 2590 TAGGCACTGTGTCTGAAGGAGACGTGGGTCAAGATCAATTCCTTGTGTCTCTAATGGG 2649
Db 1415 TAGGCACTGTGTCTGAAGGAGACGTGGGTCAAGATCAATTCCTTGTGTGTCTCTAATGGG 1474
Qy 2650 TCGCTGAAGGCTGTCTCTGAAGTGAAGACCCCAAGCGGTGAAGATCACTCTCTCTG 2709
Db 1475 TCGCTGAAGGCTGTCTCTGAAGTGAAGACCCCAAGCGGTGAAGATCACTCTCTCTG 1534
Qy 2710 AAGCGAGCACTTGGGTGTGCTGAGCTCAACAGTCTTGAAGGAGGTGCAAGGGAACCTG 2769
Db 1535 AAGCGAGCACTTGGGTGTGCTGAGCTCAACAGTCTTGAAGGAGGTGCAAGGGAACCTG 1594
Qy 2770 TGTCTTTTATCTTCATACATGACGCTGGCAGAGAGCGCTGTCTTAAAGTTTCAATGAA 2829

Db 1595 TGTCTTTTATCTTCATACATGACGCTGGGCGAGAGCGCTGTCTTAAAGTTTCCATGAA 1654
Qy 2830 TGTCTTTTATTTAAATATCTTAAAGATGAATACCTTATACCTGTGTGCTTGAACCTGTGA 2889
Db 1655 TGTCTTTTATTTAAATATCTTAAAGATGAATACCTTATACCTGTGTGCTTGAACCTGTGA 1714
Qy 2890 AAAATGTTCAATTAACATTGATAGTCTAGTCTTAAATGATAGCTTAAGTGTGGGTGGC 2949
Db 1715 AAAATGTTCAATTAACATTGATAGTCTAGTCTTAAATGATAGCTTAAGTGTGGGTGGC 1774
Qy 2950 TTTGAATAACATGTTTATTCGAACAGAAACGAATGTGACAGCTTTGGGGGCGT 3009
Db 1775 TTTGAATAACATGTTTATTCGAACAGAAACGAATGTGACAGCTTTGGGGGCGT 1834
Qy 3010 ATGTGTGCCAGCTCTTAACATTTCCAGTCTAATTAATCTTGGGTGAGTCTGTGGCAACC 3069
Db 1835 ATGTGTGCCAGCTCTTAACATTTCCAGTCTAATTAATCTTGGGTGAGTCTGTGGCAACC 1884
Qy 3070 ACACACAGTGCACATGTGTAATGCTGCGGTGCTTGTCTGTGCTTGAAGTGTG 3129
Db 1895 ACACACAGTGCACATGTGTAATGCTGCGGTGCTTGTCTGTGCTTGAAGTGTG 1954
Qy 3130 GCAACTTGAAGCCACAGGCTTAAGACTCAATTAATAATTCCTCTTGTGAACCTCAGTG 3189
Db 1955 GCAACTTGAAGCCACAGGCTTAAGACTCAATTAATAATTCCTCTTGTGAACCTCAGTG 2014
Qy 3190 CTGGGAGCTGAGGAGACCCCTCAGGTCGCTGAGAGCAACAGTCTTGGGGAAGAGGTG 3249
Db 2015 CTGGGAGCTGAGGAGACCCCTCAGGTCGCTGAGAGCAACAGTCTTGGGGAAGAGGTG 2074
Qy 3250 CAGGAGAGCTGTGTTTATCTCAACAGCAATGAAATTAATAATTAATTAATTAATTA 3309
Db 2075 CAGGAGAGCTGTGTTTATCTCAACAGCAATGAAATTAATAATTAATTAATTAATTA 2134
Qy 3310 CTTTGAACATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3369
Db 2135 CTTTGAACATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2194
Qy 3370 TCAATTTTGTAGGTGATGTGGATAGGATAGTGTGTTGGGGGTATGGGGGAGTGTTC 3429
Db 2195 TCAATTTTGTAGGTGATGTGGATAGGATAGTGTGTTGGGGGTATGGGGGAGTGTTC 2254
Qy 3430 TGAAGTGTCTTGGCAGAGTGTCTTCGACCTCAGCAGTGTGGGGGTGCGCCCAAGGCGG 3489
Db 2255 TGAAGTGTCTTGGCAGAGTGTCTTCGACCTCAGCAGTGTGGGGGTGCGCCCAAGGCGG 2314
Qy 3490 TTCTTGAATGTAATAAGATGTGGCACTTAAGCTGTGTAACTTCACTGTGTCCCA 3549
Db 2315 TTCTTGAATGTAATAAGATGTGGCACTTAAGCTGTGTAACTTCACTGTGTCCCA 2374
Qy 3550 TAGGGTGTCTTGAATAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3609
Db 2375 TAGGGTGTCTTGAATAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2454
Qy 3610 CAAACATGTACCTGTGCGCTGTATATGATAGATTAATTAATTAATTAATTAATTAATTA 3669
Db 2435 CAAACATGTACCTGTGCGCTGTATATGATAGATTAATTAATTAATTAATTAATTAATTA 2494
Qy 3670 ATGTGAATCTGTGGCAGAGATTAATTTTCCATGTGACGAGAAATATCCAGCTGTGAACCTG 3729
Db 2495 ATGTGAATCTGTGGCAGAGATTAATTTTCCATGTGACGAGAAATATCCAGCTGTGAACCTG 2554
Qy 3730 GCTATGTTTAAATATGCTCAATGTGCTTAACTGTGTGAGCTGCTGAGGAGCAAG 3789
Db 2555 GCTATGTTTAAATATGCTCAATGTGCTTAACTGTGTGAGCTGCTGAGGAGCAAG 2614
Qy 3790 AAGTTCATTTGATGTCAATTAAGCAAGTACTTGTCTTGTGAANCTGAATAAA 3849
Db 2615 AAGTTCATTTGATGTCAATTAAGCAAGTACTTGTCTTGTGAANCTGAATAAA 2674
Qy 3850 AAAAAAAAA 3858
Db 2675 AAAAAAAAA 2683

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RESULT 10
US-10-658-904-3
; Sequence 3, Application US/10658904
; Publication No. US20040048305A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 14171 Protein Kinase, A No. US20040048305A1 Human
TITLE OF INVENTION: Protein Kinase and Uses Thereof
FILE REFERENCE: MP100-0101RCP1M
CURRENT APPLICATION NUMBER: US/10/658,904
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 09/781,882
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/182,096
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-658-904-3

Query Match      61.0%; Score 2355; DB 18; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGAGGCGACCGCGGAGACCCATAGGCGCTGCGCTGCGACCTTTCAGACGCGGAGC 76
DB 1 ATGAGAGGCGACCGCGGAGACCCATAGGCGCTGCGCTGCGACCTTTCAGACGCGGAGC 60
QY 77 GAGTTACGCGGCTGGAGAAAGTGGGCTCGGCGGCTTCGGGAGGTTGTAACAAGTGGCC 136
DB 61 GAGTTACGCGGCTGGAGAAAGTGGGCTCGGCGGCTTCGGGAGGTTGTAACAAGTGGCC 120
QY 137 CATGTCACCTGAGAAAGCTGGCTGACCATCAAGTGTCTGCGCCAGCTTGCACGTCAGAC 196
DB 121 CATGTCACCTGAGAAAGCTGGCTGACCATCAAGTGTCTGCGCCAGCTTGCACGTCAGAC 180
QY 197 AGGAGCGCATGAGAGCTTTTGGAGAAAGCCAAAGATGAGATGAGATGAGATGAGATGAG 256
DB 181 AGGAGCGCATGAGAGCTTTTGGAGAAAGCCAAAGATGAGATGAGATGAGATGAGATGAG 240
QY 257 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGTCAATGAGATGAGATGAG 316
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGTCAATGAGATGAGATGAG 300
QY 317 ACGGAGCTCCCTGAGAAAGCTGTGAGCTTGGAGCCATATGAGATGAGATGAGATGAGATGAG 376
DB 301 ACGGAGCTCCCTGAGAAAGCTGTGAGCTTGGAGCCATATGAGATGAGATGAGATGAGATGAG 360
QY 377 ATATATCAAGAGACGCGGCTGGGAGATGAATTTCTGTCATGATGAGATGAGATGAGATGAG 436
DB 361 ATATATCAAGAGACGCGGCTGGGAGATGAATTTCTGTCATGATGAGATGAGATGAGATGAG 420
QY 437 CACTGGAACCTCAAGCCCGGAAATCTCTGCTGATGAGCCCAATACAGAGTCAAGATTTCT 496
DB 421 CACTGGAACCTCAAGCCCGGAAATCTCTGCTGATGAGCCCAATACAGAGTCAAGATTTCT 480
QY 497 GATTTGTGTGCGCAAGTGCACACGAGCTGTCCACTGCGATGACCTCAGCATGAGATGAG 556
DB 481 GATTTGTGTGCGCAAGTGCACACGAGCTGTCCACTGCGATGACCTCAGCATGAGATGAG 540
QY 557 CTGTTTGGGCAATCGCTCACTTCCCTCCAGAGCGATCAAGGAGAAAGCGGCTCTTC 616
DB 541 CTGTTTGGGCAATCGCTCACTTCCCTCCAGAGCGATCAAGGAGAAAGCGGCTCTTC 600
QY 617 GACACCAAGACAGATGATACAGCTTTCAGATGATGATGATGATGATGATGATGATGATGATG 676
DB 601 GACACCAAGACAGATGATACAGCTTTCAGATGATGATGATGATGATGATGATGATGATGATG 660
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QY 677 AAGCGTTTGGAGATGAGAAAGATCTTGCATCATGATGAGATGAGATGAGATGAGATGAGATGAG 736
DB 661 AAGCGTTTGGAGATGAGAAAGATCTTGCATCATGATGAGATGAGATGAGATGAGATGAGATGAG 720
QY 737 CGCCCCGAGCTGCGCGCGTGTGAGAGCCCGGCGCGCTTGCAGACCATCTTAATACG 796
DB 721 CGCCCCGAGCTGCGCGCGTGTGAGAGCCCGGCGCGCTTGCAGACCATCTTAATACG 780
QY 797 CTATGACGCGGTGTGCGAGAGGAGATCCGGAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 856
DB 781 CTATGACGCGGTGTGCGAGAGGAGATCCGGAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 840
QY 857 TCTGAAACCGAGAGACCTGTGTGAAAGAGCTGATGACGAAAGTGAAGAAATGCTCATGAT 916
DB 841 TCTGAAACCGAGAGACCTGTGTGAAAGAGCTGATGACGAAAGTGAAGAAATGCTCATGAT 900
QY 917 CTGAGAGTGAAGAGCCCGCGAGCCGAGAGCGAGAGTGTGCTTGCAGAGCTCAAGCGG 976
DB 901 CTGAGAGTGAAGAGCCCGCGAGCCGAGAGCGAGAGTGTGCTTGCAGAGCTCAAGCGG 960
QY 977 GCCTTGCCTCCACCTTGTATTAAGATCAAGCTCTTCCAGAGCTTCTCAAGCTGAGAC 1036
DB 961 GCCTTGCCTCCACCTTGTATTAAGATCAAGCTCTTCCAGAGCTTCTCAAGCTGAGAC 1020
QY 1037 TCTGAGATTTCCAGAGCTGTGAGAGGAGCCGAGAGAGCTCAAGCGAGCTCTTGAATCC 1096
DB 1021 TCTGAGATTTCCAGAGCTGTGAGAGGAGCCGAGAGAGCTCAAGCGAGCTCTTGAATCC 1080
QY 1097 AAGCTGCAATGATCTGCGAGAGTGGAGAGAGCTTTCGAGAGAGTGTCTGATGAGATCTGCGC 1156
DB 1081 AAGCTGCAATGATCTGCGAGAGTGGAGAGAGCTTTCGAGAGAGTGTCTGATGAGATCTGCGC 1140
QY 1157 TTCTTTTCCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTTCACAGAGATCTG 1216
DB 1141 TTCTTTTCCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTTCACAGAGATCTG 1200
QY 1217 GGTACCAAGAGCTGCGAGAGAGAGAGAGCTTGTGATGCAATGCTGCGGAGACACAGC 1276
DB 1201 GGTACCAAGAGCTGCGAGAGAGAGAGAGCTTGTGATGCAATGCTGCGGAGACACAGC 1260
QY 1277 AAATGATGAAGATCTCTCAAGCGCGAGAGAGTGAACCTTGCATGAGACAGCGGTCCAGC 1336
DB 1261 AAATGATGAAGATCTCTCAAGCGCGAGAGAGTGAACCTTGCATGAGACAGCGGTCCAGC 1320
QY 1337 CTGCTGCACTGCGCGGTGAGAGCGCGGCAAGAGATGCGCAATGCTGCTGCTCAAC 1396
DB 1321 CTGCTGCACTGCGCGGTGAGAGCGCGGCAAGAGATGCGCAATGCTGCTGCTCAAC 1380
QY 1397 AATGCAACCCCAACCTTGAAGCAACGTTAGAGGCTTCAACCGGTTGCAATGAGCGGTGAG 1456
DB 1381 AATGCAACCCCAACCTTGAAGCAACGTTAGAGGCTTCAACCGGTTGCAATGAGCGGTGAG 1440
QY 1457 AGGAGGCTGCGGAGTGTGTGAGAGCTCTGCTGAGCAAGAGATGATGATGATGATGATGATGATG 1516
DB 1441 AGGAGGCTGCGGAGTGTGTGAGAGCTCTGCTGAGCAAGAGATGATGATGATGATGATGATGATG 1500
QY 1517 GATGAGAGCAAGTGAACAGCTTTCATTTGAGAGCTTTCAGAGAGGAGATGATGATGATGATG 1576
DB 1501 GATGAGAGCAAGTGAACAGCTTTCATTTGAGAGCTTTCAGAGAGGAGATGATGATGATGATG 1560
QY 1577 CGGCTGCTGTTGAGAAAGAGAGAGCTTTCAGAGAGGAGATGATGATGATGATGATGATGATG 1636
DB 1561 CGGCTGCTGTTGAGAAAGAGAGAGCTTTCAGAGAGGAGATGATGATGATGATGATGATGATGATG 1620
QY 1637 ATGCAAGTGAAGCTTGCAGAGCGGAGAGATATGATGATGATGATGATGATGATGATGATGATG 1696
DB 1621 ATGCAAGTGAAGCTTGCAGAGCGGAGAGATATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1697 GTGAGAGTGAAGCTTGCAGAGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1756
DB 1681 GTGAGAGTGAAGCTTGCAGAGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1740
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QY 1757 GGCACCTGCCCCATGCTGCAAGCTGTGGCCAAAGACGCGGGGGTGAAGTGAACGCCCCAG 1816
DB 1741 GGCACCTGCCCCATGCTGCAAGCTGTGGCCAAAGACGCGGGGGTGAAGTGAACGCCCCAG 1800
QY 1817 ACGCTGATGAGGAGACGCCATTGCACTGTGCGGCAAGCGCGGCACTAACCGCGTGGCC 1876
DB 1801 ACGCTGATGAGGAGACGCCATTGCACTGTGCGGCAAGCGCGGCACTAACCGCGTGGCC 1860
QY 1877 GCGATCTCATGCACTGTGTCTCGACGCTCAAGCTGTGCAAGCTGTGCGCAAGACACC 1936
DB 1861 GCGATCTCATGCACTGTGTCTCGACGCTCAAGCTGTGCGCAAGCTGTGCGCAAGACACC 1920
QY 1997 CTGCACTGTGCGGCGGAGACGCGGGGCAAGCACTGCGAAGCTGTCTCTGATGAGGAGC 1996
DB 1921 CTGCACTGTGCGGCGGAGACGCGGGGCAAGCACTGCGAAGCTGTCTCTGATGAGGAGC 1980
QY 1997 GCTGGCAAGAGGCGGTGACCTGACAGCGGCTTGAACCGGCTGTGCACTGTGCGGCAAC 2056
DB 1981 GCTGGCAAGAGGCGGTGACCTGACAGCGGCTTGAACCGGCTGTGCACTGTGCGGCAAC 2040
QY 2057 GGAACCTGTGGCACTGTGCAAGCTGTGTGAGAGAGAGCGGATGTGCGCGGAG 2116
DB 2041 GGAACCTGTGGCACTGTGCAAGCTGTGTGAGAGAGAGCGGATGTGCGCGGAG 2100
QY 2117 CCCCAGAACGAGCGGCTGACCTGTGCGGCGGCAAGCGGCACTGTGCGGAGTGGAG 2176
DB 2101 CCCCAGAACGAGCGGCTGACCTGTGCGGCGGCAAGCGGCACTGTGCGGAGTGGAG 2160
QY 2177 GAGTTGTGACGCGGATGTCAATTGACCTGTGTGAGAGAGAGGCGCTGAC 2236
DB 2161 GAGTTGTGACGCGGATGTCAATTGACCTGTGTGAGAGAGAGGCGCTGAC 2220
QY 2237 CTGCGCGGCGGAGCGGCGGCAAGCAAGAGGCTGTGAGAGCTGTGAGAGCGGCGGAG 2296
DB 2221 CTGCGCGGCGGAGCGGCGGCAAGCAAGAGGCTGTGAGAGCGGCGGCGGAG 2280
QY 2297 ATCAACCTGTGAGAGCGGCTCAAGTTTCAAGGGCGGCGCAATGGCGCGGCGGCACTCTGCGG 2356
DB 2281 ATCAACCTGTGAGAGCGGCTCAAGTTTCAAGGGCGGCGCAATGGCGCGGCGGCACTCTGCGG 2340
QY 2357 CGAAGCAAGACCTAG 2371
DB 2341 CGAAGCAAGACCTAG 2355

RESULT 11
US-10-128-174-15
/ Sequence 15, Application US/10128174
/ Publication No. US2003019462A1
/ GENERAL INFORMATION:
/ APPLICANT: Nunez, Gabriel
/ APPLICANT: Inohara, Naohiro
/ TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
/ FILE REFERENCE: UM-06967
/ CURRENT APPLICATION NUMBER: US/10/128,174
/ CURRENT FILING DATE: 2002-04-23
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15
/ LENGTH: 2355
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-128-174-15

Query Match 60.3%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 17 AAGGAGGCGGAGCGGCGGAGCCCCATGAGGCGCTGTGCGGCACTTGAAGCGGCGC 76
DB 1 AAGGAGGCGGAGCGGCGGAGCCCCATGAGGCGCTGTGCGGCACTTGAAGCGGCGC 60
QY 77 GAGTTCAAGGCTGTGGAGAAAGGTGGGCTCGGCGGCGCTTGGGCAAGGTGAGCGC 136

DB 61 GAGTTCAAGGCTGTGGAGAAAGGTGGGCTCGGCGGCGCTTGGGCAAGGTGAGCGC 120
QY 137 CATGTCACTGAGAAAGACTGTGGCTTGGCACTAAGTGTCTGCCAGGCTGTGCAAGTGAAGAC 136
DB 121 CATGTCACTGAGAAAGACTGTGGCTTGGCACTAAGTGTCTGCCAGGCTGTGCAAGTGAAGAC 180
QY 197 AAGGAGGCGGAGCGGCTTGTGAAAGAGCAAGAAAGATGAGATGGCAAGTTTCGTAC 256
DB 181 AAGGAGGCGGAGCGGCTTGTGAAAGAGCAAGAAAGATGAGATGGCAAGTTTCGTAC 240
QY 257 ATCTGCGCTGTGATGAGCACTGTGCGGGAACCTGTGCGGCTGTGATGAGATGAGAG 316
DB 241 ATCTGCGCTGTGATGAGCACTGTGCGGGAACCTGTGCGGCTGTGATGAGATGAGAG 300
QY 317 ACGGCGCTCTGGAAGAGCTGTGGCTTGGAGAGCAATGGCAATGGATCTCCGTTCCGA 376
DB 301 ACGGCGCTCTGGAAGAGCTGTGGCTTGGAGAGCAATGGCAATGGATCTCCGTTCCGA 360
QY 377 ATCAATCAAGAGACGCGGGGTGGGATGAACCTTCTGTGCACTGCAATGGCGGCGCACTCTG 436
DB 361 ATCAATCAAGAGACGCGGGGTGGGATGAACCTTCTGTGCACTGCAATGGCGGCGCACTCTG 420
QY 437 CACCTGACCTTCAAGCGCGGGAACATCTGTGATGAGCCCACTAACAAGTATTTCT 496
DB 421 CACCTGACCTTCAAGCGCGGGAACATCTGTGATGAGCCCACTAACAAGTATTTCT 480
QY 497 GATTTGGTGTGGCAAGTGAACAGGAGCTGTCCACTGTGCAATGCACTGACATGAGATGGC 556
DB 481 GATTTGGTGTGGCAAGTGAACAGGAGCTGTCCACTGTGCAATGCACTGACATGAGATGGC 540
QY 557 CTGTTTGGCAATATGCGCTTACCTCTCCAGAGGCGCATAGGGAGAGAGCGGCTTTC 616
DB 541 CTGTTTGGCAATATGCGCTTACCTCTCCAGAGGCGCATAGGGAGAGAGCGGCTTTC 600
QY 617 GACACCAAGCAGATGATATACAGCTTTGCAATGCTATCTTGGGCGTGTCAACAAG 676
DB 601 GACACCAAGCAGATGATATACAGCTTTGCAATGCTATCTTGGGCGTGTCAACAAG 660
QY 677 AAGCGCTTTGCAATGAGAAAGAAACATCTGTGCAATCATGTGTGAAGGTGTGAAGGGCAC 736
DB 661 AAGCGCTTTGCAATGAGAAAGAAACATCTGTGCAATCATGTGTGAAGGTGTGAAGGGCAC 720
QY 737 GCGCCCGAGCGGCGCGGCTGTGAGAGCGGCGGCGGCGGCGGCTGTGAGAGCGGCGGCGGCGG 796
DB 721 GCGCCCGAGCGGCGGCGGCTGTGAGAGCGGCGGCGGCGGCGGCGGCTGTGAGAGCGGCGGCGG 780
QY 797 CTCATGAGCGGCTGTGAGAGGAGGAGATCCGAGATTAGGCGCACCTTCCAAAGAAATTA 856
DB 781 CTCATGAGCGGCTGTGAGAGGAGGAGATCCGAGATTAGGCGCACCTTCCAAAGAAATTA 840
QY 857 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGTGATGAGAGGAGAAAGAAAGCTGTGATGAT 916
DB 841 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGTGATGAGAGGAGAAAGAAAGCTGTGATGAT 900
QY 917 CTGAGCGTGAAGAAAGCGGCGGAGCGGAGAGCGAGGTGTGTCTGCGAGGCTCAAGCGG 976
DB 901 CTGAGCGTGAAGAAAGCGGCGGAGCGGAGAGCGAGGTGTGTCTGCGAGGCTCAAGCGG 960
QY 977 GCGTGTGCGGCGGCGGCTTGTGATGAGATGAGGCTTCTGAGGCTTCTGATGAGGAGC 1036
DB 961 GCGTGTGCGGCGGCGGCTTGTGATGAGATGAGGCTTCTGAGGCTTCTGATGAGGAGC 1020
QY 1037 TCTGAGATTTTCCAGAGGCTGTGAGAGGCGGCGGAGAGAGTCAAGCGGAGCTCTGAGATGCC 1096
DB 1021 TCTGAGATTTTCCAGAGGCTGTGAGAGGCGGCGGAGAGAGTCAAGCGGAGCTCTGAGATGCC 1080
QY 1097 AAGCGGCAATGATCGGAGAGTGAAGAGGCTCTCGGAGGAGTCTCTGAGTGAAGCTCGGCGC 1156
DB 1081 AAGCGGCAATGATCGGAGAGTGAAGAGGCTCTCGGAGGAGTCTCTGAGTGAAGCTCGGCGC 1140
QY 1157 TTCTTTTCAAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCAACGAGGATCTG 1216

Db	1141	TTCTCTTCCAGAGGATCACTGTCCCTGTCTCTTTAGGGGAAACCTTCAACGAGGATCTG	1200
Qy	1217	GGTACCAAGACCGTCCAGAGAGAAAGACTTGTGAATGCCATCTGTCTC--GGACACACAG	1275
Db	1201	GGCACAC--AAGCGTCCAGAGAGAAAGAACTTGTGAATGCCATCTGTCTCCGGGACACAG	1259
Qy	1276	CAACATGATGAAGATCCGTGCAGCCGCGAGAGATGAGACCTGGCACTGGACAGCGGTGCAG	1335
Db	1260	CAAACTGATGAAGATCTCTGCAGCCGCGAGAGAGTGAACCTGGCACTGGACAGCGGTGCAG	1319
Qy	1336	CTGTCTGCACCTGGCGGTGCAGAGCGCGGACAAAGAGAGTGCACAGTGGGTCTGCTCAA	1395
Db	1320	CTGTCTGCACCTGGCGGTGCAGAGCGCGGACAAAGAGAGTGAACCTGGCACTGGACAGCGGTGCAG	1379
Qy	1396	CAATGCCAAACCCCAACTGAGCAACCGTAGGGGCTCCACCCCGTTGCAATATGCGCTGGAA	1455
Db	1380	CAATGCCAAACCCCAACTGAGCAACCGTAGGGGCTCCACCCCGTTGCAATATGCGCTGGAA	1439
Qy	1456	GAGAGAGGATGGGGGGTGTCTGTGAGACTTCCTGCTGGCACGAAAGATCATGTGCACGCGCAA	1515
Db	1440	GAGAGAGGATGGGGGGTGTCTGTGAGACTTCCTGCTGGCAAGATCATGTGCACGCGCAA	1499
Qy	1516	GGAATGAGAACCAATGAGACAGCCCTTCACTTTGCAGCCCAAGAACGAGGATGAGTCTAGCAC	1575
Db	1500	GGATTAAGAACCAATGAGACAGCCCTTCACTTTGCAGCCCAAGAACGAGGATGAGTCTAGCAC	1559
Qy	1576	ACGGCTGCTGTGTGAGAGAAAGAACGCGCTCGGTCAACGAGGTGACATTTGAGGGCGGACGCC	1635
Db	1560	ACGGCTGCTGTGTGAGAGAAAGAACGCGCTCGGTCAACGAGGTGACATTTGAGGGCGGACGCC	1619
Qy	1636	CATGCACTGTGAGCTTGCCACAGCACGGGCGAGAGAAATATCGTGGCAATCCTGCTGCCGCCAGG	1695
Db	1620	CATGCACTGTGAGCTTGCCACAGCACGGGCGAGAGAAATATCGTGGCAATCCTGCTGCCGCCAGG	1679
Qy	1696	CGTGAACGTGAGCCTGCGAGGGGCAAGATGCGTGGCTGCGACCTGCACCTACAGCTGCTGGACA	1755
Db	1680	CGTGAACGTGAGCCTGCGAGGGGCAAGATGCGTGGCTGCGACCTGCACCTACAGCTGCTGGACA	1739
Qy	1756	GGGCAACCTGAGCCATCGTCAAGCTGCTGGCCAGAGAGCGGGGGTGAATGTGAACGCCCA	1815
Db	1740	GGGCAACCTGAGCCATCGTCAAGCTGCTGGCCAGAGAGCGGGGGTGAATGTGAACGCCCA	1799
Qy	1816	GACGCTGATGGAGAGAGCGCCATTGCACTGTGCGGCAAGAGCGGGGCACTAACCGCGTGGC	1875
Db	1800	GACGCTGATGGAGAGAGCGCCATTGCACTGTGCGGCAAGAGCGGGGCACTAACCGCGTGGC	1859
Qy	1876	CGGCAATCCATATGACCTGTGCTCGAGCGTCAACGTCTGCAGCGCTGCGGACAGACAC	1935
Db	1860	CGGCAATCCATATGACCTGTGCTCGAGCGTCAACGTCTGCAGCGCTGCGGACAGACAC	1919
Qy	1936	CTTGCACGTGAGCGCGGAGACCGGGGCAACAGACACTGCAGCGCTGCTCTGCATCGGGG	1995
Db	1920	CTTGCACGTGAGCGCGGAGACCGGGGCAACAGACACTGCAGCGCTGCTCTGCATCGGGG	1979
Qy	1996	CGCTGGCAAGAGAGCGGTGAACCTCAGACGAGCTAACCGCTTGCACCTGGCTGCCCGGAA	2055
Db	1980	CGCTGGCAAGAGAGCGGTGAACCTCAGACGAGCTAACCGCTTGCACCTGGCTGCCCGGAA	2039
Qy	2056	CGGACACTGTGGCACTGTCAACCTGCTTGTGAGAGAGAAAGCGATGTGCTGGCCCGGGG	2115
Db	2040	CGGACACTGTGGCACTGTCAACCTGCTTGTGAGAGAGAAAGCGATGTGCTGGCCCGGGG	2099
Qy	2116	ACCCCTGAACAGAGCGGCGTGCACCTGTGCTGCGCCACAGGACACTCGAGAGTGTGGA	2175
Db	2100	ACCCCTGAACAGAGCGGCGTGCACCTGTGCTGCGCCACAGGAGTGTGGA	2159
Qy	2176	GGAGTTGTCAAGCGCGGATGTCAATTGAACCTGTTCAACGACGAGGAGCTCAGCGCTGCA	2235
Db	2160	GGAGTTGTCAAGCGCGGATGTCAATTGAACCTGTTCAACGACGAGGAGCTCAGCGCGCTGCA	2219
Qy	2236	CTGTGGCGCCAGAGGCGGCGACGACAGAGCGTGAAGATCTGCTCAAGGCAATGGGCGCA	2295
Db	2220	CTGTGGCGCCAGAGGCGGCGACGACAGAGCGTGAAGATCTGCTCAAGGCAATGGGCGCA	2279

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OY      2286 CATCACTGCAGACGCTTCAAGTTCCAGGGCGGCCATGTCCCCGGCACCACA CTCTGGG   2355
        |||||||
Db       2280 CATTAACTTCGAAGA GACTTCAAAGTTTCAGAGCGCGCATGGCCCCGGCCGACCACTCTGGG   2339
                                         |
OY       2356 GGGAAGCAAGACTTAG   2371
        |||||
Db        2340 GGGAAGCAAGACTTAG   2355

RESULT 12
US-10-128-174-16
; Sequence 16, Application US/10128174
; Publication NO. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEO ID NO 16
; LENGTH: 2355
TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-16
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Query Match	60.3%	Score 2327.2;	DB 16;	Length 2355;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2351; Conservative	0;	Mismatches 3;	Indels 2;	Gaps 2.

QY	17	ATGAGAGGGGGAAGGGGGGAGCCCGCATGAGGGCCCTGGGGCACCCTTCAGACGGGGG	76
Db	1	ATGAGAGGGGGAAGGGGGGAGCCCGCATGAGGGCCCTGGGGCACCCTTCAGACGGGGG	60
QY	77	GAGTTCACGGGCTGGGAGAGGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAAGTGGC	136
Db	61	GAGTTCACGGGCTGGGAGAGGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAAGTGGC	120
QY	137	CATGTCCACTGGAAGACTGGCTGGCCATCAGTGGCTCGGCCAGCCTGCACCTTCAGAC	196
Db	121	CATGTCCACTGGAAGACTGGCTGGCCATCAGTGGCTCGGCCAGCCTGCACCTTCAGAC	180
QY	197	AAGGAGCGCATGAGCGCTTTTGGAGAAGGCCAAGAAATGAGATGAGATGGCCAAAGTTCCGTAC	256
Db	181	AAGGAGCGCATGAGCGCTTTTGGAGAAGGCCAAGAAATGAGATGAGATGGCCAAAGTTCCGTAC	240
QY	257	ATCCGACCTGTGTATATGGCATCTGCCCGCAACCTGTCCGGCTGGTCAATGAGTACATGAG	316
Db	241	ATCCGACCTGTGTATATGGCATCTGCCCGCAACCTGTCCGGCTGGTCAATGAGTACATGAG	300
QY	317	ACGGGCTCCCTGGAAGAGCTGCTGGCTTGGAGCCATTGCAATGGATCTCCGGTTCCGA	376
Db	301	ACGGGCTCCCTGGAAGAGCTGCTGGCTTGGAGCCATTGCAATGGATCTCCGGTTCCGA	360
QY	377	ATCATCATCAGAGACGGCGGGTGGGCAAGAACTTCCTGCACTGCAATGGCCCGGCACATCCTG	436
Db	361	ATCATCATCAGAGACGGCGGGTGGGCAAGAACTTCCTGCACTGCAATGGCCCGGCACATCCTG	420
QY	437	CACCTGGACCTCAAGCCCGCGAATCATCTGCTGGATGGCCCATACCACTCAAGATTCT	496
Db	421	CACCTGGACCTCAAGCCCGCGAATCATCTGCTGGATGGCCCATACCACTCAAGATTCT	480
QY	497	GATTTTGGTCTGGCCAAAGTGCACCGGGCTGTCCCATTCGATATGACTCAGCATGATGGC	556
Db	481	GATTTTGGTCTGGCCAAAGTGCACCGGGCTGTCCCATTCGATATGACTCAGCATGATGGC	540
QY	557	CTGTTTGGCAATATGCCCTAATCTCCCTCCAGAGGGCATCAGGGAGAGAGCCGGCTTTC	616
Db	541	CTGTTTGGCAATATGCCCTAATCTCCCTCCAGAGGGCATCAGGGAGAGAGCCGGCTTTC	600

QY	617	GACACCAAGCA	CGATGTTATACGTTTGCCATTCGTCACTTGGGGCGGTCTCA	CAAGAAAG	616
Db	601	GACACCAAGCA	CGATGTTATACGCTTTGGCCATCTGGGGCGGTCTCA	CAAGAAAG	660
QY	617	AAGCGGTTTGG	AGATGAGAAAGCAATCCGTGACATCAATGGTGAAGGTGGTGAAGGGGCAC	736	
Db	661	AAGCGGTTTGG	AGATGAGAAAGCAATCTTGCAATCAATGGTGAAGGTGGTGAAGGGGCAC	720	
QY	737	CGCCCCGAGCTG	CGCCCGGTGGAGAGCCCGGCGCGCGCGCTTGACAGCCACTTGATACGC	796	
Db	721	CGCCCCGAGCTG	CGCCCGGTGGAGAGCCCGGCGCGCGCGCTTGACAGCCACTTGATACGC	780	
QY	797	CTCATGCA	CGCGGTGCTGGCAGGGGGATCCGCGAGTTAGGCCCACTTCCAGAAATTAATCT	856	
Db	781	CTCATGCA	CGCGGTGCTGGCAGGGGGATCCGCGAGTTAGGCCCACTTCCAGAAATTAATCT	840	
QY	857	TCTGAAACCG	AGGAGACTGTGTGAAAGGCTGATGACGAATGAAAGAAATCGCTCATGAT	916	
Db	841	TCTGAAACCG	AGGAGACTGTGTGAAAGGCTGATGACGAATGAAAGAAATCGCTCATGAT	900	
QY	917	CTGACAGTGA	AAAAAGCCCCCGGAGGCCGAGAGCGAGGTGGTCCCTGCGAGGCTCAAGCGG	976	
Db	901	CTGACAGTGA	AAAAAGCCCCCGGAGGCCGAGAGCGAGGTGGTCCCTGCGAGGCTCAAGCGG	960	
QY	977	GCGCTTGG	CCCCCACTTTGATTAACAATACAGCTCTTCCAGGCTTCTCTCAACAGCTGAC	1036	
Db	961	GCGCTTGG	CCCCCACTTTGATTAACAATACAGCTCTTCCAGGCTTCTCTCAACAGCTGAC	1020	
QY	1097	TCTGAGGTTTCC	CAGGCTGTGAGGGGCCCCGAGGAGCTCAGCCGAGGCTCTCTGAGTCC	1096	
Db	1021	TCTGAGGTTTCC	CAGGCTGTGAGGGGCCCCGAGGAGCTCAGCCGAGGCTCTCTGAGTCC	1080	
QY	1097	AAGCTGCA	TCGTCCGGCAGTGGAAAGAGCTCTTGCGGGGTGTCTCTGGTGAATCTCCGC	1156	
Db	1081	AAGCTGCA	TCGTCCGGCAGTGGAAAGAGGCTCTTGCGGGGTGTCTCTGGTGAATCTCCGC	1140	
QY	1157	TTCTCTTCC	AGAGATCACTGTCCGTTCCTTTGAGCGGGAACTTTCAACAGCGATCTG	1216	
Db	1141	TTCTCTTCC	AGAGATCACTGTCCGTTCCTTTGAGCGGGAACTTTCAACAGCGATCTG	1200	
QY	1217	GGTACCA	CAAGACGTCGAGAAAGAAAGACTTGTGGATGCCATTCGATCC--GGGACACAG	1275	
Db	1201	GGTACCA	CA--AGCGTCGAGAAAGAAAGACTTGTGTGATCCATTCGATTCGGGGACACAG	1259	
QY	1276	CAAACTGTA	GAAGATCTCTGACGCCGACAGACGTGGACCTGGCACTGGCAAGCGGTGCAG	1335	
Db	1260	CAAACTGTA	GAAGATCTCTGACGCCGACAGACGTGGACCTGGCACTGGCAAGCGGTGCAG	1319	
QY	1336	CCTGCTGCA	CTCGCGGTGGAGAGCGGGCAAGAGAGTGGCCAAATGGTGGCTTGCTCA	1395	
Db	1320	CCTGCTGCA	CTCGCGGTGGAGAGCGGGCAAGAGAGTGGCCAAATGGTGGCTTGCTCA	1379	
QY	1396	CAATGCC	CAAAACCCCAACCTGAGCAACCGTAAAGGGGCTCAACCCCGTTTGGCAATGGCGGTGA	1455	
Db	1380	CAATGCC	CAAAACCCCAACCTGAGCAACCGTAAAGGGGCTCAACCCCGTTTGGCAATGGCGGTGA	1439	
QY	1456	GAGGAGGGGTG	CGGGGTGTCTGTGAGACTCTGCTGGCAGGAAAGATCAAGTGTCAACGCGCAA	1515	
Db	1440	GAGGAGGGGTG	CGGGGTGTCTGTGAGACTCTGCTGGCAGGAAAGATCAAGTGTCAACGCGCAA	1499	
QY	1516	GGATAGAGA	CGATGAGCAAGCCCTTCACTTTGACGCCAGAAACGGGGATGAGTCTAGAC	1575	
Db	1500	GGATAGAGA	CGATGAGCAAGCCCTTCACTTTGACGCCAGAAACGGGGATGAGTCTAGAC	1559	
QY	1576	AAGGCTGCTGT	TGGAGAGAAAGCCCTCGGTCAACAGAGTGAACCTTTGAGGGCCCGAGCGCC	1635	
Db	1560	AAGGCTGCTGT	TGGAGAGAAAGCCCTCGGTCAACAGAGTGAACCTTTGAGGGCCCGAGCGCC	1619	
QY	1636	CATGCA	CGTGGCTCGCAGCAAGGACAGGAGAAATATCGTGGCATCTCTGCTCGCCGAGG	1695	
Db	1620	CATGCA	CGTGGCTCGCAGCAAGGACAGGAGAAATATCGTGGCATCTCTGCTCGCCGAGG	1679	
QY	1696	CGTGA	CGTGAAGCTTGCAGAGGCAAGATGCTGTGCTGCACCTGACATGACATGCGTGCCTGGCA	1755	

Db	1680	CGTGACCTGTAGCCTTGCAAGGGCCAAAGATGCTTGGCTGCCACTGCACTAAGCTGCGTGGCA	1739
QY	1756	GAGGCACCTGCCCCATCGTCAAAGCTGCTGACCACAAGACCCGAGGGTGAAGTTGAACGCCCA	1815
Db	1740	GAGGCACCTGCCCATCGTCAAGCTGCTGACCACAAGACCCGAGGGTGAAGTTGAACGCCCA	1799
QY	1816	GAAGCTGGAATGGAGAAGAGCCATTGGACACTTGCCGCCCAAGAGCCGGGACCTAACCGGTGGC	1875
Db	1800	GAAGCTGGAATGGAGAAGAGCCATTGGACACTTGCCGCCCAAGAGCCGGGACCTAACCGGTGGC	1859
QY	1876	CCGATCTCTCAATCGACCTGTGCTCCGACGATCAAGCTCTGACGCTGTGGCAACAACAAC	1935
Db	1860	CCGATCTCTCAATCGACCTGTGCTCCGACGATCAAGCTCTGACGCTGTGGCAACAACAAC	1919
QY	1936	CTTGACACGTGGCCCGGCAAGACCGGGCACACAGACATGCGCAAGCTTCTCTGATCGGGG	1995
Db	1920	CTTGACACGTGGCCCGGCAAGACCGGGCACACAGACATGCGCAAGCTTCTCTGATCGGGG	1979
QY	1996	CGCTGGCAAAGAGGCGCTGTAACCTCAAGAGGCTTACACCGCTCTGCAACTTGGCTGCCGCA	2055
Db	1980	CGCTGGCAAAGAGGCGCTGTAACCTCAAGAGGCTTACACCGCTCTGCAACTTGGCTGCCGCA	2039
QY	2056	CGGACACCTGGGCACTGTCAAGCTGCTTGTGAGAGGAAGAGCGGATGTCTGACCCGGGG	2115
Db	2040	CGGACACCTGGGCACTGTCAAGCTGCTTGTGAGAGGAAGAGCGGATGTCTGACCCGGGG	2099
QY	2116	ACCCCTGAACCAAGACGAGCGCTGCACTTGCTGCGGCCACCGGCACTCGAGGTGTGGA	2175
Db	2100	ACCCCTGAACCAAGACGAGCGCTGCACTTGCTGCGGCCACCGGCACTCGAGGTGTGGA	2159
QY	2176	GAGATTGGTCAGAGCGGCGGATGTATTGACCTGTTCACACGACGAGGGGCTCAAGCGCTGCA	2235
Db	2160	GAGATTGGTCAGAGCGGCGGATGTATTGACCTGTTCACACGAGGGGCTCAAGCGCTGCA	2219
QY	2236	CTTGACCGGCGGACGAGCGGCGGCAAGACGAGCTGTGAGAGCTTGTCTACAGGCTATGGGCCCA	2295
Db	2220	CTTGACCGGCGGACGAGCGGCGGCAAGACGAGCTGTGAGAGCTTGTCTACAGGCTATGGGCCCA	2279
QY	2296	CATCAACCTGCAGAGCCTTCAAGTTCCAAGGACGAGCCCGCCGCCAACTCTTGCG	2355
Db	2280	CATCAACCTGCAGAGCCTTCAAGTTCCAAGGACGAGCCCGCCGCCAACTCTTGCG	2339
QY	2356	GCGAAGCAAGACTTAG 2371	
Db	2340	GCGAAGCAAGACTTAG 2355	
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US-10-128-174-18			
; Sequence 18, Application US/10128174			
; Publication No. US20030199462A1			
; GENERAL INFORMATION:			
; APPLICANT: Inohara, Naohiro			
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling			
; FILE REFERENCE: UM-06967			
; CURRENT APPLICATION NUMBER: US/10/128,174			
; CURRENT FILING DATE: 2002-04-23			
; NUMBER OF SEQ ID NOS: 44			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 18			
; LENGTH: 2355			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-128-174-18			
 Query Match 60.3%; Score 2357.2; DB 16; Length 2355;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;			
QY	17	ATGAGAGGGGAGAGGGCGGAGCCCACATGGGCGCTGGCGCTGTGGCACTTTCAGACGGGGGC	76

Db 1 ATGAGGGGAGACGGGGGAGACCCCATGGGCGCTGGCGCTGGCGACATCTTCGACGCGGGC 60
Qy 77 GAGTTCAAGGAGTGGAGAGAGTGGGCTTCGGGCGGCTTCGGGCAAGTGGCG 136
Db 61 GAGTTCAAGGAGTGGAGAGAGTGGGCTTCGGGCGGCTTCGGGCAAGTGGCG 120
Qy 137 CATGTCACATGGAAGACCTGGCTGGCTCATCAAGTCTGGCCGACGTGACACGAC 196
Db 121 CATGTCACATGGAAGACCTGGCTGGCTCATCAAGTCTGGCCGACGTGACACGAC 180
Qy 197 AAGGAGCGCATGAGACTTTTGGAGAGGCAAGAGATGAGATGGCCAGTTTGGCTAC 256
Db 181 AAGGAGCGCATGAGACTTTTGGAGAGGCAAGAGATGAGATGGCCAGTTTGGCTAC 240
Qy 257 ATCTGGCTGTGTATGAGCATCTGGCGGAACTGTGGGCTGTGTATGAGATGAG 316
Db 241 ATCTGGCTGTGTATGAGCATCTGGCGGAACTGTGGGCTGTGTATGAGATGAG 300
Qy 317 AAGGAGCTCCCTGGAGAAAGCTGTGGCTTGGAGGCACTTGGCATGGGATCTCCGGTTCCGA 376
Db 301 AAGGAGCTCCCTGGAGAAAGCTGTGGCTTGGAGGCACTTGGCATGGGATCTCCGGTTCCGA 360
Qy 377 ATCATCCAGAGACGGGCGGTGGGCAATGAACTTCCTGCACTGCAATGGCCCGGCACTCTG 436
Db 361 ATCATCCAGAGACGGGCGGTGGGCAATGAACTTCCTGCACTGCAATGGCCCGGCACTCTG 420
Qy 437 CACTGGACCTCAAGCCCGGCAATCTGTGAGATGCCACTACACAGTCAAGATTTCT 496
Db 421 CACTGGACCTCAAGCCCGGCAATCTGTGAGATGCCACTACACAGTCAAGATTTCT 480
Qy 497 GATTTTGTGTGGCCAAAGTGCACAGGGCTGTCCCATCTGGCATGACCTTCAGCATGATGGC 556
Db 481 GATTTTGTGTGGCCAAAGTGCACAGGGCTGTCCCATCTGGCATGATGATGGC 540
Qy 557 CTGTTTGGGCAATGGCTTACCTCCCTCCAGAGCGCATGAGGAGAAAGCGGCTTTC 616
Db 541 CTGTTTGGGCAATGGCTTACCTCCCTCCAGAGCGCATGAGGAGAAAGCGGCTTTC 600
Qy 617 GACACCAAGACGATGTATACAGCTTTGGCATGTGATCTGGGGCGTGTCAACAGAG 676
Db 601 GACACCAAGACGATGTATACAGCTTTGGCATGTGATCTGGGGCGTGTCAACAGAG 660
Qy 677 AAGCCGTTTGGCAGATGAGAAAGCATCTGCAATGATGATGAGTGGAGGCGCAC 736
Db 661 AAGCCGTTTGGCAGATGAGAAAGCATCTGCAATGATGATGAGTGGAGGCGCAC 720
Qy 737 CGCCCGGAGCTGCGGCGGTGGCAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 796
Db 721 CGCCCGGAGCTGCGGCGGTGGCAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Qy 797 CTGATGCAAGGCTGTGGCAGGAGGATCCGAGATTAGGCCACTTTCAGAAATTAAT 856
Db 781 CTGATGCAAGGCTGTGGCAGGAGGATCCGAGATTAGGCCACTTTCAGAAATTAAT 840
Qy 857 TCTGAAACCGAGGACCTGTGTGAAAAGCTGATGACGAAATGAAAATCTGCTATGAT 916
Db 841 TCTGAAACCGAGGACCTGTGTGAAAAGCTGATGACGAAATGAAAATCTGCTATGAT 900
Qy 917 CTGGAAGTGAAGACCCCGGAGGCCAGGAGGAGGTGGCTGCGAGGCTCAAGCGG 976
Db 901 CTGGAAGTGAAGACCCCGGAGGCCAGGAGGAGGTGGCTGCGAGGCTCAAGCGG 960
Qy 977 GCCTGCGCCCACTTTCGATTAACGATACAGCCTCTCCGAGCTTCTTCAAGCTGAC 1036
Db 961 GCCTGCGCCCACTTTCGATTAACGATACAGCCTCTCCGAGCTTCTTCAAGCTGAC 1020
Qy 1037 TCTGAGTTTCCAGGCTGTGTGAGGGCCCGGAGAGGCTCAGCGGCACTCTTGAATCC 1096
Db 1021 TCTGAGTTTCCAGGCTGTGTGAGGGCCCGGAGAGGCTCAGCGGCACTCTTGAATCC 1080
Qy 1097 AAGCTGCAATGTCGGCAGTGGAGAGAGGCTCTCGGGGGTGTCTCGGTGACCTCGCC 1156
Db 1081 AAGCTGCAATGTCGGCAGTGGAGAGAGGCTCTCGGGGGTGTCTCGGTGACCTCGCC 1140

Qy 1157 TTCTCTTCAGAGGATCATGTCGTGCTCTTGTAGGCGGAACTTCAACGAGGATCTG 1216
Db 1141 TTCTCTTCAGAGGATCATGTCGTGCTCTTGTAGGCGGAACTTCAACGAGGATCTG 1200
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Qy 1336 CCGTGTGACCTGGCGGTGGAGGCGGCGGCAAGAGAGTGGCCCAAGTGGCTGTGCA 1395
Db 1320 CCGTGTGACCTGGCGGTGGAGGCGGCGGCAAGAGAGTGGCCCAAGTGGCTGTGCA 1379
Qy 1396 CAATGCCAACCCCAACTGACCAACCGTAGGGGCTCCACCCTGTGCAATGGCGGTGGA 1455
Db 1380 CAATGCCAACCCCAACTGACCAACCGTAGGGGCTCCACCCTGTGCAATGGCGGTGGA 1439
Qy 1456 GAGAGGGGTGGGGGTGTGTGAGACTCTGTGTGACAGAGATCAATGTCAACGCCAA 1515
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Qy 1516 GAGATGAGGACGAGTGGACAGGCTTCACCTTTCAGGCCGAGAACGGGAGATGATCTAGAC 1575
Db 1500 GAGATGAGGACGAGTGGACAGGCTTCACCTTTCAGGCCGAGAACGGGAGATGATCTAGAC 1559
Qy 1576 AAGGCTGTGTGTGAGAGAAAGGCTCGGTCAAGAGGTGACCTTTGAGGGCGGAGCGC 1635
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Db 1620 CATGCACTGTGCTGTGACAGCGGCAAGAAATTCGTGGCATCTGTGCGGCGGAG 1679
Qy 1656 CCGTGGACGTGAGCCCTGGCAAGGCGCAAGATGCGTGGCTGCACTGACCTGCTGGCA 1755
Db 1640 CCGTGGACGTGAGCCCTGGCAAGGCGCAAGATGCGTGGCTGCACTGACCTGCTGGCA 1739
Qy 1756 GGGCCACTGTGCATCTGTCAGAGCTGTGGCCAGAGCGGGGGTGAATGTGAACGCCCA 1815
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Qy 1816 GACGCTGATGAGAGAGAGCGCAATTCACCTGGCGGCAAGCGGCGGCACTACCGGCTGGC 1875
Db 1800 GACGCTGATGAGAGAGAGCGCAATTCACCTGGCGGCAAGCGGCGGCACTACCGGCTGGC 1859
Qy 1876 CCGCATCTGTCAATCCAGCTGTGTCCAGAGTCAACGTCTGGCAGGCGGCTGGGCAAGAACCC 1935
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Qy 1936 CCGTGAAGTGGCGGCGGAGAGCGGGCAACAGAGCACTGCAAGGCTGTCTTGGCATCGGGG 1995
Db 1920 CCGTGAAGTGGCGGCGGAGAGCGGGCAACAGAGCACTGCAAGGCTGTCTTGGCATCGGGG 1979
Qy 1996 CGCTGGCAAGAGAGCGGTGACCTGACAGCGGCTTTCAGAGGAGAGGCGGAGTGGCTGGCCCGGGG 2055
Db 1980 CGCTGGCAAGAGAGCGGTGACCTGACAGCGGCTTTCAGAGGAGAGGCGGAGTGGCTGGCCCGGGG 2039
Qy 2056 CGGACACTGGGCACTGTGCAAGCTGTGTGAGAGAGAGGCGGAGTGGCTGGCCCGGGG 2115
Db 2040 CGGACACTGGGCACTGTGCAAGCTGTGTGAGAGAGAGGCGGAGTGGCTGGCCCGGGG 2099
Qy 2116 ACCCTGAAACAGAGCGGCGTGCACCTGAGCTGCGGCCCAAGGCACTGAGAGTGGTGA 2175
Db 2100 ACCCTGAAACAGAGCGGCGTGCACCTGAGCTGCGGCCCAAGGCACTGAGAGTGGTGA 2159
Qy 2176 GAGATTGTGACGCGCGGATGTCAATTGACTGTTCAGACAGAGGGGCTCAGCGGCTGCA 2235
Db 2160 GAGATTGTGACGCGCGGATGTCAATTGACTGTTCAGACAGAGGGGCTCAGCGGCTGCA 2219

Db	1620	CATGACGCTGGCTCTCCACGACACGGGACAGGAAATATCGTGCGCATCTGTCTCGCCGAGG	1679
QY	1696	CGTGGACGCTGAGCCTCTGCACAGGGCAAGATATGCTCTGCTCCACTGCATACGCTGCTGGCA	1755
Db	1680	CGTGGACGTGAGCCTCTGCACAGGGCAAGATATGCTCTGCTCCACTGCATACGCTGCTGGCA	1739
QY	1756	GGGCGCACCTGGCCCATCGTCAACGATCTGGCCAAAGACGGCGGGGGGAGAGTGTAAAGGCCA	1815
Db	1740	GGGCGCACCTGGCCCATCGTCAACGATCTGGCCAAAGACGGCGGGGGGAGAGTGTAAAGGCCA	1799
QY	1816	GACGCTGATGGAGGAGACGCAATTGCACCTGTGCGCCACAGCGCGGGCACTACCGCGTGGC	1875
Db	1800	GACGCTGATGGAGGAGACCGCCATTGCACCTGTGCGCCACAGCGCGGGCACTACCGCGTGGC	1859
QY	1876	CCGATCTCTCATGACACTGTGTCTCCGACGTCAACGTCTGACGCTGTGGCAACAGACAC	1935
Db	1860	CCGATCTCTCATGACACTGTGTCTCCGACGTCAACGTCTGACACCTGTGGCAACAGACAC	1919
QY	1936	CCTGACGCTGGCGCGGGAGACGGGGGACACAGAGCATGCGCAGGCTGTCTCATATCGGGG	1995
Db	1920	CCTGACGCTGGCGCGGGAGACGGGGGACACAGAGCATGCGCAGGCTGTCTCATATCGGGG	1979
QY	1996	CGCTGGCAAGAGGCGCGTGAACCTCAGACGGGCTACACCGCTCTGCACCTGGCTGCCGCA	2055
Db	1980	CGCTGGCAAGAGGCGCGTGAACCTCAGACGGGCTACACCGCTCTGCACCTGGCTGCCGCA	2039
QY	2056	CGGACACCTGGCCACTGTCAAGCTGTTGTCAAGAGAAAGCCGATGTGCTGGCCCGGGG	2115
Db	2040	CGGACACCTGGCCACTGTCAAGCTGTTGTCAAGAGAAAGCCGATGTGCTGGCCCGGGG	2099
QY	2116	ACCCCTGAAACGAGCGGCGCTGCACCTGGCTGCCCGCCACCGGCACTCGAGGTGGTGA	2175
Db	2100	ACCCCTGAAACGAGCGGCGCTGCACCTGGCTGCCCGCCACCGGCACTCGAGGTGGTGA	2159
QY	2176	GGAGTTGGTCAAGCGCGGATGTCAATTGACCTGTTCAGACGAGAGGGCTCAGGCGCTGCA	2235
Db	2160	GGAGTTGGTCAAGCGCGGATGTCAATTGACCTGTTCAGACGAGAGGGCTCAGGCGCTGCA	2219
QY	2236	CGTGGCGGCCCAAGGGCGGGCAAGACAGACGAGTGAAGACTCTGTCTCAGGCAATGGGCGCA	2295
Db	2220	CGTGGCGGCCCAAGGGCGGGCAAGACAGACGAGTGAAGACTCTGTCTCAGGCAATGGGCGCA	2279
QY	2296	CATCAACCTGCAGAGCTTCAAGTTCAGAGGGCGGGCCATGGCCCGCGGCAACTCCTGGG	2355
Db	2280	CATCAACCTGCAGAGCTTCAAGTTCAGAGGGCGGGCCATGGCCCGCGGCAACTCCTGGG	2339
QY	2356	GCGAAGCAAGACCTAG 2371	
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RESULT 15
US-10-128-174-1

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; Sequence 1, Application US/10128174
; Publication No. US20030199462A1
;
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-128-174-1

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Query Match	60.2%;	Score 2325.6;	DB 16;	Length 2355;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 2350;	Conservative	0;	Mismatches 4;	Indels 2;
				Gaps 2;

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OY	77	GAGTTCAAGGAGCTGAGGAG	AGTGTGGCTCGGAGCGCTT	CGGAGAGTTTACAAAGTGTGC		136
Db	61	GAGTTTCAAGGAGCTGAGGAG	AGTGTGGCTCGGAGCGCTT	CGGAGAGTTTCAAGTGTGC		120
OY	137	CATGTCCACTGGAAGAC	CTTGCTGGCCATTAATGTCTCGCCGAC	CGCTGCACCGTCAAGC		196
Db	121	CATGTCCACTGGAAGAC	CTTGCTGGCCATTAATGTCTCGCCGAC	CGCTGCACCGTCAAGC		180
OY	197	AGGAGGCGCATGAGAGCTTTT	TGAAAGAACCAAGATGAGATGAG	CGCAAGTTTCGTAC		256
Db	181	AGGAGGCGCATGAGAGCTTTT	TGAAAGAACCAAGATGAGATGAG	CGCAAGTTTCGTAC		240
OY	257	ATCTGCTCTGTGTATGAG	CACTCTGCGCGAACCTTGCGAGCTTGAT	CTATGAGTTACATGAGAG		316
Db	241	ATCTGCTCTGTGTATGAG	CACTCTGCGCGAACCTTGCGAGCTTGAT	CTATGAGTTACATGAGAG		300
OY	317	ACGGAGCTCCCTGGAAAG	CTGTGGAGCTTCCGAGCATTTGCATGAG	ATCTCTCCGTTTCGA		376
Db	301	ACGGAGCTCCCTGGAAAG	CTGTGGAGCTTCTGAGCATTTGCATGAG	ATCTCTCCGTTTCGA		360
OY	377	ATCATCCACAGACAGGCG	GGTGGGATGAACCTTCTGCACTTGCA	TGAGCGCCGCCACCTCTCG		436
Db	361	ATCATCCACAGACAGGCG	GGTGGGATGAACCTTCTGCACTTGCA	TGAGCGCCGCCACCTCTCG		420
OY	437	CACCTGGAACCTCAAG	CGCCCGGAAACATCTCTGTGGAATGCCA	CTAACACAGTCAAGATTCT		496
Db	421	CACCTGGAACCTCAAG	CGCCCGGAAACATCTCTGTGGAATGCCA	CTAACACAGTCAAGATTCT		480
OY	497	GATTTGGTCTGAGCAAG	TGCAAGCGGCTGTCCCACTCGCATGA	CTCAGCATGAGTGGC		556
Db	481	GATTTGGTCTGAGCAAG	TGCAAGCGGCTGTCCCACTCGCATGA	CTCAGCATGAGTGGC		540
OY	557	CTGTTTGGCACAATCG	CCCTACCTTCCCTTCAGAGCGCAT	CAGGAGAAAGACCGGCTCTTC		616
Db	541	CTGTTTGGCACAATCG	CCCTACCTTCCCTTCAGAGCGCAT	CAGGAGAAAGACCGGCTCTTC		600
OY	617	GACACCAAGACAGATG	TATACAGCTTTTGGCATGCTCATCTG	GGGCGTGTCTCACACAGAG		676
Db	601	GACACCAAGACAGATG	TATACAGCTTTTGGCATGCTCATCTG	GGGCGTGTCTCACACAGAG		660
OY	677	AAGCGGTTTGAGATG	AGAAAGATCTTGCACTCATCTG	CAATCTGTAAGGTGTGAAAGGCGCAC		736
Db	661	AAGCGGTTTGAGATG	AGAAAGATCTTGCACTCATCTG	CAATCTGTAAGGTGTGAAAGGCGCAC		720
OY	737	CGCCCGGAGCTGCGG	CGCGGTGTGAGAGCCCGGCGGCGCG	CTGCAAGCATCTGATACGC		796
Db	721	CGCCCGGAGCTGCGG	CGCGGTGTGAGAGCCCGGCGGCGCG	CTGCAAGCATCTGATACGC		780
OY	797	CTCATGCAAGCGGTCT	GAGGAGATCTCGAGTTTAGGCCCACTT	CCAAGAAATTAAT		856
Db	781	CTCATGCAAGCGGTCT	GAGGAGATCTCGAGTTTAGGCCCACTT	CCAAGAAATTAAT		840
OY	857	TCGTGAACCGAGAC	CTGTGTGAAAGCTGTATGACAGATG	GAAGAAACCTGCTCATGAT		916
Db	841	TCGTGAACCGAGAC	CTGTGTGAAAGCTGTATGACAGATG	GAAGAAACCTGCTCATGAT		900
OY	917	CTGAGACGTGAAGAG	CGCCCGGAGCGCCAGAGCGAGAGTGTG	CTGCAAGGCTCAAGCGG		976
Db	901	CTGAGACGTGAAGAG	CGCCCGGAGCGCCAGAGCGAGAGTGTG	CTGCAAGGCTCAAGCGG		960
OY	977	GCTCTGCGCCCACTT	GATTAAGACTTCTTCGAGCTTCTCTCA	CAGCTGAGC		1036
Db	961	GCTCTGCGCCCACTT	GATTAAGACTTCTTCGAGCTTCTCTCA	CAGCTGAGC		1020
OY	1037	TCGTGAAGTTTCCAG	GGCTGTGAGAGGCGCCGAGAGGCTC	AGCGCAGCTCTCTGAAGTCC		1096
Db	1021	TCGTGAAGTTTCCAG	GGCTGTGAGAGGCGCCGAGAGGCTC	AGCGCAGCTCTCTGAAGTCC		1080

QY 1097 AAGCTGCCATGTCCTGGGCAATGGGAAGAGCTCTGGGGGTTGTCCTCGGTGGACCTCCGCC 1156
DB 1091 AAGCTGCCATGTCCTGGGCAATGGGAAGAGCTCTGGGGGTTGTCCTCGGTGGACCTCCGCC 1140
QY 1157 TTCTCTTCGAGAGATCACTGTCGCTGTCCTTTGAGCGGGAACTTCAACGAGCATCTG 1216
DB 1141 TTCTCTTCGAGAGATCACTGTCGCTGTCCTTTGAGCGGGAACTTCAACGAGCATCTG 1200
QY 1217 GGTACCAAGAGCTTCAGAGAGAGAGCTTGTGATGTCATGTTGCC-GGACACAG 1275
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QY 1276 CAATCTGATGAGATCTGCAAGCGGACGAGAGCTGAGACCTGAGCAAGCGGTCAG 1335
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QY 1396 CAATGCCAACCCCAACTGAGCAACCTGAGGGCTTCACCCCGTTGCAATGGCCGTGA 1455
DB 1380 CAATGCCAACCCCAACTGAGCAACCTGAGGGCTTCACCCCGTTGCAATGGCCGTGA 1439
QY 1456 GAGGAGGGGTGGGGGTGTTGTTGAGAGTCTGCTGGCAAGAGATCAATGTCAGCCAA 1515
DB 1440 GAGGAGGGGTGGGGGTGTTGTTGAGAGTCTGCTGGCGGAGAGATCAATGTCAGCCAA 1499
QY 1516 GAGTGAAGGACAGTGGACAGCCCTCACTTTGACAGCCCAAGACGGGATGATCTAGCA 1575
DB 1500 GAGTGAAGGACAGTGGACAGCCCTCACTTTGACAGCCCAAGACGGGATGATCTAGCA 1559
QY 1576 ACGGCTGCTGTTGAGAGAGAGAGCTTCGTCACAGAGTGAATTTGAGGGCCGACGCC 1635
DB 1560 ACGGCTGCTGTTGAGAGAGAGAGCTTCGTCACAGAGTGAATTTGAGGGCCGACGCC 1619
QY 1636 CATGACGTCGCTGTCAGCAGCGGAGAGAGATTCGTCGATCCTGCTGCGCGAGAG 1695
DB 1620 CATGACGTCGCTGTCAGCAGCGGAGAGAGATTCGTCGATCCTGCTGCGCGAGAG 1679
QY 1696 CTTGACGTCGACCTGCAAGGGCAAGATGCTGAGCTGCCACTGCACTAGCTGCTGCA 1755
DB 1680 CTTGACGTCGACCTGCAAGGGCAAGATGCTGAGCTGCCACTGCACTAGCTGCTGCA 1739
QY 1756 GGGCCCACTGCCCCATGTCATGTAAGCTGTGCGCAAGCGGCGGTGAGTGAAGCCCA 1815
DB 1740 GGGCCCACTGCCCCATGTCATGTAAGCTGTGCGCAAGCGGCGGTGAGTGAAGCCCA 1799
QY 1816 GACGCTGATGGAGAGAGCGCATTTGCACTTGGCCGCAAGCGGCGCACTACCGGTGGC 1875
DB 1800 GACGCTGATGGAGAGAGCGCATTTGCACTTGGCCGCAAGCGGCGCACTACCGGTGGC 1859
QY 1876 CCGCATCTCTCATGACCTGTGCTCCGACGTCAACGTCTGACAGCTTGGGCAAGACACC 1935
DB 1860 CCGCATCTCTCATGACCTGTGCTCCGACGTCAACGTCTGACAGCTTGGGCAAGACACC 1919
QY 1936 CTTGACGTCGCGCGGAGAGAGCGGGGCAAGAGCACTGCGCAAGCTGCTGCAATCGGG 1995
DB 1920 CTTGACGTCGCGCGGAGAGAGCGGGGCAAGAGCACTGCGCAAGCTGCTGCAATCGGG 1979
QY 1996 CGCTGAGAGAGAGCGGTGACCTCAGACGGCTTACACCGCTTGCACCTTGGCTGCCGCA 2055
DB 1980 CGCTGAGAGAGAGCGGTGACCTCAGACGGCTTACACCGCTTGCACCTTGGCTGCCGCA 2039
QY 2056 CGGACACCTGACCTGTCAGCTGCTTGTGAGAGAGAGCGCATGTCGTCGCGCGGG 2115
DB 2040 CGGACACCTGACCTGTCAGCTGCTTGTGAGAGAGAGCGCATGTCGTCGCGCGGG 2099
QY 2116 ACCCTTGAACAGACGGCGCTGCACTGCTGTCGCGCGCACTCGGAGTGTGTGA 2175
DB 2100 ACCCTTGAACAGACGGCGCTGCACTGCTGTCGCGCGCACTCGGAGTGTGTGA 2159
QY 2176 GAGGTTGATCAAGCGCGATGTATTTGACCTGTTCAGAGAGGGGCTCAGCGCGCTGCA 2235

DB 2160 GAGATTGATCAAGCGCCCATATGTCATTTGACTGTTGAGAGAGAGGAGGCTCAGCGGCTGCA 2219
QY 2236 CTTGCGCGCCCAAGGCGCGGCAAGAGAGAGAGAGCTTGTCTAGAGCATGGGCGCCA 2295
DB 2220 CTTGCGCGCCCAAGGCGCGGCAAGAGAGAGAGAGCTTGTCTAGAGCATGGGCGCCA 2279
QY 2296 CATCACTTGAAGAGCTTCAAGGCTTCAAGGCGGCGCATGCGCGCGCAACTTGGCG 2355
DB 2280 CATCACTTGAAGAGCTTCAAGGCTTCAAGGCGGCGCATGCGCGCGCAACTTGGCG 2339
QY 2356 GCGAAGCAAGACTAG 2371
DB 2340 GCGAAGCAAGACTAG 2355

Search completed: September 17, 2005, 02:18:44
Job time : 8808.61 secs

Db 1 ATGAGAGGCGACGGCGGGACCCCATGgggCCCTGGCGCTGCTCGGCACTTTCGACGCGGGC 60
Qy 61 GAGTTCAcGgGCTGGGAGAAgGTGGgCTCGGGCGGCTTCGGGCAgGTGTACAAGGTGGC 120
Db 61 GAGTTCAcGgGCTGGGAGAAgGTGGgCTCGGGCGGCTTCGGGCAgGTGTACAAGGTGGC 120
Qy 121 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTgCTCGCCAGCCTTCGACGTGCAcGAC 180
Db 121 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTgCTCGCCAGCCTTCGACGTGCAcGAC 180
Qy 181 AGGAGCGCATGAGACTTTTGAAGAAAGCCAAAGATGAGATGAGCCCAAGTTTCGCTAC 240
Db 181 AGGAGCGCATGAGACTTTTGAAGAAAGCCAAAGATGAGATGAGCCCAAGTTTCGCTAC 240
Qy 241 ATCTGCTGTGTATGGCACTGCGCGGACACTGTGGCCTGTGTCAATGAGATTAATGAG 300
Db 241 ATCTGCTGTGTATGGCACTGCGCGGACACTGTGGCCTGTGTCAATGAGATTAATGAG 300
Qy 301 ACGGGCTCCCTGGAAGAGCTGGCTTCGGAGCCATTGGCCATGGGANTCTCGGTTCCGA 360
Db 301 ACGGGCTCCCTGGAAGAGCTGGCTTCGGAGCCATTGGCCATGGGANTCTCGGTTCCGA 360
Qy 361 ATCAATCCAGAGCGGCGGTGGGCAATGAATCTTCGCACTGCAATGGCCCGCACTCCTG 420
Db 361 ATCAATCCAGAGCGGCGGTGGGCAATGAATCTTCGCACTGCAATGGCCCGCACTCCTG 420
Qy 421 CACCTGGAACCTCAAGCCCGGCAACATCTGTGTGATGCGCACTACCAAGTCAAGTTTCT 480
Db 421 CACCTGGAACCTCAAGCCCGGCAACATCTGTGTGATGCGCACTACCAAGTCAAGTTTCT 480
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Db 721 CGCCCCGAGCTGGCGCCGCTGTGCAAGAGCCGGCCGCGGCTTCGACCCACCTGATAGC 780
Qy 781 CTCAATGCAcGGGTGTGGCAAGGGGATTCGGAGGTTAAGGCCCACTTTCAGAAATTAAT 840
Db 781 CTCAATGCAcGGGTGTGGCAAGGGGATTCGGAGGTTAAGGCCCACTTTCAGAAATTAAT 840
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Db 901 CTGGAACGTGAAGAGCCCGCGAGGCCAGAGCGAGGTGTGTGCTGCGAGGCTCAAGCGG 960
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Qy 1141 TTCTCTTCCAGAGATTAATGTCGTGTCTCTTTGAAGCGGGAACCTTCAACAGCGATCTG 1200
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Qy 1201 GGTACCAAGAGCGTCCAGAGAAAGAGTGTGATGCCATGTCGTCCGGGACACCAAGC 1260
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Db 1321 CTGCTGCACTGGCGGTGAGAGCGCGGCAAGAGAGTGGCGCAAGTGGCTGTCTCAAC 1380
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Db 1381 AATGCCAACCCCAACCTGAGCAACCGTAAGGAGCTCAACCCCGTTTGCATATGAGGAG 1440
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Db 1441 AGAGGCTGCGGGTGTCTGAGAGCTCTGTGCAcGAGAAATCAATGTCAACGCCAAG 1500
Qy 1501 GATGAGGACGAGTGGACAGGCCCTCACTTTGCAAGCCAGAAcGGGGATGAGTCAAGACA 1560
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Qy 1561 CGGCTGTGTTTGAAGAAAGAAcGGCTCGGTCAACAGAGTGAATTTTGAAGGCGGACGCCC 1620
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Db 1621 ATGCACTGGCTTCGCAAGCCCGGCAAGAAATATGTTGGCATCTGTCTGCGCCAGAGC 1680
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Db 1741 GGGCACTGGCCCATCTGTCAAGCTGTGCGCAAGCAAGCCGGGGGTGAGTGAAGCGCCAG 1800
Qy 1801 ACGTGAATGGAGAGAGCGCATTTGCACTTGGCCGCAcAGCGGGGCACTACCGCGTGGCC 1860
Db 1801 ACGTGAATGGAGAGAGCGCATTTGCACTTGGCCGCAcAGCGGGGCACTACCGCGTGGCC 1860
Qy 1861 CGCATCTCAATGCACTGTGCTCGAAGTCAAGCGTCTGCAAGCTGTGGCAAGACACC 1920
Db 1861 CGCATCTCAATGCACTGTGCTCGAAGTCAAGCGTCTGCAAGCTGTGGCAAGACACC 1920
Qy 1921 CTGCACTGTGCGCGGAGAGCGGGGCAcAGAGCACTGCAAGGCTGTCTCTGATCGGGGC 1980
Db 1921 CTGCACTGTGCGCGGAGAGCGGGGCAcAGAGCACTGCAAGGCTGTCTCTGATCGGGGC 1980
Qy 1981 GCTGGCAAGAGCGCGTGAACCTTGAAGAGCGCTTACCGCTTGTGCACTGGGTGCGCGAAC 2040
Db 1981 GCTGGCAAGAGCGCGTGAACCTTGAAGAGCGCTTACCGCTTGTGCACTGGGTGCGCGAAC 2040
Qy 2041 GGAACACTGGCACTGTCAAGCTGTGTGAGAGAAAGGCGGATGTGTGCGCGGGGA 2100
Db 2041 GGAACACTGGCACTGTCAAGCTGTGTGAGAGAAAGGCGGATGTGTGCGCGGGGA 2100
Qy 2101 CCCCTGAACCAAGACGGGCTTGAACCTTGGCTGCGGCCACGGGCACTTGAAGGTGTGAG 2160
Db 2101 CCCCTGAACCAAGACGGGCTTGAACCTTGGCTGCGGCCACGGGCACTTGAAGGTGTGAG 2160
Qy 2161 GAGTTGTGACCGCGCAATGTATTAAGCTGTGAGAGAGAGGAGCTCAAGCGGCTGAC 2220
Db 2161 GAGTTGTGACCGCGCAATGTATTAAGCTGTGAGAGAGAGGAGCTCAAGCGGCTGAC 2220

[illegible]

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RESULT 2
US-10-658-904-1
? Sequence 1, Application US/10658904
? Publication No. US20040048305A1
? GENERAL INFORMATION:
? APPLICANT: Kapeller-Libermann, Rosana
? APPLICANT: Millennium Pharmaceuticals, Inc.
? TITLE OR INVENTION: 1417 Protein Kinase, A No. US20040048305A1 Human
? FILE REFERENCE: MP100-010P1RCP1M
? CURRENT APPLICATION NUMBER: US/10/658,904
? PRIOR FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: 09/781,882
? PRIOR FILING DATE: 2001-02-12
? PRIOR APPLICATION NUMBER: 60/182,096
? PRIOR FILING DATE: 2000-02-11
? NUMBER OF SEQ ID NOS: 29
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 3860
? TYPE: DNA
? ORGANISM: H. sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (17)...(2371)
? OTHER INFORMATION:
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(3860)
? OTHER INFORMATION: n = A,T,C or G
US-10-658-904-1

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Query Match	100.0%;	Score 2355;	DB 18;	Length 3860;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2355; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

QY	1	ATGAGAGGGGAGCGGGGAGACCCCATATGGGCGCTGGCGCTGTCGCACTTTCACACGGGGC	60
Db	17	ATGAGAGGGGAGCGGGGAGACCCCATATGGGCGCTGGCGCTGTCGCACTTTCACACGGGGC	76
QY	61	GAGTTTCA CGGCGCTGGAGAGGTGGGCTCTGGGCGGCTTTGGGCAAGTGTACAAAGTGGGC	120
Db	77	GAGTTTCA CGGCGCTGGAGAGGTGGGCTCTGGGCGGCTTTGGGCAAGTGTACAAAGTGGGC	136
QY	121	CATGTCTCACTGGAGA C CTGGCTGGGCATCAAGTGTCTGCCAGCCTGCACGCTGCAGC	180
Db	137	CATGTCTCACTGGAGA C CTGGCTGGGCATCAAGTGTCTGCCAGCCTGCACGCTGCAGC	196
QY	181	AGGAGCGCATGAGCTTTTGGAGAGGCCAAGAGATGGAATGGCCAAAGTTTCGCTAC	240
Db	197	AGGAGCGCATGAGCTTTTGGAGAGGCCAAGAGATGGAATGGCCAAAGTTTCGCTAC	256
QY	241	ATCTGCCTGTGTATGCACTTCGCCGAACTGTTCGGCTGGTCACTGAGAGTACATGAG	300
Db	257	ATCTGCCTGTGTATGCACTTCGCCGAACTGTTCGGCTGGTCACTGAGAGTACATGAG	316
QY	301	ACGGGCTCCCTGGAAAAGCTGCTGGCTTTGGAGCCATTGGCATGGGATCTTCGGGTTCCGA	360
Db	317	ACGGGCTCCCTGGAAAAGCTGCTGGCTTTGGAGCCATTGGCATGGGATCTTCGGGTTCCGA	376

QY	361	ATCATCCAGAGACGGGGGTGGGCATGAACCTTCCTGACATGACATGGCCCGGCACCTCCTG	420
Db	377	ATCATCCAGAGACGGGGGTGGGCATGAACCTTCCTGACATGACATGGCCCGGCACCTCCTG	436
QY	421	CACCTGGACCTCAAGCCCGGAAACATCTCTGGATGCCACTTACACGTCACAAATTTCT	480
Db	437	CACCTGGACCTCAAGCCCGGAAACATCTCTGGATGCCACTTACACGTCACAAATTTCT	496
QY	481	GATTTTGGTCTGGCCAAGTGCACAGGGCTGTCCACTTCGATGACTTCAGATGATGGC	540
Db	497	GATTTTGGTCTGGCCAAGTGCACAGGGCTGTCCACTTCGATGACTTCAGATGATGGC	556
QY	541	CTGTTTGGCACATCGCTTACCTTCCCTCAGAGGGCATCAAGGAGAAAGCCGCTCTTC	600
Db	557	CTGTTTGGCACAAATCGCTTACCTTCCCTCAGAGGGCATCAAGGAGAAAGCCGCTCTTC	616
QY	601	GACACCAAGACGATGTATACAGCTTTGGCATGCTCATCTGGGGCGTGTCAACACAAG	660
Db	617	GACACCAAGACGATGTATACAGCTTTGGCATGCTCATCTGGGGCGTGTCAACACAAG	676
QY	661	AAGCGTTTGGAGATGAGAAAGAACATCTGCACTACATATGTTGAAGTGTGAAGGGCCAC	720
Db	677	AAGCGTTTGGAGATGAGAAAGAACATCTGCACTACATATGTTGAAGTGTGAAGGGCCAC	736
QY	721	CGCCCCAGCTGCCGCCCGCTGTGTGAGAGCCCGCGCGCGCTGCAACCACTGATACG	780
Db	737	CGCCCCAGCTGCCGCCCGCTGTGTGAGAGCCCGCGCGCGCTGCAACCACTGATACG	796
QY	781	CTCATGCAAGCGGATGCTGGCAGGGGGATCCGCGAATTATAGGCCCACTTCCAAAGAAATTACT	840
Db	797	CTCATGCAAGCGGATGCTGGCAGGGGGATCCGCGAATTATAGGCCCACTTCCAAAGAAATTACT	856
QY	841	TCTGAAACCGAGGACTGTGTGAAAGCCTGATGACGAAATGAAAGAACTGCTCATGAT	900
Db	857	TCTGAAACCGAGGACTGTGTGAAAGCCTGATGACGAAATGAAAGAACTGCTCATGAT	916
QY	901	CTGACAGTGAAAGACCCCCCGGAGCCCAAGAGCGAGGTGTGTCTGCGAGGCTCAAGGG	960
Db	917	CTGACAGTGAAAGACCCCCCGGAGCCCAAGAGCGAGGTGTGTCTGCGAGGCTCAAGGG	976
QY	961	GCCCTGCGCCCCCACTTTCGATTAAGCATACAGCCCTCCGAGCTTCTCTCAAGCTGTGAC	1020
Db	977	GCCCTGCGCCCCCACTTTCGATTAAGCATACAGCCCTCTCCAGGCTTCTCTCAAGCTGTGAC	1036
QY	1021	TCTGAGATTTCCAGAGCTGTGAGGGGCCCGAGGAGCTCAAGCCGACGCTCTCTGAGTCC	1080
Db	1037	TCTGAGATTTCCAGAGCTGTGAGGGGCCCGAGGAGCTCAAGCCGACGCTCTCTGAGTCC	1096
QY	1081	AAGCTGCCATGTGTCCGGCATGTGGGAAGAGCTTCTCGGGGGTGTCTCGGTGATCTCCGC	1144
Db	1097	AAGCTGCCATGTGTCCGGCATGTGGGAAGAGCTTCTCGGGGGTGTCTCGGTGATCTCCGC	1156
QY	1141	TTTCTTTCACAGGATCACTGTGCTGTCTTTGAGCGGAACTTCAACAGCGATCTG	1200
Db	1157	TTTCTTTCACAGGATCACTGTGCTGTCTTTGAGCGGAACTTCAACAGCGATCTG	1216
QY	1201	GGTACCAAGACGTCAGAGAAAGACTTGTGATGTCATGTGTTCGGGACACAGC	1260
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QY	1261	AAACTGATGAAGATCTTGCAACCGCAGGACCTGTGACCTGTGGACATGGGTGCCAGC	1320
Db	1277	AAACTGATGAAGATCTTGCAACCGCAGGACCTGTGACCTGTGGACATGGGTGCCAGC	1336
QY	1321	CTGCTGCACCTGGCGGTGTGAAGGCGGGAAGAGTGCAGCAATGTGCTCTGTCAAC	1380
Db	1337	CTGCTGCACCTGGCGGTGTGAAGGCGGGAAGAGTGCAGCAATGTGCTCTGTCAAC	1396
QY	1381	AATGCCAACCCCAACTTGAGCAACCTGTAGGGGCTTCAACCCCGTTTGCAATGACCGTGGAG	1440
Db	1397	AATGCCAACCCCAACTTGAGCAACCTGTAGGGGCTTCAACCCCGTTTGCAATGACCGTGGAG	1456
QY	1441	AGAGAGGTGCGGGGTGTGTGAGACTCTTGCTGGCACGAAAGATCATGTGTCAAGCCCAAG	1500

Db 1457 AGGAGGCGCGGGGTGTGTGAGACTCTGCTGGACGGAAAGATCAAGTGAACGCCAAG 1516
Qy 1501 GATGAGACGATGAGACAGCCCTTCCATTTCAGCCCAAGCGGGATGAGTCTTACACA 1560
Db 1517 GATGAGACGATGAGACAGCCCTTCCATTTCAGCCCAAGCGGGATGAGTCTTACACA 1576
Qy 1561 CGGCTGCTGTGGAGAAAGAGCCCTCGGTCAACAGAGTGGACCTTGGAGGGCCGACGCC 1620
Db 1577 CGGCTGCTGTGGAGAAAGAGCCCTCGGTCAACAGAGTGGACCTTGGAGGGCCGACGCC 1636
Qy 1621 ATGCACTGAGCTGCGACAGCGGAGGAGATATCTGCGCATCTGCTGCGCGAGAGC 1680
Db 1637 ATGCACTGAGCTGCGACAGCGGAGGAGATATCTGCGCATCTGCTGCGCGAGAGC 1696
Qy 1681 GTGACGCTGAGCTGCGACAGCGGAGGAGATCTGCTGCGCATCTGCTGCGCGAG 1740
Db 1697 GTGACGCTGAGCTGCGACAGCGGAGGAGATCTGCTGCGCATCTGCTGCGCGAG 1756
Qy 1741 GGGCACTGCGCATCTGCTGAGCTGTGCGCAAGCAGCGGGGGTGAAGTGAAGGCCAG 1800
Db 1757 GGGCACTGCGCATCTGCTGAGCTGTGCGCAAGCAGCGGGGGTGAAGTGAAGGCCAG 1816
Qy 1801 ACGCTGATGGAGAGAGCGCATTTGCACTTGGCCGACAGCGCGGCACTACCGGCTGCGC 1860
Db 1817 ACGCTGATGGAGAGAGCGCATTTGCACTTGGCCGACAGCGCGGCACTACCGGCTGCGC 1876
Qy 1861 CGCATCTCATGAGCTGTGCTCGGACGTCAACGTCTGCGACCTGCTGCGCAACAGACCC 1920
Db 1877 CGCATCTCATGAGCTGTGCTCGGACGTCAACGTCTGCGACCTGCTGCGCAACAGACCC 1936
Qy 1921 CTGACCGTGGCGCGGAGAGCGGGGCAAGAGCACTGCGCAAGCTGCTGCAATCGGGGC 1980
Db 1937 CTGACCGTGGCGCGGAGAGCGGGGCAAGAGCACTGCGCAAGCTGCTGCAATCGGGGC 1996
Qy 1981 GCTGGCAAGAGAGCGCGTGAACCTGACAGCGGCTTACACCGCTTGCACCTTGGCCCGCAAC 2040
Db 1997 GCTGGCAAGAGAGCGCGTGAACCTGACAGCGGCTTACACCGCTTGCACCTTGGCCCGCAAC 2056
Qy 2041 GGAACACTGCGCATCTGTCAAGCTGTCTTTCAGAGAGAAAGCCGATGTCTGGCCCGGAGA 2100
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Qy 2101 CCCCTGAACAGAGCGGGGCTGCACTGCTGCGCGCCGACGCGGCACTCGGAGTGGTGGAG 2160
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Qy 2161 GAGTTGTCAAGCGCGGATGTCAATTGACCTGTTTCAGAGCAAGGGGCTCAGCGCGCTGCAC 2220
Db 2177 GAGTTGTCAAGCGCGGATGTCAATTGACCTGTTTCAGAGCAAGGGGCTCAGCGCGCTGCAC 2236
Qy 2221 CTGCGCGCGCCAGAGCGCGGCAAGCAAGCGGTGAGAGATCTGTCTAAGGCAATGGGGCCAC 2280
Db 2237 CTGCGCGCGCCAGAGCGCGGCAAGCAAGCGGTGAGAGATCTGTCTAAGGCAATGGGGCCAC 2296
Qy 2281 ATCAACTGCGAGAGCTCAAGTTCCAGAGGCGGCACTGAGCCCGGCGCACTCTCTGCGG 2340
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Db 2357 CGAAGCAAGACTTAA 2371

RESULT 3
US-10-354-358-37
; Sequence 37, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying

APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14111, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
FILE REFERENCE: MP102-020P1R0N0N1M
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 37
LENGTH: 3860
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (17)...(2371)
US-10-354-358-37

Query Match 99.0%; Score 2332; DB 16; Length 3860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2354; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy 61 GAGTTCAAGGCTGGAGAGAGTGGGCTCGGGCGGCTTCGGGAGAGTGTACAAAGTGGC 120
Db 77 GAGTTCAAGGCTGGAGAGAGTGGGCTCGGGCGGCTTCGGGAGAGTGTACAAAGTGGC 136
Qy 121 CATGTCACTGGAAGACTTGGCTGGCATCAAGTGTGCTGCCAGGCTGCAGTGCAGAC 180
Db 137 CATGTCACTGGAAGACTTGGCTGGCATCAAGTGTGCTGCCAGGCTGCAGTGCAGAC 196
Qy 181 AGGAGGCGATGAGAGCTTTTGGAGAAAGCCCAAGAGTGAAGATGGCCAGTTCCGTAC 240
Db 197 AGGAGGCGATGAGAGCTTTTGGAGAAAGCCCAAGAGTGAAGATGGCCAGTTCCGTAC 256
Qy 241 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGCGGCTGTGATGAGTATGAGAG 300
Db 257 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGCGGCTGTGATGAGTATGAGAG 316
Qy 301 ACGGCTCCCTGAAAAGCTGTGGCTTCGAGCCCATGTGCATGGAGATCTCGGTTCCGA 360

D	b	317	ACGGGCTTCCTGGAAAAAGCTCTGGCTTCGGAGGCATTGGCCATGGGATCTCCGGTTCCGA	376
Q	y	361	ATCATCCACGAGACGGCGGTGGGAGTAATCTTCGTGACCTGCATGAGTGGCCCGGCACCTCTG	420
D	b	377	ATCATCCACGAGACGGCGGTGGGAGTAATCTTCGTGACCTGCATGAGTGGCCCGGCACCTCTG	436
Q	y	421	CACCTGGACCTCAAGCCCGCGCAACATCTGTGGATGCGCACTACACAGTCACAGATTCTC	480
D	b	437	CACCTGGACCTCAAGCCCGCGCAACATCTGTGGATGCGCACTACACAGTCACAGATTCTC	496
Q	y	481	GATTGGTCTGGCGCAAGTGGACAGGCTGTGCCACTGTCATGACCTCAGCATGATGGC	540
D	b	497	GATTGGTCTGGCGCAAGTGGACAGGCTGTGCCACTGTCATGACCTCAGCATGATGGC	556
Q	y	541	CTGTTTGGCACAATTCGCTCACTCCCTCCACAGCGCATCAGAGGAAGAGCCGCTCTTC	600
D	b	557	CTGTTTGGCACAATTCGCTCACTCCCTCCACAGCGCATCAGAGGAAGAGCCGCTCTTC	616
Q	y	601	GACACCAAGCACGATGTATACAGCTTTGGATCTGTCATCTGGGGCTGTCTACACAGAG	660
D	b	617	GACACCAAGCACGATGTATACAGCTTTGGATCTGTCATCTGGGGCTGTCTACACAGAG	676
Q	y	661	AAGCGTTTGGAGATGAGAAAGAACCTCTGCATCATGTGTAAGAGTGTGAAGGGCAC	720
D	b	677	AAGCGTTTGGAGATGAGAAAGAACCTCTGCATCATGTGTAAGAGTGTGAAGGGCAC	736
Q	y	721	CGCCCGGAGCTGCGCGCCGTGTGACAGACCAGCGCGCGCTGCAAGCATCTGATAGC	780
D	b	737	CGCCCGGAGCTGCGCGCCGTGTGACAGACCAGCGCGCGCTGCAAGCATCTGATAGC	796
Q	y	781	CTCATGCAAGCGGTGTGGCAGGAGGATTCGCGAGTTAGGCCACCTTCCAAAGAAATTACT	840
D	b	797	CTCATGCAAGCGGTGTGGCAGGAGGATTCGCGAGTTAGGCCACCTTCCAAAGAAATTACT	856
Q	y	841	TCTGAAACCGAGAGACCTGTGTGAAAGAGCTGATGACGAAGTAAGAAAGAAACGTGCATGAT	900
D	b	857	TCTGAAACCGAGAGACCTGTGTGAAAGAGCTGATGACGAAGTAAGAAAGAAACGTGCATGAT	916
Q	y	901	CTGACGCTGAAAAGGCCCCCGGAGGCCAGAGACGAGGTGTGCTGCGAGGCTCAAGCGG	960
D	b	917	CTGACGCTGAAAAGGCCCCCGGAGGCCAGAGACGAGGTGTGCTGCGAGGCTCAAGCGG	976
Q	y	961	GCTCTGCGCCCACTCTGATTAACGACTACAGCTTCTCGAGCTTCTTCAACAGCTGAC	1020
D	b	977	GCTCTGCGCCCACTCTGATTAACGACTACAGCTTCTCGAGCTTCTTCAACAGCTGAC	1036
Q	y	1021	TCTGAGATTTCCCAAGGCTGTGAGGGGCCCGGAGAGCTCAACCCGACGTCCTTGAATGCC	1080
D	b	1037	TCTGAGATTTCCCAAGGCTGTGAGGGGCCCGGAGAGCTCAACCCGACGTCCTTGAATGCC	1096
Q	y	1081	AAGCTGCATCGTCCGGGACGTGGAAAGAGCTCTCGGAGGTGTCTCGTGGATCTCGGC	1140
D	b	1097	AAGCTGCATCGTCCGGGACGTGGAAAGAGCTCTCGGAGGTGTCTCGTGGATCTCGGC	1156
Q	y	1141	TTCTCTTCCAGAGATCACTGTGCTGTCTTTGACGGAAACCTTCAACAGCGATCTG	1200
D	b	1157	TTCTCTTCCAGAGATCACTGTGCTGTCTTTGACGGAAACCTTCAACAGCGATCTG	1216
Q	y	1201	GGTACCAAGACGTTCCAGAGAAAGAGACTTGTGGATGTCATCGTGTCC-GGACACAG	1259
D	b	1217	GGTACCAAC-AGACGTTCAGAGAAAGAAACCTTGTGATCCATCGTGTCCGGGACACAG	1275
Q	y	1260	CAAACTGATGAAGATCTCGAGCGGCGCAAGACGTGACCTGGACCTGACAGAGGTCAG	1319
D	b	1276	CAAACTGATGAAGATCTCGAGCGGCGCAAGACGTGACCTGGACCTGACAGAGGTCAG	1335
Q	y	1320	CTGCTGCACTTGCGCGTGGAGGCGCGGCAAGAGAGTGCAGAGTGGCTGTGCTCAA	1379
D	b	1336	CTGCTGCACTTGCGCGGCGTGGAGGCGCGGCAAGAGAGTGCAGAGTGGCTGTGCTCAA	1395
Q	y	1380	CAATGCCAAACCCCAACTGAGCAACCTGTAAGGGGGCTTCAACCCGTTTGCACTAGCCGTGGA	1439
D	b	1396	CAATGCCAAACCCCAACTGAGCAACCTGTAAGGGGGCTTCAACCCGTTTGCACTAGCCGTGGA	1455

QY	1440	GAGGAGGGTGGCGGGGTGTCTGTGAAGCTCTCTGCTGAGCAAGGAAGATCAAGTCTCAACGGCCA	1449
Db	1456	GAGGAGGGGTGGGGGTGTCTGTGAGGCTCTCTGTGGCAAGGAAGTCAAGTCTCAACGGCCA	1515
QY	1500	GGATGAGGAGCCAGTGGAGCAGGCCCTCACTTTGAGCCCGAGAACGGGGATGAGTCTTACAC	1559
Db	1516	GGATGAGGAGCCAGTGGAGCAGGCCCTTCCACTTTGAGCCCGAGAACGGGGATGAGTCTTACAC	1575
QY	1560	ACGGCTGTGTTTGAGAGAGAACGGCTTGGGTCAACGAGGTGGAATTTTAGAGGGCCGGACGCC	1619
Db	1576	ACGGCTGTGTTTGAGAGAGAACGGCTTGGGTCAACGAGGTGGAATTTTAGAGGGCCGGACGCC	1635
QY	1620	CATGCACTGTGGCTCTGCCAGCACGGGCGAGAGAAATATGTGCGCATCTCTGCTGGCCGAGG	1679
Db	1636	CATGCACTGTGGCTCTGCCAGCACGGGCGAGAGAAATATGTGCGCATCTCTGCTGGCCGAGG	1695
QY	1680	CGTGGACGTGAGCGCTGCAGGGCGAAGGATGACCTGGCTGCCACTGCACTTACGCTGCTTGACA	1739
Db	1696	CGTGGACGTGAGCGCTGCAGGGCGAAGGATGACCTGGCTGCCACTGCACTTACGCTGCTTGACA	1755
QY	1740	GGGGCACCTGGCCCATCTGTCAAGCTGTGGCCAGACCGGGGGTGAAGTGAACGCCCA	1799
Db	1756	GGGGCACCTGGCCCATCTGTCAAGCTGTGGCCAGACCGGGGGTGAAGTGAACGCCCA	1815
QY	1800	GACCGTGAATGGAGAGAACCCATTGTCACCTTGGCTGGCACAGCGGGGCACTTACCGCTGTGC	1859
Db	1816	GACCGTGAATGGAGAGAACCCATTGTCACCTTGGCTGGCACAGCGGGGCACTTACCGCTGTGC	1875
QY	1860	CGGATCTCTATTCAGCCGTGTGCTGCCAGCGTCAACGTCGTGAGCGCTGTGGGCAAGACAC	1919
Db	1876	CGGATCTCTATTCAGCCGTGTGCTGCCAGCGTCAACGTCGTGAGCGCTGTGGGCAAGACAC	1935
QY	1920	CCTGCACGTGGCCCGCGAGAGACGGGGCACACGAGCATTCGAGGCTGTCTGTCAATCGGGG	1979
Db	1936	CCTGCACGTGGCCCGCGAGAGACGGGGCACACGAGCATTCGAGGCTGTCTGTCAATCGGGG	1995
QY	1980	CGCTGCGAAGAGGCGCTGTGACCTTGAAGACGCTTACACCGCTCTGTGACCTGTGGCTGCGCGAA	2039
Db	1996	CGCTGCGAAGAGGCGCTGTGACCTTGAAGACGCTTACACCGCTCTGTGACCTGTGGCTGCGCGAA	2055
QY	2040	CGGACACCTGGCCACTGTCAAGCTGTCTGTGAGAGAGAGGCGAGTGTCTGGCCCGGGG	2099
Db	2056	CGGACACCTGGCCACTGTCAAGCTGTCTGTGAGAGAGAGGCGAGTGTCTGGCCCGGGG	2115
QY	2100	AACCCCTGAACGAGACGGGCGTGCACCTTGGCTGCCCGCCACGGGCACTTCGAGGTGTGGA	2155
Db	2116	AACCCCTGAACGAGACGGGCGTGCACCTTGGCTGCCCGCCACGGGCACTTCGAGGTGTGGA	2171
QY	2160	GGAGTTTGGTCAAGCGCCGATGTCTTATTTGACCTGTTTGAGAGAGAGGGGCTCAAGCGGCTGCA	2219
Db	2176	GGAGTTTGGTCAAGCGCCGATGTCTTATTTGACCTGTTTGAGAGAGAGGGGCTCAAGCGGCTGCA	2235
QY	2220	CCTGGCGGCCAGAGGGCCGGGACGCAAGACGGTGAAGACTTGTGCTCAGGCACTTGGGGCCCA	2279
Db	2236	CCTGGCGGCCAGAGGGCCGGGACGCAAGACGGTGAAGACTTGTGCTCAGGCACTTGGGGCCCA	2295
QY	2280	CATCAACTGTGAGAGCCTCAAGTTTCAAGGGGGGCGCATAGCCCGCGCCGACACTTCTTGG	2339
Db	2296	CATCAACTGTGAGAGCCTCAAGTTTCAAGGGGGGCGCATAGCCCGCGCCGACACTTCTTGG	2355
QY	2340	GGGAAGCAAGACTTNG 2355	
Db	2356	GGGAAGCAAGACTTNG 2371	

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RESULT 4
US-10-172-118-1840
; Sequence 1840, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yidong

```

APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1840
LENGTH: 3879
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_020639
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1840

Query Match 99.0%; Score 2330.4; DB 17; Length 3879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2353; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

1 ATGAGAGGCGACGGCGGAGCCCGCANTGGCCCTGGCGCTGGCCACCTTGAGAGCGGGC 60
49 ATGAGAGGCGACGGCGGAGCCCGCANTGGCCCTGGCGCTGGCCACCTTGAGAGCGGGC 108
61 GAGTTCAAGGCTGGGAGAGAGTGGGCTCGGGCGGCTTCGGGAGGTGTACAAAGGTGGC 120
109 GAGTTCAAGGCTGGGAGAGAGTGGGCTCGGGCGGCTTCGGGAGGTGTACAAAGGTGGC 168
121 CATGTCCATCGAAGAGCTGGCTGGCCATCAAGTGTCTGCCCAAGCTTGACGTGAGAGC 180
169 CATGTCCATCGAAGAGCTGGCTGGCCATCAAGTGTCTGCCCAAGCTTGACGTGAGAGC 228
181 AGGAGGCGCATGGAGCTTTTGAAGAAGCCAAAGAGATGAGATGGCCATTTCGGCTAC 240
229 AGGAGGCGCATGGAGCTTTTGAAGAAGCCAAAGAGATGAGATGGCCATTTCGGCTAC 288
241 ATCTGCTGTGTATGGCATCTGCCGAGAACCTGTGGCTGTGTATGAGATGAGAG 300
289 ATCTGCTGTGTATGGCATCTGCCGAGAACCTGTGGCTGTGTATGAGATGAGAG 348
301 ACGGAGCTCTGGAAAGCTGTGGCTTGGAGCCATTGGCATGGAGATCTCGGTTCCGA 360
349 ACGGAGCTCTGGAAAGCTGTGGCTTGGAGCCATTGGCATGGAGATCTCGGTTCCGA 408
361 ATCATCCAGAGAGCGCGGTGGGATGAACTTCCGTGCACTGCAATGGCCCGGCACTCTCG 420
409 ATCATCCAGAGAGCGCGGTGGGATGAACTTCCGTGCACTGCAATGGCCCGGCACTCTCG 468
421 CACCTGAGACTCAAGCCCGGAGACATCTGTGTGATGGCCACTACAGTCAAGATTTCT 480
469 CACCTGAGACTCAAGCCCGGAGACATCTGTGTGATGGCCACTACAGTCAAGATTTCT 528
481 GATTTGGTCTGGCCAGTGAAGGAGCTGTGCCACTGTGATGACCTTCAGATGAGTGGC 540
529 GATTTGGTCTGGCCAGTGAAGGAGCTGTGCCACTGTGATGACCTTCAGATGAGTGGC 588
541 CTGTTGGCAATGAGCTTACCTCCCTCAAGAGGCACTCAAGGAGAGAGCGGCTCTTC 600
589 CTGTTGGCAATGAGCTTACCTCCCTCAAGAGGCACTCAAGGAGAGAGCGGCTCTTC 648
601 GACACCAAGCAGATGTATACAGCTTTGCAATGCTGATCTGGGCGTGTCTCAACAAG 660
649 GACACCAAGCAGATGTATACAGCTTTGCAATGCTGATCTGGGCGTGTCTCAACAAG 708
661 AAGCGTTTGCAGATGAGAAAGACATCTGTGACATCATGTGTGAAGTGTGAAGGCGCAC 720
709 AAGCGTTTGCAGATGAGAAAGACATCTGTGACATCATGTGTGAAGTGTGAAGGCGCAC 768

Qy 721 CGCCCCAGCTGCGCGCCGTGTGACAGAGCCCGGCGGCTGACAGCCATTGATACGC 780
Db 769 CGCCCCAGCTGCGCGCCGTGTGACAGAGCCCGGCGGCTGACAGCCATTGATACGC 828
Qy 781 CTATGACAGGCTGTGGCAGAGGGGATCCGCGATTAGGCCACTTCCAGAAATTAAT 840
Db 829 CTATGACAGGCTGTGGCAGAGGGGATCCGCGATTAGGCCACTTCCAGAAATTAAT 888
Qy 841 TCTGAACCGAGAGACCTGTGTGAAGAGCTGTGAAGTGAAGTGAAGAAATGTCTATGAT 900
Db 889 TCTGAACCGAGAGACCTGTGTGAAGAGCTGTGAAGTGAAGTGAAGAAATGTCTATGAT 948
Qy 901 CTGAGACTGAAAGAGCCCGGAGAGCCAGAGAGCGAGGTGTGCTGAGAGCTCAAGCG 960
Db 949 CTGAGACTGAAAGAGCCCGGAGAGCCAGAGAGCGAGGTGTGCTGAGAGCTCAAGCG 1008
Qy 961 GCCTTGGCCCGCACTTTCATTAACATCAAGCTTCTCGAGCTTCTCAAGCTGGAC 1020
Db 1009 GCCTTGGCCCGCACTTTCATTAACATCAAGCTTCTCGAGCTTCTCAAGCTGGAC 1068
Qy 1021 TCTGAGATTTCAGAGCTGTGAGAGGCGCCGAGAGAGTCAAGCGGCTCTGAGTCC 1080
Db 1069 TCTGAGATTTCAGAGCTGTGAGAGGCGCCGAGAGAGTCAAGCGGCTCTGAGTCC 1128
Qy 1081 AAGCTGCATCTGTCCGAGAGTGGAAAGAGCTCTCGAGGCTGTCTCGATGACCTCGGC 1140
Db 1129 AAGCTGCATCTGTCCGAGAGTGGAAAGAGCTCTCGAGGCTGTCTCGATGACCTCGGC 1188
Qy 1141 TTCTCTTCAGAGATCACTGTGCTGTCTTTGAGCGGAGACCTTCAACAGCATCTG 1200
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Db 1249 GGTACCAAGAGAGTCCAGAGAAAGAGCTGTGAGATGCCATGATGTC -GGGAGACACAG 1307
Qy 1260 CAAACTGATGAGATCTGTGAGCGCGAGAGCTGTGACCTGTGACCTGTGACAG 1319
Db 1308 CAAACTGATGAGATCTGTGAGCGCGAGAGCTGTGACCTGTGACAGCGGTGACAG 1367
Qy 1320 CTGTGTCACCTGTGGGTGTGAGAGCGCGGAGAGAGAGTGTGCGCATAGTGTCTCTCA 1379
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Qy 1380 CAATGCCAACCCCAACCTGAGCAACGCTAGGGGCTCCACCCGTTGACATGGCCGTGGA 1439
Db 1428 CAATGCCAACCCCAACCTGAGCAACGCTAGGGGCTCCACCCGTTGACATGGCCGTGGA 1487
Qy 1440 GAGGAGGCTCGGGGTGTGTGTGAGCTCTGTGAGCAGAGAGATCAGTGTCAACGCCAA 1499
Db 1488 GAGGAGGCTCGGGGTGTGTGTGAGCTCTGTGAGCAGAGAGATCAGTGTCAACGCCAA 1547
Qy 1500 GATGAGAGCAAGTGAAGAGCTTCCACTTTGACAGCCAGAGCGGGATGATGTAGAC 1559
Db 1548 GATGAGAGCAAGTGAAGAGCTTCCACTTTGAGAGCCAGAGCGGGATGATGTAGAC 1607
Qy 1560 ACGGCTGCTGTGAGAGAGAGCGCTGTGAGAGAGTGTGAGAGGCGGAGCGC 1619
Db 1608 ACGGCTGCTGTGAGAGAGAGCGCTGTGAGAGAGTGTGAGAGGCGGAGCGC 1667
Qy 1620 CATGCAAGTGGCTGCGAGCAGGAGGAGAGATATGTGAGAGCTGTGAGCGCGAGG 1679
Db 1668 CATGCAAGTGGCTGCGAGCAGGAGGAGAGATATGTGAGAGCTGTGAGCGCGAGG 1727
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Db 1728 GTGAGAGTGAAGCTGTGAGAGGCAAGATGCTGTGAGCTGCACTGAGCTGTGAGCA 1787
Qy 1740 GGGGCACTTGCATCTGTCAAGCTGTGAGAGAGCGCGGGGTGAGTGAAGCGCCA 1799
Db 1788 GGGGCACTTGCATCTGTCAAGCTGTGAGAGAGCGCGGGGTGAGTGAAGCGCCA 1847

QY 1800 GACCTGATGGAGAGACCCATTGCACTTGGCCGACAGCGCGGCACTACCGCTGGC 1859
 Db 1848 GACCTGATGGAGAGACCCATTGCACTTGGCCGACAGCGCGGCACTACCGCTGGC 1907
 QY 1860 CCGATCTCTATTCAGCTGTGTCTCCAGTGAAGTCTGAGCGCTGAGGCAAGACACC 1919
 Db 1908 CCGATCTCTATTCAGCTGTGTCTCCAGTGAAGTCTGAGCGCTGAGGCAAGACACC 1967
 QY 1920 CCGTCACTGGCCGCGAGAGACGCGGCAACAGACACTGCGAGCTGCTCTGCAATCGGG 1979
 Db 1968 CCGTCACTGGCCGCGAGAGACGCGGCAACAGACACTGCGAGCTGCTCTGCAATCGGG 2027
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 Db 2028 CCGTGGCAAGAGCGCGTGAAGCTGACAGAGGCTACACCGCTCTGCACTGCTGCGGAA 2087
 QY 2040 CCGACACTGGCCATGTCAGAGCTGCTGTGAGGAGAAAGCCATGTGTGCTGACCGGG 2099
 Db 2088 CCGACACTGGCCATGTCAGAGCTGCTGTGAGGAGAAAGCCATGTGTGCTGACCGGG 2147
 QY 2100 ACCCTGAGACGAGCGCGCTGCACTGCTGCGCCGACGCGGCACTGAGAGTGTGA 2159
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 Db 2268 CCGGCGCGCCGAGCGCGGCAACAGACAGCGTGGAGACTGCTCAGGCAATGCGGCGCA 2327
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 Db 2388 GCGAGCAAGACTTAG 2403

RESULT 5
 US-10-342-887-1840
 ; Sequence 1840, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yundong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernard, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1840
 ; LENGTH: 3879
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-1840

Query Match 99.0%; Score 2330.4; DB 18; Length 3879;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 2353; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 QY 1 ATGAGAGGCGACCGCGGGAACCCATGAGCCCTGCGCTGTGAGCACTTCAGACGCGGGC 60
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 Db 109 GAGTTTCAAGGAGTGGAGAGAGTGGCTGGGCGGCTTCGAGGAGGTGTACAAAGTGGC 168
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 Db 169 CATGTCACTGGAAGACTGAGCTGGCCATGAGTGTCTGCGCAAGCTTCAGAGTCAAGAC 228
 QY 181 AGGAGGCGCATGAGAGCTTTTGGAAAGAACCAAGAAATGAGATGCGCAAGTTTGGCTAC 240
 Db 229 AGGAGGCGCATGAGAGCTTTTGGAAAGAACCAAGAAATGAGATGCGCAAGTTTGGCTAC 288
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 QY 301 ACGGCTCTCTGGAAGAGCTGAGCTTGGAGAGCAATTCAGATGGATCTTCGCTTCCA 360
 Db 349 ACGGCTCTCTGGAAGAGCTGAGCTTGGAGAGCAATTCAGATGGATCTTCGCTTCCA 408
 QY 361 ATCATTCACAGAGAGCGGCTGGATGAATCTTCTGCACTGCAATGAGCGCGGCACTCTG 420
 Db 409 ATCATTCACAGAGAGCGGCTGGATGAATCTTCTGCACTGCAATGAGCGCGGCACTCTG 468
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 Db 469 CACCTGAGCTCAAGCCCGGCAACATCTGCTGAGATCCCACTACAGTCAAGATTTCT 528
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 QY 709 AAGCGTTTGGAGATGAGAAACATCTGCAATCATGATGAGTGTGAAGGCGCAC 768
 Db 721 CGCCCGAGCTGCGCGCTGTGCAAGAGCCCGGCGCGGCTGTGACAGCACTGATAGC 780
 QY 769 CGCCCGAGCTGCGCGCTGTGCAAGAGCCCGGCGCGGCTGTGACAGCACTGATAGC 828
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 QY 1069 TCTGAGATTTCAGAGCTGTGAGAGGCGCGAGAGAGTCAAGCGGAGTCTCTTGAATTC 1128

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Db	1129	AAGCTGCATGCTCCGAGCATGTGGAGAAAGGCTCTCCGGGGGTGTCTCCGTGTGACATCTCCGC	1188
QY	1141	TTCTCTTCCAAAGGATCACTGTCCGTGTCTTTTGAGCGGAACTTCAACAGCGATCTG	1200
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QY	1201	GGTACCAACAAGCTGTCCGAAGAGAGACTTGTGATATGCAATCGTGTCC - GGAGACCAAG	1259
Db	1249	GGTACCAAC - AAGCTGTCCGAAGAGAGAAACTTGTGATATGCAATCGTGTCCGGGAGACACAG	1307
QY	1260	CAAACTGTATGAAGATCTCTGACAGCCGACAGAGAGCTGTGACCTGTGACCTGTGACAGCGGTGACAG	1319
Db	1308	CAAACTGTATGAAGATCTCTGACAGCCGACAGAGAGCTGTGACCTGTGACCTGTGACAGCGGTGACAG	1367
QY	1320	CTGTCTGACACTGTGGCGGTGTGAGAGCCGGGCAAGAAGATGTGCGCAAGTGTCTGTCTCA	1379
Db	1368	CTGTCTGACACTGTGGCGGTGTGAGAGCCGGGCAAGAAGATGTGCGCAAGTGTCTGTCTCA	1427
QY	1380	CAATGCCAACCCCAACTGACGCAACCGTAAGGGGCTCCACCCCGTTTGACATAGCCCGTGTGA	1439
Db	1428	CAATGCCAACCCCAACTGACGCAACCGTAAGGGGCTCCACCCCGTTTGACATAGCCCGTGTGA	1487
QY	1440	GAGAGAGGTGGCGGGTGTCTGTGAGAGCTCTGTCTGTGACGGAAGATCACTGTCAACGCCAA	1499
Db	1488	GAGAGAGGTGGCGGGTGTCTGTGAGAGCTCTGTCTGTGACGGAAGATCACTGTCAACGCCAA	1547
QY	1500	GGATGAGGACCAAGTGTGACAGCCCTTCACTTTTGACAGCCCAAGAACGGGGATGATGTAGTACAC	1559
Db	1548	GGATGAGGACCAAGTGTGACAGCCCTTCACTTTTGACAGCCCAAGAACGGGGATGATGTAGTACAC	1607
QY	1560	ACGGCTGTCTGTGAGAGAAAGCGCTCGGTCAACAGAGGTGTGACTTTGAGGGCCGGACGCC	1619
Db	1608	ACGGCTGTCTGTGAGAGAAAGCGCTCGGTCAACAGAGGTGTGACTTTGAGGGCCGGACGCC	1667
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QY	1680	CGTGGACGTGAGCCGTGCGAGGGCCAAAGATAGCCGTGCTGTGACCTGTGACCTACAGCTACGCTGTGCA	1739
Db	1728	CGTGGACGTGAGCCGTGCGAGGGCCAAAGATAGCCGTGCTGTGACCTGTGACCTACAGCTACGCTGTGCA	1787
QY	1740	GGGCGCACTGTGCCATCTGTCAAGCTGTGTGGCCCAAGCAGCGCGGGGTGATGTGTAAACGCCCA	1799
Db	1788	GGGCGCACTGTGCCATCTGTCAAGCTGTGTGGCCCAAGCAGCGCGGGGTGATGTGTAAACGCCCA	1847
QY	1800	GACGTGTGATGTGGAGAGAGCCCATTTGTACACTGTGGCCGACAGCGCGGGGCACTACCGCGTGTGGC	1859
Db	1848	GACGTGTGATGTGGAGAGAGCCCATTTGTACACTGTGGCCGACAGCGCGGGGCACTACCGCGTGTGGC	1907
QY	1860	CGGCATCTCTACATCGACTGTGTGCTCCGAGCTCAACCGTGTGTGACAGCCGTGTGGACACAGACACC	1919
Db	1908	CGGCATCTCTACATCGACTGTGTGCTCCGAGCTCAACCGTGTGTGTGACAGCCGTGTGGACACAGACACC	1967
QY	1920	CTGTGCACTGTGCGCGGAGACGGGGCAACAGACACTGTCCAGCGCTGTCTTGTCAATCGGGG	1979
Db	1968	CTGTGCACTGTGCGCGGAGACGGGGCAACAGACACTGTCCAGCGCTGTCTTGTCAATCGGGG	2027
QY	1980	CGCTGTGCAAGAGAGGCGCGTGAACCTCAAGAGGGCTACACCGCTGTGTGACCTGTGGCGCGGCA	2039
Db	2028	CGCTGTGCAAGAGAGGCGCGTGAACCTCAAGAGGGCTACACCGCTGTGTGACCTGTGGCGCGGCA	2087
QY	2040	CGGACACTGTGGCACTGTCAAGCTGTGTGTGAGAGAGAAAGCCGATGTGTGTGCGCCGGGG	2099
Db	2088	CGGACACTGTGGCACTGTCAAGCTGTGTGTGAGAGAGAAAGCCGATGTGTGTGTGCGCCGGGG	2147
QY	2100	ACCTCTGAACCAAGATGCGCGCTGTGCATCTGTGGCTGTGCGGCCAATGTGAGATGTGTGTGA	2159
Db	2148	ACCTCTGAACCAAGATGCGCGCTGTGCATCTGTGGCTGTGCGGCCAATGTGAGATGTGTGTGA	2207

QY	2160	GGAAGTGTGTCAGCGCCCATGTGCATTGACCTGTTGCAAGCAGCAGGGGCTCAGCGCGCTGCA	2219
Db	2208	GGAAGTGTGTCAGCGCCCATGTGCATTGACCTGTTGCAAGCAGCAGGGGCTCAGCGCGCTGCA	2267
QY	2220	CCTGGCGGCCCGCAGGGGCGGCGCACGACGAGCGATGAGACTCTGCTCAGAGGATGAGGCCCA	2279
Db	2268	CTTGCGCGGCCCGCAGGGGCGGCGCACGACGAGCGATGAGACTCTGCTCAGAGGATGAGGCCCA	2327
QY	2280	CATCAACCTGCAGAGCCTCAAGTTCCAGGGCGGCGCATGCGCCCGCGCCACACTCTCTGG	2339
Db	2328	CATCAACCTGCAGAGCCTCAAGTTCCAGGGCGGCGCATGCGCCCGCGCCACACTCTCTGG	2387
QY	2340	GCGAAGCAAGACCCTAG 2355 	
Db	2388	GCGAAGCAAGACCCTAG 2403 	
RESULT 6			
US-10-648-593-16			
; Sequence 16, Application US/10648593			
; Publication No. US20040106132#1			
; GENERAL INFORMATION:			
; APPLICANT: Bristol-Myers Squibb Company			
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT			
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR			
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS			
; FILE REFERENCE: D0273 NP			
; CURRENT APPLICATION NUMBER: US/10/648,593			
; CURRENT FILING DATE: 2003-08-26			
; PRIOR APPLICATION NUMBER: 60/406,385			
; PRIOR FILING DATE: 2002-08-27			
; NUMBER OF SEQ ID NOS: 557			
; SOFTWARE: Patentin version 3.2			
; SEQ ID NO 16			
; LENGTH: 3879			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-648-593-16			
Query Match 99.0%; Score 2330.4; DB 19; Length 3879;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 2353; Conservative 0; Mismatches 1; Indels 2; Gaps 2;			
QY	1	ATGGAGGGCGGACGGCGGGGACCCCATGGGCGCTGGCGCTGCGGCACCTTCGACGGCGGC	60
Db	49	ATGGAGGGCGGACGGCGGGGACCCCATGGGCGCTGGCGCTGCTGCGGCACCTTCGACGGCGGC	108
QY	61	GAGTTCAAGGCTCTGGGAGAAGTAGTGGGCTCGGGCGGCTTCGGGCGAGGTGTAACAAGTGGCG	120
Db	109	GAGTTCAAGGCTCTGGGAGAAGTAGTGGGCTCGGGCGGCTTCGGGCGAGGTGTAACAAGTGGCG	168
QY	121	CATGTCCACTGGAAGACTGTGGCTGCGCATCAAGTGTCTGCGCCAGCTTGCACGTTCGACGAC	180
Db	169	CATGTCCACTGGAAGACTGTGGCTGCGCATCAAGTGTCTGCGCCAGCTTGCACGTTCGACGAC	228
QY	181	AGGAGGCGCATGAGAGCTTTTGGAGAAAGCCAAAGATGAGAGATGAGCAAGTTTCGCTAC	240
Db	229	AGGAGGCGCATGAGAGCTTTTGGAGAAAGCCAAAGATGAGAGATGAGCAAGTTTCGCTAC	288
QY	241	ATCTGCTCTGTGTATGGCATCTGCGCGGAACCTGTGCGGCTGTGTCATGAGTACATGAG	300
Db	289	ATCTGCTCTGTGTATGGCATCTGCGCGGAACCTGTGCGGCTGTGTCATGAGTACATGAG	348
QY	301	ACGGGCTCTCTGGAAGAAAGCTGTGGCTTCGAGAGCCATTGCGATGGAGATCTTCGGTTCCGA	360
Db	349	ACGGGCTCTCTGGAAGAAAGCTGTGGCTTCGAGAGCCATTGCGATGGAGATCTTCGGTTCCGA	408
QY	361	ATTCATCCACGAGAGCGGCGGTGGGATGAACTTCCTGACATGCATAGGCGCCGCCACTCTCTG	420
Db	409	ATTCATCCACGAGAGCGGCGGTGGGATGAACTTCCTGACATGCATAGGCGCCGCCACTCTCTG	468
QY	421	CACCTGGACTCAAGCCCGCGAATCATCTGTGTGATGCCCACTAACAGCTCAAGATTCT	480

Db 469 CACCTGGAACCTCAGAGCCGCGAACAATCCTGCTGAGATGCCCACTAACAGATTTCT 528
Qy 481 GATTTTGTCTGCGCAAGTGCACACGGGCTGTCCCACTGCAATGACCTTCAAGATGATGAC 540
Db 529 GATTTTGTCTGCGCAAGTGCACACGGGCTGTCCCACTGCAATGACCTTCAAGATGATGAC 588
Qy 541 CTGTTTGGCAACAATGCTTACTCTCCCTCCAGAGCGCATCAGAGGANAAGCCGCTCTTC 600
Db 589 CTGTTTGGCAACAATGCTTACTCTCCCTCCAGAGCGCATCAGAGGANAAGCCGCTCTTC 648
Qy 601 GACACCAAGCAAGATGATATACAGCTTTGCGATGCTCATCTGAGGCGTCTCAACAGAG 660
Db 649 GACACCAAGCAAGATGATATACAGCTTTGCGATGCTCATCTGAGGCGTCTCAACAGAG 708
Qy 661 AAGCGTTTGCAGATGAGAGAAACATCTTGCAATCATGATGAGAGTGTGAGAGGCGAC 720
Db 709 AAGCGTTTGCAGATGAGAGAAACATCTTGCAATCATGATGAGAGTGTGAGAGGCGAC 768
Qy 721 CGCCCGAGAGCTGCGCCGCTGTGCAAGAGCCCGCGCGCTGCAAGCCTGATAGC 780
Db 769 CGCCCGAGAGCTGCGCCGCTGTGCAAGAGCCCGCGCGCTGCAAGCCTGATAGC 828
Qy 781 CTGATGACGCGGTGCTGAGAGGAGATCCGAGATTAGGCGCACTTCCAGAAATTAAT 840
Db 829 CTGATGACGCGGTGCTGAGAGGAGATCCGAGATTAGGCGCACTTCCAGAAATTAAT 888
Qy 841 TCTGAACCGAGAGACCTGTGTGAAAAAGCTGTGATGACAGATGAGAAAGAACTGCTCATGAT 900
Db 889 TCTGAACCGAGAGACCTGTGTGAAAAAGCTGTGATGACAGATGAGAAAGAACTGCTCATGAT 948
Qy 901 CTGAGACGTGAAAAAGCCCCCGAGAGCCAGAGAGCGAGTGTGCTGCGAGGCTCAAGCGG 960
Db 949 CTGAGACGTGAAAAAGCCCCCGAGAGCCAGAGAGCGAGTGTGCTGCGAGGCTCAAGCGG 1008
Qy 961 GCGTGTGCGCCGACCTTGATTAACAGATCAAGCTCTCCGAGCTTCTCAAGCTGAGAC 1020
Db 1009 GCGTGTGCGCCGACCTTGATTAACAGATCAAGCTCTCCGAGCTTCTCAAGCTGAGAC 1068
Qy 1021 TCTGAGATTTCAGAGCTGTGAGAGGCGCCGAGAGCTCAAGCTCTCTGATGTC 1080
Db 1069 TCTGAGATTTCAGAGCTGTGAGAGGCGCCGAGAGCTCAAGCTCTCTGATGTC 1128
Qy 1081 AAGCTGCTCATGCTCGGCGAGTGTGAGAGAGCTCTCGGAGGTTCCTCGGTGAGACTCCGCG 1140
Db 1129 AAGCTGCTCATGCTCGGCGAGTGTGAGAGAGCTCTCGGAGGTTCCTCGGTGAGACTCCGCG 1188
Qy 1141 TCTCTTCCAGAGAGATCACTGTGCTGTGCTTGAAGCGGAACTTCAACAGAGCATGTC 1200
Db 1189 TCTCTTCCAGAGAGATCACTGTGCTGTGCTTGAAGCGGAACTTCAACAGAGCATGTC 1248
Qy 1201 GGTACCAACAAGAGCTGCAAGAGAGAGAGCTTGTGATGCTGATGTC-GGAGACACAG 1259
Db 1249 GGTACCAACAAGAGCTGCAAGAGAGAGAGCTTGTGATGCTGATGTC-GGAGACACAG 1307
Qy 1260 CAAATGATGAGAGATCTGCAAGCGGAGAGCTGAGACTGAGACTGAGAGAGGAGTCCAG 1319
Db 1308 CAAATGATGAGAGATCTGCAAGCGGAGAGAGCTGAGACTGAGACTGAGAGAGGAGTCCAG 1367
Qy 1320 CCGTGTGACCTGCGGAGTGTGAGAGGCGGAGAGAGAGAGTGTGAGAGTGTGCTGCA 1379
Db 1368 CCGTGTGACCTGCGGAGTGTGAGAGGCGGAGAGAGAGTGTGAGAGTGTGCTGCTCA 1427
Qy 1380 CAATGCAACCCCAACCTGAGCAACCGTGTGAGGCTTCAACCGTTTGCACATGTGCGTGTGA 1439
Db 1428 CAATGCAACCCCAACCTGAGCAACCGTGTGAGGCTTCAACCGTTTGCACATGTGCGTGTGA 1487
Qy 1440 GAGGAGGAGTGTGCGGAGTGTGAGAGTCTCTGCTGAGAGAGAGATAGTGTCAAGCCCA 1499
Db 1488 GAGGAGGAGTGTGCGGAGTGTGAGAGTCTCTGCTGAGAGAGATAGTGTCAAGCCCA 1547
Qy 1500 GATGAGAGACAGTGTGAGAGCCCTTCACTTTTGCAGGCCAGAGAGGAGATGATGTAGCAC 1559
Db 1548 GATGAGAGACAGTGTGAGAGCCCTTCACTTTTGCAGGCCAGAGAGGAGATGATGTAGCAC 1607

Qy 1560 ACCGCTGCTGTGTGAGAGAGAGAGCGCTGCTCAAGAGTGTGACTTTGAGAGGCGGACGCC 1619
Db 1608 ACCGCTGCTGTGTGAGAGAGAGAGCGCTGCTCAAGAGTGTGACTTTGAGAGGCGGACGCC 1667
Qy 1620 CATGCAAGTGTGCTGTGAGAGAGAGAGAGAGTATGTGTGCGATCTGTGCTGTGCGGAGG 1679
Db 1668 CATGCAAGTGTGCTGTGAGAGAGAGAGAGAGTATGTGTGCGATCTGTGCTGTGCGGAGG 1727
Qy 1680 CTGTGAGAGTGTGAGAGAGAGAGAGAGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCA 1739
Db 1728 CTGTGAGAGTGTGAGAGAGAGAGAGAGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCA 1787
Qy 1740 GGGGCACTGTGCTGTGCAAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1799
Db 1788 GGGGCACTGTGCTGTGCAAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1847
Qy 1800 GACGCTGATGTGAG 1859
Db 1848 GACGCTGATGTGAG 1907
Qy 1860 CCGCATCTCTCATGTGAG 1919
Db 1908 CCGCATCTCTCATGTGAG 1967
Qy 1920 CCGCATCTCTCATGTGAG 1979
Db 1968 CCGCATCTCTCATGTGAG 2027
Qy 1980 CCGCATCTCTCATGTGAG 2039
Db 2028 CCGCATCTCTCATGTGAG 2087
Qy 2040 CCGCATCTCTCATGTGAG 2099
Db 2088 CCGCATCTCTCATGTGAG 2147
Qy 2100 ACCCTGAAACAG 2159
Db 2148 ACCCTGAAACAG 2207
Qy 2160 GAGATGTGTGAG 2219
Db 2208 GAGATGTGTGAG 2267
Qy 2220 CCGTGTGCGCCAG 2279
Db 2268 CCGTGTGCGCCAG 2327
Qy 2280 CATCAACCTGTGAG 2339
Db 2328 CATCAACCTGTGAG 2387
Qy 2340 GCGAAGCAAG 2355
Db 2388 GCGAAGCAAG 2403

RESULT 7
US-10-128-174-15
; Sequence 15, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: US-06967
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 2355

TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-15
Query Match 98.8%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 1 ATGAGGGCGACGGCGGGAGCCCATGGGCGCTGGCTGCTGCGCACCTTGAGCGCGGC 60
DB 1 ATGAGGGCGACGGCGGGAGCCCATGGGCGCTGGCTGCTGCGCACCTTGAGCGCGGC 60
QY 61 GAGTTCAAGGCTGGGAGAGAGTGGGCTGGGCGGCTTGCGGACGATGATCAAGGTGGC 120
DB 61 GAGTTCAAGGCTGGGAGAGAGTGGGCTGGGCGGCTTGCGGACGATGATCAAGGTGGC 120
QY 121 CATGTCCATGGAAGACTGGCTGGCCATCAAGTCTGCGCCAGCTTGACGTCGACGAC 180
DB 121 CATGTCCATGGAAGACTGGCTGGCCATCAAGTCTGCGCCAGCTTGACGTCGACGAC 180
QY 181 AGGAGCCGATGAGAGCTTTTGAAGAGCCCAAGAGATGAGATGGCCAACTTTCGCTAC 240
DB 181 AGGAGCCGATGAGAGCTTTTGAAGAGCCCAAGAGATGAGATGGCCAACTTTCGCTAC 240
QY 241 ATCCGCTGTGTATGGCATCTGCGCGAACCTGTGCGCTGTGTATGAGATCAATGAG 300
DB 241 ATCCGCTGTGTATGGCATCTGCGCGAACCTGTGCGCTGTGTATGAGATCAATGAG 300
QY 301 ACGGAGCTCCCTGGAAGAGCTGTGCTTTCGAGGCCATTTGCAATGGATCTTCGAGTCCGA 360
DB 301 ACGGAGCTCCCTGGAAGAGCTGTGCTTTCGAGGCCATTTGCAATGGATCTTCGAGTCCGA 360
QY 361 ATCATCCAGAGACGGCGGTGGGCAATGAACTTCCCTGCACTGCAATGGCCCGCCACTCTG 420
DB 361 ATCATCCAGAGACGGCGGTGGGCAATGAACTTCCCTGCACTGCAATGGCCCGCCACTCTG 420
QY 421 CACCTGACCTCAAGCCGCGCAACATCTGCTGATGAGCCCACTACAGTCAAGATTCT 480
DB 421 CACCTGACCTCAAGCCGCGCAACATCTGCTGATGAGCCCACTACAGTCAAGATTCT 480
QY 481 GATTTGGTCTGGCCAAATGCAACGGGCTGTCCCATCTGCATGACCTTGAGATGAGTGGC 540
DB 481 GATTTGGTCTGGCCAAATGCAACGGGCTGTCCCATCTGCATGACCTTGAGATGAGTGGC 540
QY 541 CTGTTTGGCAATATGCTTACTCTCCCTCAAGAGCGCAATCAAGGAGAAAGCGGCTTTC 600
DB 541 CTGTTTGGCAATATGCTTACTCTCCCTCAAGAGCGCAATCAAGGAGAAAGCGGCTTTC 600
QY 601 GACACCAAGCAGATGTATACAGCTTTGCAATCGTCACTGGGCGTCTCAACAGAG 660
DB 601 GACACCAAGCAGATGTATACAGCTTTGCAATCGTCACTGGGCGTCTCAACAGAG 660
QY 661 AAGCGTTTGCAGATGAGAGAAACATCTTGCAATCATGTGTGAGGTGTAAGGGCAC 720
DB 661 AAGCGTTTGCAGATGAGAGAAACATCTTGCAATCATGTGTGAGGTGTAAGGGCAC 720
QY 721 CGCGCCGAGCTGCGCGCGTGTGCAAGACCGCGCGCGCTTGAGGCACTGATTAAGC 780
DB 721 CGCGCCGAGCTGCGCGCGTGTGCAAGACCGCGCGCGCTTGAGGCACTGATTAAGC 780
QY 781 CTATGACAGCGGTGTGCAAGAGGAGATCGGAGTTAGGCCCACTTCCAAAGAAATTACT 840
DB 781 CTATGACAGCGGTGTGCAAGAGGAGATCGGAGTTAGGCCCACTTCCAAAGAAATTACT 840
QY 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTGATGACGAAGTGAAGAAACTGCTATGAT 900
DB 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTGATGACGAAGTGAAGAAACTGCTATGAT 900
QY 901 CTGGAACGTAAGAGCCCCCGAGAGCCGAGAGCGAGGTGTGCTGCGAAGGCTCAAGGG 960
DB 901 CTGGAACGTAAGAGCCCCCGAGAGCCGAGAGCGAGGTGTGCTGCGAAGGCTCAAGGG 960
QY 961 GCCTCTGCCCCCACTTGATTAAGACTTCTCCAGCTTCTCAAGCTGAGC 1020

DB 961 GCCTCTGCCCCCACTTGATTAAGACTTCTCCAGCTTCTCAAGCTGAGC 1020
QY 1021 TCTGAAGTTTCCAGAGCTGTGAGGGCCCGAGAGACTCAGCCGAGCTCTTGAGTCC 1080
DB 1021 TCTGAAGTTTCCAGAGCTGTGAGGGCCCGAGAGACTCAGCCGAGCTCTTGAGTCC 1080
QY 1081 AAGCTGCATGTGCGCGAGTGGAGAGAGGCTGCGGGGGTGTCTCGGTGAGCTCGGC 1140
DB 1081 AAGCTGCATGTGCGCGAGTGGAGAGAGGCTTCCGGGGTGTCTCGGTGAGCTCGGC 1140
QY 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGGGGGAACCTTCAACAGCATCTG 1200
DB 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGGGGGAACCTTCAACAGCATCTG 1200
QY 1201 GGTATCCAAAGAGCTCCAGAAAGAAAGCTTTGTGATGCTCATGTGTCC-GGGACACAG 1259
DB 1201 GGCACAC-AGAAGTCCAGAAAGAAAGCTTTGTGATGCTCATGTGTCCGGGACACAG 1259
QY 1260 CAAACTGATGAGATCTGTGAGCGCGAGAGAGTGGACCTTGCACTGGACAGCGGTGCAG 1319
DB 1260 CAAACTGATGAGATCTGTGAGCGCGAGAGAGTGGACCTTGCACTGGACAGCGGTGCAG 1319
QY 1320 CTGTCTGCACTGTGCGGTGAGGCGGGCAAGAGAGTGGCCAACTGTGCTCTCAA 1379
DB 1320 CTGTCTGCACTGTGCGGTGAGGCGGGCAAGAGAGTGGCCAACTGTGCTCTCAA 1379
QY 1380 CAATGCCAACCCCACTGAGCAACGCTTAGGGCTCAACCCGTTGCACTTGGCCGTGGA 1439
DB 1380 CAATGCCAACCCCACTGAGCAACGCTTAGGGCTCAACCCGTTGCACTTGGCCGTGGA 1439
QY 1440 GAGGAGGGTGTGAGGAGTGTGAGAGCTCTGTGAGCGAGAAATCATGTCAACGCGCAA 1499
DB 1440 GAGGAGGGTGTGAGGAGTGTGAGAGCTCTGTGAGCGAGAAATCATGTCAACGCGCAA 1499
QY 1500 GATGAGAGACCAATGAGCAAGCCCTTCACTTTGCAAGCCAGAACCGGAGTATGCTTACAC 1559
DB 1500 GATGAGAGACCAATGAGCAAGCCCTTCACTTTGCAAGCCAGAACCGGAGTATGCTTACAC 1559
QY 1560 ACGGCTCTGTGTGAGAAAGACGCTGTGTCACAGAGTGGACTTTGAGGGCCGAGAGGCC 1619
DB 1560 ACGGCTCTGTGTGAGAAAGACGCTGTGTCACAGAGTGGACTTTGAGGGCCGAGAGGCC 1619
QY 1620 CATGCAAGTGGCTGCGCAGCAGGAGGAGAAATATGTCGCACTCTGCTGGCCGAGG 1679
DB 1620 CATGCAAGTGGCTGCGCAGCAGGAGGAGAAATATGTCGCACTCTGCTGGCCGAGG 1679
QY 1680 CGTGAAGTGAAGCTTGAAGGAGCAAGATGCTGTGTCGACCTGACCTGCTGCGCA 1739
DB 1680 CGTGAAGTGAAGCTTGAAGGAGCAAGATGCTGTGTCGACCTGACCTGCTGCGCA 1739
QY 1740 GGGCAACCTGCCCCATGCTCAAGCTGTGCGCAAGACCGGGGTGAGTGGAAAGCCCA 1799
DB 1740 GGGCAACCTGCCCCATGCTCAAGCTGTGCGCAAGACCGGGGTGAGTGGAAAGCCCA 1799
QY 1800 GAGCGTGAATGAGAGAGCGCATTTGCACTGTGCGCAACGCGGGGCACTAACCGCGTGGC 1859
DB 1800 GAGCGTGAATGAGAGAGCGCATTTGCACTGTGCGCAACGCGGGGCACTAACCGCGTGGC 1859
QY 1860 CCGGATCTCATGCACTGTGTCTCCAGCTCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGC 1919
DB 1860 CCGGATCTCATGCACTGTGTCTCCAGCTCAAGCTGTGCAAGCTGTGCAAGCTGTGCAAGC 1919
QY 1920 CTGCAAGTGGCGCGGAGAGCGGGGCAAGAGCATGCGCAAGGCTGTCTCTGCAATGGGG 1979
DB 1920 CTGCAAGTGGCGCGGAGAGCGGGGCAAGAGCATGCGCAAGGCTGTCTCTGCAATGGGG 1979
QY 1980 CGCTGCAAGAGAGCGCTGACCTTCAAGCGGCTACACCGCTTCTGCACTGTGCTGCGCAA 2039
DB 1980 CGCTGCAAGAGAGCGCTTGAAGCTTCAAGCGGCTTCAAGCGGCTTCTGCACTGTGCTGCGCAA 2039
QY 2040 CGGCAACTGGCCACTGTCAAGCTGTGTGAGAGAGAGCGGATGTGTGCGCGGG 2099

Db	2040	CGGACACCTGGCGCACTGTCAAGCTGCTGTGAGAGGAAAGCCGATGTGCTGGCCCGGGAG	2029
QY	2100	ACCCCTGAACCAAGACGGCGCTGGCACTTGCGCTGCCGCCCACTGGAGGTGTGTGA	2155
Db	2100	AACCCCTGAACCAAGAGGGCGCTGGCACTTGCGCTGCCGCCCACTGGAGGTGTGTGA	2155
QY	2160	GGAGTGTGTCAAGCGCGCGATGTGATTTGACCTGTTCCAGCAGCAGGAGGCTCAAGCGCGCTGCA	2219
Db	2160	GGAGTGTGTCAAGCGCGCGATGTGATTTGACCTGTTCCAGCAGCAGGAGGCTCAAGCGCGCTGCA	2219
QY	2220	CTTGGCCCGCCCAAGGGCCGGGCACACGCAACACGGTGTGAAGCTCTGTCTCAAGCAATGGGGCCCA	2279
Db	2220	CTTGGCCCGCCCAAGGGCCGGGCACACGCAACACGGTGTGAAGCTCTGTCTCAAGCAATGGGGCCCA	2279
QY	2280	CATCAACTGTGAGAGCTCTCAAGTTCCAGGGCCGGCCATGAGCCCGCCGACCACTTCCTGCG	2335
Db	2280	CATCAACTGTGAGAGCTCTCAAGTTCCAGGGCCGGCCATGAGCCCGCCGACCACTTCCTGCG	2335
QY	2340	GCGAAGCAAGACTTAG	2355
Db	2340	GCGAAGCAAGACTTAG	2355

RESULT 8

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US-10-128-174-16
; Sequence 16, Application US/10128174
; Publication No. US2003019462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-16

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Query Match . 98.8%; Score 2327.2; DB 16; Length 2355;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2.

Qy	1	ATGAGAGGGCGA	CGGCGGGAGCCCATAGGAGCCCTGGCGCTCTGCGCACTTTCGACGCGGGC	60
Db	1	ATGAGAGGGCGA	CGGCGGGAGCCCATAGGAGCCCTGGCGCTCTGCGCACTTTCGACGCGGGC	60
Qy	61	GAGTTCA	CGGGGCTGGGAGAAAGGTGGGCTCGGGCGGCTTTGGGCAAGTGTAAAGAGGTGGCG	120
Db	61	GAGTTCA	CGGGGCTGGGAGAAAGGTGGGCTCGGGCGGCTTTGGGCAAGTGTAAAGAGGTGGCG	120
Qy	121	CATGTCCATGGA	AGACTGTGGCTGGGCGCATCAAGTGTGCGCCAGAGCTTGACGTCGACGAC	180
Db	121	CATGTCCATGGA	AGACTGTGGCTGGGCGCATCAAGTGTGCGCCAGAGCTTGACGTCGACGAC	180
Qy	181	AGGGAGCGCAT	GTAGAGCTTTTGGAGAAAGCCAGAAAGATGGAAGATGGCCAAAGTTTGGCTAC	240
Db	181	AGGGAGCGCAT	GTAGAGCTTTTGGAGAAAGCCAGAAAGATGGAAGATGGCCAAAGTTTGGCTAC	240
Qy	241	ATTCGAGCGT	GTGATATGGCATCTGCCGGAACCTGTGGGCTGGTCAATGGAAGTACATGTAG	300
Db	241	ATTCGAGCGT	GTGATATGGCATCTGCCGGAACCTGTGGGCTGGTCAATGGAAGTACATGTAG	300
Qy	301	ACGGGCTCCCT	GAAAAAGCTGCTGCGGCTTGGAGCCATTGCCATGGAGATCTCCGGTTCCGA	360
Db	301	ACGGGCTCCCT	GAAAAAGCTGCTGCGGCTTGGAGCCATTGCCATGGAGATCTCCGGTTCCGA	360
Qy	361	ATCATTCACAG	AGACGGCGGTGGGCAATTAATTCGTCATCGATGGCCCCGGCACAATCCG	420
Db	361	ATCATTCACAG	AGACGGCGGTGGGCAATTAATTCGTCATCGATGGCCCCGGCACAATCCG	420

QY	421	CACCGGACCTCAAGCCCGGAAATCATCTCTGGAATGCCACATCAACGCTCAAGATTCT	480
Db	421	CACCTGACCTCAAGCCCGGAAATCATCTCTGGAATGCCACATCAACGCTCAAGATTCT	480
QY	481	GATTTTGGTCTGAGCCAAATGACAAAGGAGTGTCCCACTCGCATGACTTCAAGATGATGAC	540
Db	481	GATTTTGGTCTGAGCCAAATGACAAAGGAGTGTCCCACTCGCATGACTTCAAGATGATGAC	540
QY	541	CTGTTTGGCAAAATGCGCTTACCTTCCACAGAGGATCAAGGGAGAAAGCCGGCTCTTC	600
Db	541	CTGTTTGGCAAAATGCGCTTACCTTCCACAGAGGATCAAGGGAGAAAGCCGGCTCTTC	600
QY	601	GACACCAAGCAGATGTATACAGCTTTGGCATCTCATCTGGGCGTCTCAACAAG	660
Db	601	GACACCAAGCAGATGTATACAGCTTTGGCATCTCATCTGGGCGTCTCAACAAG	660
QY	661	AAGCGTTTGGCAGATGAGAGAAATCTCTGCACTATCTGTGAAGGTGTGAAGGGCCAC	720
Db	661	AAGCGTTTGGCAGATGAGAGAAATCTCTGCACTATCTGTGAAGGTGTGAAGGGCCAC	720
QY	721	CGCCCGGACGTGCGCCCGGTGTGACAGAGCCCGGCGCGCTGCACGCACTGATACGC	780
Db	721	CGCCCGGACGTGCGCCCGGTGTGACAGAGCCCGGCGCGCTGCACGCACTGATACGC	780
QY	781	CTCATGCAAGCGGTCTGCGAGGGGGAATCCGGAATTAGGCCACCTTCCAGAAATTAAT	840
Db	781	CTCATGCAAGCGGTCTGCGAGGGGGAATCCGGAATTAGGCCACCTTCCAGAAATTAAT	840
QY	841	TCTGAACACCGAGACCTGTGTGAAAAGCCGTGAATGACGAATGAAAGAAACGTGCTCATGAT	900
Db	841	TCTGAACACCGAGACCTGTGTGAAAAGCCGTGATGACGAATGAAAGAAACGTGCTCATGAT	900
QY	901	CTGACGATGAAGAACCCCGGAGCCGACGAGCAGAGGTGTGTCTGCGAGGCTCAAGCGG	960
Db	901	CTGACGATGAAGAACCCCGGAGCCGACGAGCAGAGGTGTGTCTGCGAGGCTCAAGCGG	960
QY	961	GCTCTGCCCCCACTTGTGATTAAGACTACAGCTCTTCCAGGCTTCTCAACACTGGAC	1020
Db	961	GCTCTGCCCCCACTTGTGATTAAGACTACAGCTCTTCCAGGCTTCTCAACACTGGAC	1020
QY	1021	TCTGAGTTTCCAGGCGTGTGAGAGGGCCCGAGAGACTCAGCGGAGCTCTCTGAATCC	1080
Db	1021	TCTGAGTTTCCAGGCGTGTGAGAGGGCCCGAGAGACTCAGCGGAGCTCTCTGAATCC	1080
QY	1081	AAGCTGCAATGATCGTCGCGCAGTGTGGAAGAGGCTCTCGGGGAGTGTCTCGGTGACTCCGCC	1140
Db	1081	AAGCTGCAATGATCGTCGCGCAGTGTGGAAGAGGCTCTCGGGGAGTGTCTCGGTGACTCCGCC	1140
QY	1141	TTCTCTTCCAGAGATCACTGTGCTGTCTTTTGAAGCGGGAACCTTCAACAGAGGATCTG	1200
Db	1141	TTCTCTTCCAGAGATCACTGTGCTGTCTTTTGAAGCGGGAACCTTCAACAGAGGATCTG	1200
QY	1201	GGTACCAAGAAGCGTCCAGAAGAAAGACTTGTGATGTGCATCGTGTCC -GGGACACAG	1258
Db	1201	GGTACCAAG -AGAAGTCCAGAAGAAAGACTTGTGATGTGCATCGTGTCCGAGGACACAG	1259
QY	1260	CAAACTGATGAAGATCTTGCAAGCCGCAAGACTGTGACTGTGCACTGCAACAGCGGTGCGG	1319
Db	1260	CAAACTGATGAAGATCTTGCAAGCCGCAAGACTGTGACTGTGCACTGCAACAGCGGTGCGG	1319
QY	1320	CGTGTGCAACCTGTGGGTGTGAGAGGCCCGGCAAGAGAGTGTGCCCAAGTGGCTGTGTCTAA	1379
Db	1320	CGTGTGCAACCTGTGGGTGTGAGAGGCCCGGCAAGAGAGTGTGCCCAAGTGGCTGTGTCTAA	1379
QY	1380	CAATGCCAAACCCCAACTTGAGCAACCGTAAAGGGGCTCAACCCCGTTGCACTATGCCGTGGA	1439
Db	1380	CAATGCCAAACCCCAACTTGAGCAACCGTAAAGGGGCTCAACCCCGTTGCACTATGCCGTGGA	1439
QY	1440	GAGAGAGGTGTGGGGTGTGTGTGAGACTCTGTGTGCGCGGAAAGATCAAGTGTCAACGCCAA	1499
Db	1440	GAGAGAGGTGTGGGGTGTGTGTGAGACTCTGTGTGCGCGGAAAGATCAAGTGTCAACGCCAA	1499

QY 1500 GGATGAGGACCAAGTGGACAGCCCTCCACTTTGACAGCCCAAGGAGATGACTAGAC 1559
DB 1500 GGATGAGGACCAAGTGGACAGCCCTCCACTTTGACAGCCCAAGGAGATGACTAGAC 1559
QY 1560 ACGGCTGCTTTGAGAGAAAGCCCTCGGTCAACGAGGTGACCTTTGAGGCGGACGCC 1619
DB 1560 ACGGCTGCTTTGAGAGAAAGCCCTCGGTCAACGAGGTGACCTTTGAGGCGGACGCC 1619
QY 1620 CATGCACTGGCTCTGACGACAGGCGAGAGAAATCTGTGGCATCTCTGCTGCGCCAGG 1679
DB 1620 CATGCACTGGCTCTGACGACAGGCGAGAGAAATCTGTGGCATCTCTGCTGCGCCAGG 1679
QY 1680 CGTGACCTGAGCCCTGACAGGCGAAGATGCTGTGCTGCACTGACCTAGCTGCTGCA 1739
DB 1680 CGTGACCTGAGCCCTGACAGGCGAAGATGCTGTGCTGCACTGACCTAGCTGCTGCA 1739
QY 1740 GGGGCACTGCGCCATCTGCAAGCTGCTGCGCAAGACCGGCGGTGAGTGTGAACGCCCA 1799
DB 1740 GGGGCACTGCGCCATCTGCAAGCTGCTGCGCAAGACCGGCGGTGAGTGTGAACGCCCA 1799
QY 1800 GACGCTGATGAGAGAGAGCCCACTTGTACCTGCGCGCAACAGCGCGGACCTACCGCTGAGC 1859
DB 1800 GACGCTGATGAGAGAGAGCCCACTTGTACCTGCGCGCAACAGCGCGGACCTACCGCTGAGC 1859
QY 1860 CGGATCTCTCAATGACCTGTGCTCGACCTTCAACGCTTGTGACCTGCTGCGACAGACACC 1919
DB 1860 CGGATCTCTCAATGACCTGTGCTCGACCTTCAACGCTTGTGACCTGCTGCGACAGACACC 1919
QY 1920 CCTGCACTGCGCGCGGAGAGCGGCGCACAGACCTGCGACGCTGCTGCTGCAATCGGAGG 1979
DB 1920 CCTGCACTGCGCGCGGAGAGCGGCGCACAGACCTGCGACGCTGCTGCTGCAATCGGAGG 1979
QY 1980 CGCTGAGCAAGAGGCGGTGACCTGACAGGCGTCAACCGCTTGTGACCTGCTGCGCGCA 2039
DB 1980 CGCTGAGCAAGAGGCGGTGACCTGACAGGCGTCAACCGCTTGTGACCTGCTGCGCGCA 2039
QY 2040 CGGACACCTGCGCACTGTCAAGCTGCTTGTGAGGAGAGGCGGATGTGTGCTGCGCGGAG 2099
DB 2040 CGGACACCTGCGCACTGTCAAGCTGCTTGTGAGGAGAGGCGGATGTGTGCTGCGCGGAG 2099
QY 2100 ACCCTGAAACGACGCGGCTGACCTTGTGCGCGCGCCCACTGCGAGGTGTGGA 2159
DB 2100 ACCCTGAAACGACGCGGCTGACCTTGTGCGCGCGCCCACTGCGAGGTGTGGA 2159
QY 2160 GAGTGTGCTGAGCGCGGATGCTTGTGACGAGGAGGCGGCTCAACGCGCTGCA 2219
DB 2160 GAGTGTGCTGAGCGCGGATGCTTGTGACGAGGAGGCGGCTCAACGCGCTGCA 2219
QY 2220 CCTGCGCGCGCGGAGCGGCGACGACAGCGGTGAGACTGTGCTCAAGCATGCGGCCCA 2279
DB 2220 CCTGCGCGCGCGGAGCGGCGACGACAGCGGTGAGACTGTGCTCAAGCATGCGGCCCA 2279
QY 2280 CATCAACCTGCAAGACCTCAAGTTTCAGGCGCGGCGGCGGCGCACTTCTGCG 2339
DB 2280 CATCAACCTGCAAGACCTCAAGTTTCAGGCGCGGCGGCGGCGCACTTCTGCG 2339
QY 2340 GCGAAGCAAGACTTG 2355
DB 2340 GCGAAGCAAGACTTG 2355

RESULT 9

US-10-128-174-18
; Sequence 18, Application US/10128174
; Publication No. US2003019462A1
; GENERAL INFORMATION:
; APPLICANT: Inohara, Naohiro
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-18
Query Match 98.8%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 1 ATGAGGCGACAGCGCGGACCCCATGAGCCCTGAGCTGTGCGACCTTGCAGCGGCG 60
DB 1 ATGAGGCGACAGCGCGGACCCCATGAGCCCTGAGCTGTGCGACCTTGCAGCGGCG 60
QY 61 GAGTTCAAGGCTGAGAGAGGTGGCTCGGGCGGCTTGGGCGAGGTGACAAAGTGGCG 120
DB 61 GAGTTCAAGGCTGAGAGAGGTGGCTCGGGCGGCTTGGGCGAGGTGACAAAGTGGCG 120
QY 121 CATGTCACTGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCTGACGTCAGAC 180
DB 121 CATGTCACTGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCTGACGTCAGAC 180
QY 181 AGGAGCGCATGAGCTTTTGAAGAGCCAGAGATGAGATGAGCAAGTTGCTAC 240
DB 181 AGGAGCGCATGAGCTTTTGAAGAGCCAGAGATGAGATGAGCAAGTTGCTAC 240
QY 241 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGCTGTGTATGAGTACATGAG 300
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGCTGTGTATGAGTACATGAG 300
QY 301 ACGGCGCTCTGGAAGAGCTGTGCTTGGAGCGATTTGCAATGAGATCTCCGGTTCGA 360
DB 301 ACGGCGCTCTGGAAGAGCTGTGCTTGGAGCGATTTGCAATGAGATCTCCGGTTCGA 360
QY 361 ATATCCAGAGACGCGGATGAGCACTTCTGTGACATGAGCGCGGCACTTCTG 420
DB 361 ATATCCAGAGACGCGGATGAGCACTTCTGTGACATGAGCGCGGCACTTCTG 420
QY 421 CACTGGAACCTCAAGCCCGGAACTATCTGCTGAGTCCCATCAACGTCAGATTTCT 480
DB 421 CACTGGAACCTCAAGCCCGGAACTATCTGCTGAGTCCCATCAACGTCAGATTTCT 480
QY 481 GATTTGTGTGCGCAAGTCAAGGCTGTCCCATCTGCGATGACCTCAGATGATGGC 540
DB 481 GATTTGTGTGCGCAAGTCAAGGCTGTCCCATCTGCGATGACCTCAGATGATGGC 540
QY 541 CTGTTTGGCACAATGCTTACTTCTTCAAGCGCATCAAGGAGAAAGCCGCTTTC 600
DB 541 CTGTTTGGCACAATGCTTACTTCTTCAAGCGCATCAAGGAGAAAGCCGCTTTC 600
QY 601 GACACCAAGACCATGTATACGTTTGCATGTCTATCTGAGGCGGTCTCAACAGAG 660
DB 601 GACACCAAGACCATGTATACGTTTGCATGTCTATCTGAGGCGGTCTCAACAGAG 660
QY 661 AAGCGTTTGCAGATGAGAGAAATCTCTGACATCATGTGAGAGGTGTGAAGGCGCAC 720
DB 661 AAGCGTTTGCAGATGAGAGAAATCTCTGACATCATGTGAGAGGTGTGAAGGCGCAC 720
QY 721 CGCCCGAGCTGCGCGCGGTGTGAGAGCCGCGCGCGGCTGCGACGCACTGTATGCG 780
DB 721 CGCCCGAGCTGCGCGCGGTGTGAGAGCCGCGCGCGGCTGCGACGCACTGTATGCG 780
QY 781 CTCATGAGAGGTGTGAGAGGAGATCCCGAGTTTGAAGGCGCACTTCCAGAAATTAAT 840
DB 781 CTCATGAGAGGTGTGAGAGGAGATCCCGAGTTTGAAGGCGCACTTCCAGAAATTAAT 840
QY 841 TCTGAACCGAGGACTGTGTGAAGAAAGCTGATGACGAAGTGAAGAACTGCTCATGAT 900
DB 841 TCTGAACCGAGGACTGTGTGAAGAAAGCTGATGACGAAGTGAAGAACTGCTCATGAT 900
QY 901 CTGACGTGAAGAGCCCGCGAGGCCAGAGCGAGGTGTGCTGTGAGGCTTCAAGCGG 960

Db	901	CTGGACGTGAAAAACCCCCCGGAGCCAGAGACGAGAGTGGTGGCTTGGAGAGCTCAAGCGG	960
Qy	961	GCCTCTGCCCCCACCTTCGATTAACGACTACGCTCTCCAGACTTCTCTCAAGCTGGAC	1020
Db	961	GCCTCTGCCCCCACCTTCGATTAACGACTACGCTCTCCAGACTGCTCTCAAGCTGGAC	1020
Qy	1021	TCTGGAGTTTCCCAAGGCTGTGGAAGGCCCCGAGAGAGCTCAAGCCGACACTCTCTGAAGTCC	1080
Db	1021	TCTGGAGTTTCCCAAGGCTGTGGAAGGCCCCGAGAGAGCTCAAGCCGACACTCTCTGAAGTCC	1080
Qy	1081	AAGCGCCATCGTCCGGCAGTGGGAGAAGAGCTCTCGGAGGAGTCTCGGTGACTCCGCC	1140
Db	1081	AAGCTGCATCGTCCGGCAGTGGGAGAAGAGCTCTCGGAGGAGTCTCGGTGACTCCGCC	1140
Qy	1141	TTCTCTTCACAGAGATCACTGTGCTGTCTTTGACGGGAACTTCAACGCGATCTG	1200
Db	1141	TTCTCTTCACAGAGATCACTGTGCTGTCTTTGACGGGAACTTCAACGCGAGACTG	1200
Qy	1201	GGTACCAACAAGCTTCGAGAGAGAAAGTGTGAGTGGCATCGTGTCC -GGGACAACAG	1259
Db	1201	GGCACACA -AGACCTCCAGAGAGAAAGAACTTGTAGATGCATCGTGTCCGGAGACAACAG	1259
Qy	1260	CAAACTGATGAAGATCTCGACGCCGACAGACGTGACCTTGACCTTGACACAGCGGTGCAG	1319
Db	1260	CAAACTGATGAAGATCTCGACGCCGACAGACGTGACCTTGACCTTGACACAGCGGTGCAG	1319
Qy	1320	CTGTGTCACCTGTGCGGTGAGAGGCGGGCAAGAGAGTGCAGAGTGGCTGTCTCAA	1379
Db	1320	CTGTGTCACCTGTGCGGTGAGAGGCGGGCAAGAGAGTGCAGAGTGGCTGTCTCAA	1379
Qy	1380	CAATGCCAACCCCAACTGAGCAACCTGAAGGAGCTCCACCCCTGTGACACATGGCCGTGGA	1439
Db	1380	CAATGCCAACCCCAACTGAGCAACCTGAAGGAGCTCCACCCCTGTGACACATGGCCGTGGA	1439
Qy	1440	GAGGAGGGGTGCGGGGTGTCTGAGAACTCTGTGGCAGAGAAATCAGTGTCAACGCAAA	1499
Db	1440	GAGGAGGGGTGCGGGGTGTCTGAGAACTCTGTGGCAGAGAAATCAGTGTCAACGCAAA	1499
Qy	1500	GGATAGAGACCAAGTGAACAGCCCTTCACTTTTGCACGCCCAAGAACCGGAGTGAAGTCTAGAC	1559
Db	1500	GGATAGAGACCAAGTGAACAGCCCTTCACTTTTGCACGCCCAAGAACCGGAGTGAAGTCTAGAC	1559
Qy	1560	ACGGCTGCTGTGAGAGAAAGACGCTCTCGGTCAACAGAGTGAACCTTGAAGGCGCGACGCC	1619
Db	1560	ACGGCTGCTGTGAGAGAAAGACGCTCTCGGTCAACAGAGTGAACCTTGAAGGCGCGACGCC	1619
Qy	1620	CATGCACTGTGGCTTGCACACAGGGCAGAGAAATTCGTGGCANTCCTGCGCGCCAGAG	1679
Db	1620	CATGCACTGTGGCTTGCACACAGGGCAGAGAAATTCGTGGCANTCCTGCGCGCCAGAG	1679
Qy	1680	CGTGGACGTGAGCTGCGAGAGGCAAGATATGCTGCTGCACCTGACCTGACCTGAC	1739
Db	1680	CGTGGACGTGAGCTGCGAGAGGCAAGATATGCTGCTGCACCTGACCTGACCTGAC	1739
Qy	1740	GGGCCACCTGCCCATCTGTCAAGCTGTGGCCAAAGACCGGGGGTGAAGTGAACGCCCA	1799
Db	1740	GGGCCACCTGCCCATCTGTCAAGCTGTGGCCAAAGACCGGGGGTGAAGTGAACGCCCA	1799
Qy	1800	GAACGCTGAATGGGAGGACGCCATTGCACTTGGCCGACACAGCCGGGGCACTAACCGGTGGC	1859
Db	1800	GAACGCTGAATGGGAGGACGCCATTGCACTTGGCCGACACAGCCGGGGCACTAACCGGTGGC	1859
Qy	1860	CGGCATCCATCGACCTGTGTCCGACGTCAACGCTTGCACGCTGCGACCTGCGACACAGACCC	1919
Db	1860	CGGCATCCATCGACCTGTGTCCGACGTCAACGCTTGCACGCTGCGACCTGCGACACAGACCC	1919
Qy	1920	CTTGGACGTGGCCGCGAGAGACGGAGGACACAGACCTGCCAGGCTTCTCTGCAATCGAGG	1979
Db	1920	CTTGGACGTGGCCGCGAGAGACGGAGGACACAGACCTGCCAGGCTTCTCTGCAATCGAGG	1979
Qy	1980	CGCTGGCAGAGAGGCGGTGACTCAACAGGACTCAACCGCTCTGCACCTGGCTGGCCCGCAA	2039
Db	1980	CGCTGGCAGAGAGGCGGTGACTCAACAGGACTCAACCGCTCTGCACCTGGCTGGCCCGCAA	2039

QY	2040	CGAACACTGGCCACTGTCAAGCTGTTGTGCGAGGAGAAAGCCGATGTGTGCTGGCCCCGGG	2039
Db	2040	CGAACACTGGCCACTGTCAAGCTGTTGTGCGAGGAGAAAGCCGATGTGTGCTGGCCCCGGG	2039
QY	2100	ACCCCTGAACCGAGCGGCGCTGCACTGGGCTGCCGCCACGGGCACTCGAGAGTGATGGA	2159
Db	2100	ACCCCTGAACCGAGCGGCGCTGCACTGGGCTGCCGCCACGGGCACTCGAGAGTGATGGA	2159
QY	2160	GGAGTTGGTCAGCGCCCGCATGTCAATTGACCTTGTCGACGAGCAGGGGCTCAGCGCGCTGCA	2219
Db	2160	GGAGTTGGTCAGCGCCCGCATGTCAATTGACCTTGTCGACGAGCAGGGGCTCAGCGCGCTGCA	2219
QY	2220	CCTGGCGCGCCAGGGCCCGGCACGCAGACGCTGAGACACTTCTCAGCGCATGGGGCCCCA	2279
Db	2220	CCTGGCGCGCCAGGGCCCGGCACGCAGACGCTGAGACACTTCTCAGCGCATGGGGCCCCA	2279
QY	2280	CATCAACTGCAAGGCTCAAGTTCGAGGGGGGCGACAGCCCGCGCGCACTCTGGCG	2339
Db	2280	CATCAACTGCAAGGCTCAAGTTCGAGGGGGGCGACAGCCCGCGCGCACTCTGGCG	2339
QY	2340	GCGAAGCAAGCCTTAG	2355
Db	2340	GCGAAGCAAGCCTTAG	2355

```

RESULT 10
US-10-128-174-19
; Sequence 19, Application US/10128174
; Publication NO. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inchausti, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06367
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;
; LENGTH: 2355
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
US-10-128-174-19

```

Query Match	98.8%	Score 2327.2;	DB 16;	Length 2355;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2351; Conservative	0;	Mismatches 3;	Indels 2;	Gaps 2

QY	1	ATGAGAGGGGCAACGGGGGGAACCCCAATGGGGCCCTGGGGGCTGGCTGGGACCTTGCACGCGGGC	60
Db	1	ATGAGAGGGGGAAGGGGGAGCCCAATGGGGCCCTGGGGGCTGGCTGGGACCTTGCACGCGGGC	60
QY	61	GAGTTCAAGGGGCTGGGAGAAAGTGGGCTTCGGGCGGCTTTCGGGACAGTGTACAAGTGGGC	120
Db	61	GAGTTCAAGGGGCTGGGAGAAAGTGGGCTTCGGGCGGCTTTCGGGACAGTGTACAAGTGGGC	120
QY	121	CATGTCCACTGGAAAGCCGGGCTGGCCATCAAGTCTCGGCCAGGCTGCACGTCGACGAC	180
Db	121	CATGTCCACTGGAAAGCCGGGCTGGCCATCAAGTCTCGGCCAGGCTGCACGCTGCACGTCGACGAC	180
QY	181	AGGGAGCGCATGAGCTTTTGGAGAAAGCCAAAGAAATGGAGATGGCCAAAGTTTGCTTAC	240
Db	181	AGGGAGCGCATGAGCTTTTGGAGAAAGCCAAAGAAATGGAGATGGCCAAAGTTTGCTTAC	240
QY	241	ATCCGACCGTATATGGGCACTGCGCGGAAACCTGTACGGCTGGTATGGAGATACATGGAG	300
Db	241	ATCCGACCGTATATGGGCACTGCGCGGAAACCTGTACGGCTGGTATGGAGATACATGGAG	300
QY	301	ACGGGCTCCCTGGAAAAGCTGGCTTGGAGCCATTGGCCATGGGAATCTCCGGTTCCGA	360
Db	301	ACGGGCTCCCTGGAAAAGCTGGCTTGGAGCCATTGGCCATGGGAATCTCCGGTTCCGA	360

QY 361 ATCATCCAGAGCGGCGGTGGGCAATGAATTTCTTGCACTGATAGGCCCCCGCACTCTG 420
 Db 361 ATCATCCAGAGCGGCGGTGGGCAATGAATTTCTTGCACTGATAGGCCCCCGCACTCTG 420
 QY 421 CACCTGAGCCTCAAGCCCGCAACATCTCTGTGATGCGCACTACAGTCAAGATTTCT 480
 Db 421 CACCTGAGCCTCAAGCCCGCAACATCTCTGTGATGCGCACTACAGTCAAGATTTCT 480
 QY 481 GATTTTGTCTGGCCAAATGCAAGGCGCTGTCCCACTGTGATGACCTTGAAGATGATGAC 540
 Db 481 GATTTTGTCTGGCCAAATGCAAGGCGCTGTCCCACTGTGATGACCTTGAAGATGATGAC 540
 QY 541 CTGTTTGGCAATGCTTACCTCCCTCCAGAGCATCAAGAGAGAGCGGCTCTTC 600
 Db 541 CTGTTTGGCAATGCTTACCTCCCTCCAGAGCATCAAGAGAGAGCGGCTCTTC 600
 QY 601 GACACCAAGCAAGATGATTAACATTTTGATGATCTGTGATCTGTGGGCGTGTCAACAGAG 660
 Db 601 GACACCAAGCAAGATGATTAACATTTTGATGATCTGTGATCTGTGGGCGTGTCAACAGAG 660
 QY 661 AAGCGTTTGGCAATGATGAAGAAATCTCTGCAATCATGTGTGAAGTGTGAAGGCGAC 720
 Db 661 AAGCGTTTGGCAATGATGAAGAAATCTCTGCAATCATGTGTGAAGTGTGAAGGCGAC 720
 QY 721 CGCCCGAGCTGCGCCGCTGTGTGAGAGCCCGGCGCGCTGTGAAGCACTGATAGC 780
 Db 721 CGCCCGAGCTGCGCCGCTGTGTGAGAGCCCGGCGCGCTGTGAAGCACTGATAGC 780
 QY 781 CTGATGCAAGCGGTGTGCAAGGAGGATCCGCGATTAGGCCCACTTTCAGAAATTAATCT 840
 Db 781 CTGATGCAAGCGGTGTGCAAGGAGGATCCGCGATTAGGCCCACTTTCAGAAATTAATCT 840
 QY 841 TCTGAACCGAGAGACTGTGTGAAAAGCTGTGATGACGAATGAAAGAAATGCTCATAT 900
 Db 841 TCTGAACCGAGAGACTGTGTGAAAAGCTGTGATGACGAATGAAAGAAATGCTCATAT 900
 QY 901 CTGAGCGTGAAGAAAGCCCCCGAGGCCAGAGAGAGTGTGCTGCGAGGCTCAAGCGG 960
 Db 901 CTGAGCGTGAAGAAAGCCCCCGAGGCCAGAGAGAGTGTGCTGCGAGGCTCAAGCGG 960
 QY 961 GCCTTGTGCCCCCACTTGATTAACGATCAAGCTCTCCAGCTTCTCTCAAGCTGAGC 1020
 Db 961 GCCTTGTGCCCCCACTTGATTAACGATCAAGCTCTCCAGCTTCTCTCAAGCTGAGC 1020
 QY 1021 TCTGAGATTTTCCAGAGCTGTGAGAGGCCCCCGAGAGCTCAAGCGGAGTCTCTTGAATCC 1080
 Db 1021 TCTGAGATTTTCCAGAGCTGTGAGAGGCCCCCGAGAGCTCAAGCGGAGTCTCTTGAATCC 1080
 QY 1081 AAGCTGCCATCGTCCGGCAGTGGGAAAGAGCTCTGCGGAGTGTCTCGGTGAGCTCCGC 1140
 Db 1081 AAGCTGCCATCGTCCGGCAGTGGGAAAGAGCTCTGCGGAGTGTCTCGGTGAGCTCCGC 1140
 QY 1141 TTCTTTCAGAGATCACTGTGTGTCTTTGAGCGGAACTTTCACACGAGATCTG 1200
 Db 1141 TTCTTTCAGAGATCACTGTGTGTCTTTGAGCGGAACTTTCACACGAGATCTG 1200
 QY 1201 GGTACCAAGAGCTGCCAGAGAGAAAGATTTGTGATGCAATCGGTGTC-GGAGACAG 1259
 Db 1201 GGTACCAAGAGCTGCCAGAGAGAAAGATTTGTGATGCAATCGGTGTC-GGAGACAG 1259
 QY 1260 CAATCTGATGAAGATCTGTGAGCCCGCAGAGCTGTGACCTGTGAGCAGGCGGTGCGAG 1319
 Db 1260 CAATCTGATGAAGATCTGTGAGCCCGCAGAGCTGTGACCTGTGAGCAGGCGGTGCGAG 1319
 QY 1320 CTTGTGTGCACTGTGCGGTGAGAGCGCGCAAGAGATGCGCAAGTGTGCTGCTCA 1379
 Db 1320 CTTGTGTGCACTGTGCGGTGAGAGCGCGCAAGAGATGCGCAAGTGTGCTGCTCA 1379
 QY 1380 CAATGCAACCCCACTGAGAGCAATGTAAGGCGTCAACCCCGTTGCAATAGCCGTGGA 1439
 Db 1380 CAATGCAACCCCACTGAGAGCAATGTAAGGCGTCAACCCCGTTGCAATAGCCGTGGA 1439
 QY 1440 GAGGAGGAGTGTGAGAGCTCTGCTGTGCAAGAGATCAATGTCAAGCCAA 1499

Db 1440 GAGGAGGAGTGTGAGAGCTCTGCTGTGCGCGGAAATCATGTGTCAACGCCAA 1499
 QY 1500 GATGAGAGCAATGAGCAAGCCCTTCCACTTTGAGGCCAGAAAGGGGATGATCTAGCAC 1559
 Db 1500 GATGAGAGCAATGAGCAAGCCCTTCCACTTTGAGGCCAGAAAGGGGATGATCTAGCAC 1559
 QY 1560 ACCGCTGTGTTGAGAGAAAGCTGTGCAAGAGTGTGAATTTGAGGGCGGAGGCC 1619
 Db 1560 ACCGCTGTGTTGAGAGAAAGCTGTGCAAGAGTGTGAATTTGAGGGCGGAGGCC 1619
 QY 1620 CATGCAAGTGTGCTGCGAGCAAGGCAAGAAATATCTGTGCGATCTGTGCGCGAGG 1679
 Db 1620 CATGCAAGTGTGCTGCGAGCAAGGCAAGAAATATCTGTGCGATCTGTGCGCGAGG 1679
 QY 1680 CTGTGAGATGAGCTGTGAGGGCAAGATGTGCTGTGCTCCACTGCACTAACCTGTGGA 1739
 Db 1680 CTGTGAGATGAGCTGTGAGGGCAAGATGTGCTGTGCTCCACTGCACTAACCTGTGGA 1739
 QY 1740 GGGCCACTGCGCCATCGTCAAGCTGTGTGCGCAAGCAGCGGGGTGATGAAAGGCCA 1799
 Db 1740 GGGCCACTGCGCCATCGTCAAGCTGTGTGCGCAAGCAGCGGGGTGATGAAAGGCCA 1799
 QY 1800 GACGCTGATGTGAGAGAGCGCATTTGCACTGTGCGCAAGCGGCGCACTAACCGCTGTGC 1859
 Db 1800 GACGCTGATGTGAGAGAGCGCATTTGCACTGTGCGCAAGCGGCGCACTAACCGCTGTGC 1859
 QY 1860 CCGGATCTCATGACCTGTGTCTCCAGCTCAACGTCTGAGAGCTGTGCGCAAGACACC 1919
 Db 1860 CCGGATCTCATGACCTGTGTCTCCAGCTCAACGTCTGAGAGCTGTGCGCAAGACACC 1919
 QY 1920 CTTGCAAGTGTGCGCGAGAGAGGGGCAAGAGCACTGCGAGGCTGTCTGTGATCGAGG 1979
 Db 1920 CTTGCAAGTGTGCGCGAGAGAGGGGCAAGAGCACTGCGAGGCTGTCTGTGATCGAGG 1979
 QY 1980 CGCTGTGAGAGAGCGCTGTGACCTTCAAGCGCTCAACCGCTTGTGCAAGGAGGAGG 2039
 Db 1980 CGCTGTGAGAGAGCGCTGTGACCTTCAAGCGCTCAACCGCTTGTGCAAGGAGGAGG 2039
 QY 2040 CGGACACTGTGCGCACTGTGACCTGTGTGAGAGAGAGGCGGATGTGTGCGCGCGG 2099
 Db 2040 CGGACACTGTGCGCACTGTGACCTGTGTGAGAGAGAGGCGGATGTGTGCGCGCGG 2099
 QY 2100 ACCCTTGAACAGAGCGCGCTGTGACCTGTGTGAGAGAGAGGCGGATGTGTGCGCGG 2159
 Db 2100 ACCCTTGAACAGAGCGCGCTGTGACCTGTGTGAGAGAGAGGCGGATGTGTGCGCGG 2159
 QY 2160 GAGATTGTGACGCGCGATGTCAATTGACCTGTGTGACGAGCGAGGCTCAAGCGCTGCA 2219
 Db 2160 GAGATTGTGACGCGCGATGTCAATTGACCTGTGTGACGAGCGAGGCTCAAGCGCTGCA 2219
 QY 2220 CTTGCGCGGCCAGGCGCGGACCGCAAGAGAGTGTGACCTGTGTGAGAGAGGAGGCCA 2279
 Db 2220 CTTGCGCGGCCAGGCGCGGACCGCAAGAGAGTGTGACCTGTGTGAGAGAGGAGGCCA 2279
 QY 2280 CATCAACTGTGAGAGCTTCAAGTTTCAAGGCGGCGCATGAGCGCGCCACACTCTGTGG 2339
 Db 2280 CATCAACTGTGAGAGCTTCAAGTTTCAAGGCGGCGCATGAGCGCGCCACACTCTGTGG 2339
 QY 2340 GCGAAGCAAGACTAG 2355
 Db 2340 GCGAAGCAAGACTAG 2355

RESULT 11
 US-10-128-174-1
 ; Sequence 1, Application US/10128174
 ; Publication No. US20030199462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nunez, Gabriel
 ; APPLICANT: Inohara, Naohiro
 ; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
 ; FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
US-10-128-174-1

Query Match 98.8%; Score 2325.6; DB 16; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2350; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 ATGAGGGCGAAGCGGGGACCCCATGGGCGCTGGCGCTGCGCACTTGACGCGGGC 60
DB 1 ATGAGGGCGAAGCGGGGACCCCATGGGCGCTGGCGCTGCGCACTTGACGCGGGC 60
QY 61 GAGTTCAAGGGCTGGGAGAGAGTGGGCTCGGCGGGCTTGCGGCAAGTGTGGC 120
DB 61 GAGTTCAAGGGCTGGGAGAGAGTGGGCTCGGCGGGCTTGCGGCAAGTGTGGC 120
QY 121 CATGTCATGGAAGACCTGGCTGGCAATCAAGTGTGGCCAGCTGCAAGTGTGGC 180
DB 121 CATGTCATGGAAGACCTGGCTGGCAATCAAGTGTGGCCAGCTGCAAGTGTGGC 180
QY 181 AGGAGCGCATGGAAGCTTTTGGAGAGCCAGAGAGATGAGATGGCCAGTTTGGTAC 240
DB 181 AGGAGCGCATGGAAGCTTTTGGAGAGCCAGAGAGATGAGATGGCCAGTTTGGTAC 240
QY 241 ATCTGCGCTGTGTATGAGCATCTGCGCGCAACCTGTGCGCTGTGTATGAGATGAG 300
DB 241 ATCTGCGCTGTGTATGAGCATCTGCGCGCAACCTGTGCGCTGTGTATGAGATGAG 300
QY 301 AGGGGCTCCCTGGAAAGCTGTGGCTTGAGAGCCATTGCAATGGATCTCCGGTTCCGA 360
DB 301 AGGGGCTCCCTGGAAAGCTGTGGCTTGAGAGCCATTGCAATGGATCTCCGGTTCCGA 360
QY 361 ATCATCAAGAGACGGCGGTGGGCAATCTTCTGCACTGCACTGAGGCGCGCACTCTG 420
DB 361 ATCATCAAGAGACGGCGGTGGGCAATCTTCTGCACTGCACTGAGGCGCGCACTCTG 420
QY 421 CACCTGGAACCTCAAGCCCGCAACATCTGCTGTGATGCCCACTAACAAGTATCT 480
DB 421 CACCTGGAACCTCAAGCCCGCAACATCTGCTGTGATGCCCACTAACAAGTATCT 480
QY 481 GATTTGTGCTGGCCAGTGAAGCAACGGGCTGTCCACTGCGATGACCTGCAAGATGAG 540
DB 481 GATTTGTGCTGGCCAGTGAAGCAACGGGCTGTCCACTGCGATGACCTGCAAGATGAG 540
QY 541 CTGTTTGGCAATCGCTCACTCCCTCGAGAGCGCATGAGGAGAGAGCGGCTTTTC 600
DB 541 CTGTTTGGCAATCGCTCACTCCCTCGAGAGCGCATGAGGAGAGAGCGGCTTTTC 600
QY 601 GACCAAGACAGATATATACAGCTTTGGGATGTATCTGGGGGCTGTCTCAACAGAG 660
DB 601 GACCAAGACAGATATATACAGCTTTGGGATGTATCTGGGGGCTGTCTCAACAGAG 660
QY 661 AAGCGCTTGGCAATGAGAGAAATCTGCAATCATGATGATGATGATGATGATGATGAT 720
DB 661 AAGCGCTTGGCAATGAGAGAAATCTGCAATCATGATGATGATGATGATGATGATGAT 720
QY 721 CCGCCGAGCTGCGCGCTGTGTCAGAGCCCGCGCGCGCTGCAAGCACTGATACGC 780
DB 721 CCGCCGAGCTGCGCGCTGTGTCAGAGCCCGCGCGCGCTGCAAGCACTGATACGC 780
QY 781 CTGATGAGAGGTGTGTCAGAGGGGATTCGGAGTTAAGCCACTTCCAAAGAAATTAAT 840
DB 781 CTGATGAGAGGTGTGTCAGAGGGGATTCGGAGTTAAGCCACTTCCAAAGAAATTAAT 840
QY 841 TCTGAAGCGAGGACCTGTGTGAAGAGCTGATGAGAGAGTGAAGAAATCTGCTATGAT 900
DB 841 TCTGAAGCGAGGACCTGTGTGAAGAGCTGATGAGAGAGTGAAGAAATCTGCTATGAT 900

QY 901 CTGGAAGTGAAGAGCCCGGAGCCCAAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
DB 901 CTGGAAGTGAAGAGCCCGGAGCCCAAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
QY 961 GCTCTGCGCCCACTTGTGATTAAGCAAGCTTCTCCAGACTTCTCTCAAGCTGAGC 1020
DB 961 GCTCTGCGCCCACTTGTGATTAAGCAAGCTTCTCCAGACTTCTCTCAAGCTGAGC 1020
QY 1021 TCTGAGTTTCCAGAGGTGTGTCAGAGGGCCCGAGAGGTGACGCACTGCTGAGTTC 1080
DB 1021 TCTGAGTTTCCAGAGGTGTGTCAGAGGGCCCGAGAGGTGACGCACTGCTGAGTTC 1080
QY 1081 AAGCTGCATGATGTCGCGGAGTGGAGAGAGCTCTCGGGGGTGTCTCGTGTGAGCTCCGC 1140
DB 1081 AAGCTGCATGATGTCGCGGAGTGGAGAGAGCTCTCGGGGGTGTCTCGTGTGAGCTCCGC 1140
QY 1141 TTCTCTTCCAGAGGATCATGTGTGCTGTCTTTGAGCGGGAACTTCAACAGCGATCTG 1200
DB 1141 TTCTCTTCCAGAGGATCATGTGTGCTGTCTTTGAGCGGGAACTTCAACAGCGATCTG 1200
QY 1201 GGTACCAAGAGCTTCCAGAGAGAGAGCTTTGTGATGCTGCTGCTGCTGCTGCTGCTG 1259
DB 1201 GGTACCAAGAGCTTCCAGAGAGAGAGCTTTGTGATGCTGCTGCTGCTGCTGCTGCTG 1259
QY 1260 CAAATGATGAAGATCTGCAAGCGCGCAAGAGCTGCACTGGAACAGCGGTGCGAG 1319
DB 1260 CAAATGATGAAGATCTGCAAGCGCGCAAGAGCTGCACTGGAACAGCGGTGCGAG 1319
QY 1320 CCTGCTGCACTGCGCGGTGAGAGCGCGGCAAGAGAGTGTGCGCAATGGCTGTCTCA 1379
DB 1320 CCTGCTGCACTGCGCGGTGAGAGCGCGGCAAGAGAGTGTGCGCAATGGCTGTCTCA 1379
QY 1380 CAATGCCAACCCCACTGAGCAACCTGAGGGGCTTCAACCCGTTTGGCAATGGCCGTGGA 1439
DB 1380 CAATGCCAACCCCACTGAGCAACCTGAGGGGCTTCAACCCGTTTGGCAATGGCCGTGGA 1439
QY 1440 GAGAGGGTGTGGGGTGTGAGAGCTCTGCTGCAAGAGATCAATGTCAAGCCAA 1499
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QY 1500 GATGAGAGACAGTGAAGAGCCCTTCACTTTCAGAGCCCAAGAGCGGAGTGAATGATGAC 1559
DB 1500 GATGAGAGACAGTGAAGAGCCCTTCACTTTCAGAGCCCAAGAGCGGAGTGAATGATGAC 1559
QY 1560 ACGGCTGTGTTGAGAGAGAGAGCTCTGCTGCAAGAGTGAATGAGGGCCGGAACCC 1619
DB 1560 ACGGCTGTGTTGAGAGAGAGAGCTCTGCTGCAAGAGTGAATGAGGGCCGGAACCC 1619
QY 1620 CATGCAAGTGTGCTGCGCAAGCGGCAAGAGAAATATGCTGGGCAATCTGCTGCGCGAGG 1679
DB 1620 CATGCAAGTGTGCTGCGCAAGCGGCAAGAGAAATATGCTGGGCAATCTGCTGCGCGAGG 1679
QY 1680 CBTGGAAGTGTGAG 1739
DB 1680 CBTGGAAGTGTGAG 1739
QY 1740 GGGCCACTGCGCAATGTCAGAGCTGTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1799
DB 1740 GGGCCACTGCGCAATGTCAGAGCTGTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1799
QY 1800 GACGCTGATGAG 1859
DB 1800 GACGCTGATGAG 1859
QY 1860 CCGCATCTCATGACCTGTGTCTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCA 1919
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QY 1920 CCTGCAAGTGTGCGCGGAG 1979
DB 1920 CCTGCAAGTGTGCGCGGAG 1979

QY	1980	CGCTGGCAAGAGGCGCTGACCTTCAGACGGCTTACACCGCTCTGCACTCTGGCTGCCCGCAA	2039
Db	1980	CGCTGGCAAGAGGCGCTGACCTTCAGACGGCTTACACCGCTCTGCACTCTGGCTGCCCGCAA	2039
QY	2040	CGGACACCTGGGCACTGTCAAGCTGCTTTCAGAGGAAAGGCGGATGTCTGGCCCGGGG	2099
Db	2040	CGGACACCTGGGCACTGTCAAGCTGCTTTCAGAGGAAAGGCGGATGTCTGGCCCGGGG	2099
QY	2100	ACCCCTGAACGAGCGGCGCTGCACCTGGGCTGCGGCCACGCGGCACTCGAGGTTGGTGA	2159
Db	2100	ACCCCTGAACGAGCGGCGCTGCACCTGGGCTGCGGCCACGCGGCACTCGAGGTTGGTGA	2159
QY	2160	GGAATTGGTCAACGCGCGGATGTATTGACCTGTTTCAGACGAGCGGGGCTCAGCGCGCTGCA	2219
Db	2160	GGAATTGGTCAACGCGCGGATGTATTGACCTGTTTCAGACGAGCGGGGCTCAGCGCGCTGCA	2219
QY	2220	CCTGGCCGGCCGAGGGCCGGCAAGACGAGTGAAGACTTCTCTCAGGCAATGGGCCCCA	2279
Db	2220	CCTGGCCGGCCGAGGGCCGGCAAGACGAGTGAAGACTTCTCTCAGGCAATGGGCCCCA	2279
QY	2280	CATCAACCTGCAGAGCTTCAAGTTTCAGGGCGGGCATGGGCCCGCGCCACACTCTTCGCG	2339
Db	2280	CATCAACCTGCAGAGCTTCAAGTTTCAGGGCGGGCATGGGCCCGCGCCACACTCTTCGCG	2339
QY	2340	GCGAAGCAAGACCTTGA	2355
Db	2340	GCGAAGCAAGACCTTGA	2355

QY	1	ATGGAGAGCGGACCGCGCGAGCCCATGAGGCGCTGCGCTGCGACCTTCGACGCGGCG	60
Db	1	ATGCGAGGCGGACCGCGCGAGCCCATGAGGCGCTGCGCTGCGACCTTCGACGCGGCG	60
QY	61	GAGTTCACGCGGCTGGGAGAAAGTGGGCTCGGCGCGCTTCGGGCAAGTGTTCAAAGTCCG	120
Db	61	GAGTTCACGCGGCTGGGAGAAAGTGGGCTCGGCGCGCTTCGGGCAAGTGTTCAAAGTCCG	120
QY	121	CATGTCACCTGGAAGACTGGCTGCGCATGATGTCTCGCCAGCTGCACTGCAAGAC	180
Db	121	CATGTCACCTGGAAGAAGCTGGCTGCGCATGATGTCTCGCCAGCTGCAAGTGAAGAC	180
QY	181	AGGAGCGCATGAGCTTTTGGAAAGAACCAAGATGAGATGGCCAAAGTTTCGCTAC	240
Db	181	AGGAGCGCATGAGCTTTTGGAAAGAACCAAGATGAGATGGCCAAAGTTTCGCTAC	240
QY	241	ATCTCCTCTGTATGATGAGCATCTGCCGGAACCTGTCCGCTGTGCATGAGATCATGAG	300
Db	241	ATCTCCTCTGTATGATGAGCATCTGCCGGAACCTGTCCGCTGTGCATGAGATCATGAG	300
QY	301	ACGGGCTCCCTGGAAAAGCTGTGGCTTCGGAGCCATTGCCAATTCGCGTTCCGA	360

D	b	301	ACGGGCTCCCTGGAAAGCTGCTGGCTTTGGAGCAATTGGCATGGGATCTCCGGTTCCGA	360
Q	y	361	ATCATCCAGAGACGGCGGTGGGCATGAACTTTCTTGCACTGCATGGCCCGGCACCTCTG	420
D	b	361	ATCATCCAGAGACGGCGGTGGGCATGAACTTTCTTGCACTGCATGGCCCGGCACCTCTG	420
Q	y	421	CACCTGACCTCAGAGCCCGCAAGCATCTGCTGATGCGCCACTACACGTCAGATTTCT	480
D	b	421	CACCTGACCTCAGAGCCCGCAAGCATCTGCTGATGCGCCACTACACGTCAGATTTCT	480
Q	y	481	GATTTTGGTCTGGCCAAAGTCAGACGGGCTGTCCACTCGCATGAACCTTCAGATGAGC	540
D	b	481	GATTTTGGTCTGGCCAAAGTCAGACGGGCTGTCCACTCGCATGAACCTTCAGATGAGC	540
Q	y	541	CTGTTTGGGCAATGGCCCTACCTCCCTCCAGAGGSCATCAAGGAGAAAGCCGCTCTTC	600
D	b	541	CTGTTTGGGCAATGGCCCTACCTCCCTCCAGAGGSCATCAAGGAGAAAGCCGCTCTTC	600
Q	y	601	GACCAACGACGATGTATACAGTTTGCATCTGTCATCTGGGCGTGTCCACAGAG	660
D	b	601	GACCAACGACGATGTATACAGTTTGCATCTGTCATCTGGGCGTGTCCACAGAG	660
Q	y	661	AAGCGTTTGCAGATGAGAAACATCTTGCACTATGATGAAAGTGTGAAGGGCAC	720
D	b	661	AAGCGTTTGCAGATGAGAAACATCTTGCACTATGATGAAAGTGTGAAGGGCAC	720
Q	y	721	CGCCCCGAGGTGCGCGCTGTGCAGAGCCGGCGCGCGCTGCAGCACCCTGATACG	780
D	b	721	CGCCCCGAGGTGCGCGCTGTGTGCAGAGCCGGCGCGCGCTGCAGCACCCTGATACG	780
Q	y	781	CTCATGACGGGTGCTGGAGGGGATCCGCGATTAGGCCCATCTTCAAGAAATTACT	840
D	b	781	CTCATGACGGGTGCTGGAGGGGATCCGCGATTAGGCCCATCTTCAAGAAATTACT	840
Q	y	841	TCGAAACCGAGGACCTGTGTGAAAAAGCTGTATGCAGAAAGAAACATGCTCATGAT	900
D	b	841	TCGAAACCGAGGACCTGTGTGAAAAAGCTGTATGCAGAAAGAAACATGCTCATGAT	900
Q	y	901	CTGGAAGTGAAGAGCCGCCCGAGGCCAGAGACGAGGTGTGTGCTGCAGGCTCAAGCG	960
D	b	901	CTGGAAGTGAAGAGCCGCCCGAGGCCAGAGACGAGGTGTGTGCTGCAGGCTCAAGCG	960
Q	y	961	GCCCTTGGCCCCACTTTCGATTAACGACTTCTCGAGCTTCTTCAACATGGAC	1020
D	b	961	GCCCTTGGCCCCACTTTCGATTAACGACTTCTCGAGCTTCTTCAACATGGAC	1020
Q	y	1021	TCGGAAGTTTCCAGGCTGTGCAGAGGCCCCGAGAGCTCAAGCCGACGCTCTTGAGTCC	1080
D	b	1021	TCGGAAGTTTCCAGGCTGTGCAGAGGCCCCGAGAGCTCAAGCCGACGCTCTTGAGTCC	1080
Q	y	1081	AAGGTGCATGTCTCCGAGTGGGAAAGAGGCTTCTGGGGGTGTCTCGGTGAGCTCGCC	1140
D	b	1081	AAGGTGCATGTCTCCGAGTGGGAAAGAGGCTTCTGGGGGTGTCTCGGTGAGCTCGCC	1140
Q	y	1141	TTCTCTTCCAGAGGATCATGTGTGCTGTCTTTCGAGCCGGAACTTCAACACGATTTG	1200
D	b	1141	TTCTCTTCCAGAGGATCATGTGTGCTGTCTTTCGAGCCGGAACTTCAACACGATTTG	1200
Q	y	1201	GGTACCAAGAGTCCAGAGAAAGCTTGTGATGTGCATGTGTCC-GGGACACAG	1259
D	b	1201	GGTACCAAGAGTCCAGAGAAAGCTTGTGATGTGCATGTGTCC-GGGACACAG	1259
Q	y	1260	CAAACTGATGAATCTCTGACGCGGAGGACCTTGGACTTGGAACAACGATGTG	1319
D	b	1260	CAAACTGATGAATCTCTGACGCGGAGGACCTTGGACTTGGAACAACGATGTG	1319
Q	y	1320	CTGTCTCACTTGCGGTGAAGGCCCGGGAAGAGATGTGCGCAAGTGGCTGTCAA	1379
D	b	1320	CTGTCTCACTTGCGGTGAAGGCCCGGGAAGAGATGTGCGCAAGTGGCTGTCAA	1379
Q	y	1380	CAATGCCAACCCCAACCTGAGCAACCTTAGGGCTTCACCCCTTTCACATGGCGTGG	1439

Db 1380 CAATGCCAACCCCACTGAGCAACCGTAAGGGGCTCCACCCCTTGGACATGGCCGTGGA 1439
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 Db 1440 GAGAGGGTGGGGGTGTCTGTGAGCTCTCTGCGCGGGAAGATCACTGTCAAAGCCAA 1499
 Qy 1500 GATGAGGACCAATGAGACAGCCCTTCACTTTTGCAGCCCAAGCGGGATGAGTCTAGAC 1559
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 Qy 1560 ACGGCTGTGTGAGGAGAAAGCCTCGGTCAAGAGGTGAGCTTTGAGGGCCGAGCC 1619
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 Qy 1620 CATGCACTGGCTCTGCGACGAGCGGACAGAAATATCTGGGCACTTGTGCGCGAGG 1679
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 Qy 1800 GACGCTGATGAGGAGAGAGCCATTGCACTGCGCCGACAGCGCGGGCACTACCGGCTGAC 1859
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 Qy 1860 CCGCATCTCTCATGACCTGTGCTCCGAGCTCAAGCTGTGCACTGCTGTGCGACAGACACC 1919
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 Qy 2040 CGGACACCTGCGCACTGTGACCTGTGCTGCGAGAGAGCGGCTGTGCGAGCGGCG 2099
 Db 2040 CGGACACCTGCGCACTGTGACCTGTGCTGCGAGAGAGCGGCTGTGCGAGCGGCG 2099
 Qy 2100 ACCCTTGAACCAAGAGCGGCTGACCTGCGCGCGCCACCGGGCACTGCGAGGCTGTGGA 2159
 Db 2100 ACCCTTGAACCAAGAGCGGCTGACCTGCGCGCGCCACCGGGCACTGCGAGGCTGTGGA 2159
 Qy 2160 GAGATTGTGACAGCGCGGATGATGACCTGTGCGAGAGAGGGGCTCAGGCGCTGGA 2219
 Db 2160 GAGATTGTGACAGCGCGGATGATGACCTGTGCGAGAGAGGGGCTCAGGCGCTGGA 2219
 Qy 2220 CTTGGCCCGCCAGGCGCGGACGCAAGAGCGGTGAGACTCTGTCTCAGGCACTGGGCGCA 2279
 Db 2220 CTTGGCCCGCCAGGCGCGGACGCAAGAGCGGTGAGACTCTGTCTCAGGCACTGGGCGCA 2279
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 Db 2340 GCGAAGCAAGACTAG 2355

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 ; Publication No. US20030199462A1
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 ; APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro
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 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 17
 LENGTH: 2355
 TYPE: DNA
 ORGANISM: Homo sapiens
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 Query Match 98.7%; Score 2324; DB 16; Length 2355;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
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 Db 1 ATGAGAGGCGACGCGCGGACCCCATGAGGACCTGCGCTGCGCACTTTCAGCGCGGCG 60
 Qy 61 GAGTTCAAGGCTGGAGAAAGTGGGCTCGGCGGCTTTCGAGAGGTGTACAGGTGCGC 120
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 Qy 181 AGGAGGCGCATGAGCTTTTGAAGAGCAAGAGATGAGATGAGCAAGTTTCGCTAC 240
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Qy 301 ACGGGCTTCCCTGGAAGAGCTCTG3CTTCCGAGCCATTGCCATG3GANTCTCCGTTCCGA 360
Db 301 ACGGGCTTCCCTGGAAGAGCTCTG3CTTCCGAGCCATTGCCATG3GANTCTCCGTTCCGA 360
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Qy 1980 CGCTG3GCAAGAGAGCGCTGACCTTCAAGCG3CTACACCG3CTG3GCACTG3GCTG3 2039
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Qy 2040 CGGACACTG3GCACTGTCAAGCTGTGTTGTGAGAGAGAGCG3CATGTGCTG3GCG3G 2099
Db 2040 CGGACACTG3GCACTGTCAAGCTGTGTTGTGAGAGAGAGCG3CATGTGCTG3GCG3G 2099
Qy 2100 ACCCTTGAACCAAGCG3GCTG3GCACTG3GCTG3GCG3GCACTG3GAGTGTG3G 2159
Db 2100 ACCCTTGAACCAAGCG3GCTG3GCACTG3GCTG3GCG3GCACTG3GAGTGTG3G 2159
Qy 2160 GGAATGTGTGAGCG3CGATGCTTGAAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2219
Db 2160 GGAATGTGTGAGCG3CGATGCTTGAAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2219
Qy 2220 CTTG3CG3GCG3GCG3GCG3GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2279
Db 2220 CTTG3CG3GCG3GCG3GCG3GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2279
Qy 2280 CATCAACTGTGAGAGCTTCAAGTTTCAAGAGCG3GCG3GCG3GCG3GCACTG3G 2339
Db 2280 CATCAACTGTGAGAGCTTCAAGTTTCAAGAGCG3GCG3GCG3GCG3GCACTG3G 2339
Qy 2340 GCGAAGCAAGCACTAG 2355
Db 2340 GCGAAGCAAGCACTAG 2355

RESULT 15
US-10-128-174-21
; Sequence 21, Application US/10128174

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Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Itohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UN-06967
CURRENT APPLICATION NUMBER: US/10/128,174
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
US-10-128-174-21

Query Match      98.7%; Score 2324; DB 16; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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DB      1 ATGAGGGCGACGGCGGACCCCATGAGCCCTGGCGCTGCTGCGCACTTGTGACGGGGC 60
QY      61 GAGTTCAAGGGCTGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGTGGC 120
DB      61 GAGTTCAAGGGCTGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGTGGC 120
QY      121 CATGTCCATGGAAGACCTGGCTGGCCATCAAGTGTCTGCCAGCCTTGACGTGACGAC 180
DB      121 CATGTCCATGGAAGACCTGGCTGGCCATCAAGTGTCTGCCAGCCTTGACGTGACGAC 180
QY      181 AGGAGCGGCATGAGGCTTTTGGAGAAAGCCAAAGAAAGTGAAGTGGCCAAAGTTTCGCTAC 240
DB      181 AGGAGCGGCATGAGGCTTTTGGAGAAAGCCAAAGAAAGTGAAGTGGCCAAAGTTTCGCTAC 240
QY      241 ATCTGCTGTGTATGTCATCTGCCGGAACCTGTGGCTGTGTCATGAGATGATGAG 300
DB      241 ATCTGCTGTGTATGTCATCTGCCGGAACCTGTGGCTGTGTCATGAGATGATGAG 300
QY      301 ACGGGCTCCCTGGAAGAGCTGCTGGCTTGGAGCCATTGCCATGGGATCTTCGGTTCCGA 360
DB      301 ACGGGCTCCCTGGAAGAGCTGCTGGCTTGGAGCCATTGCCATGGGATCTTCGGTTCCGA 360
QY      361 ATCATCCAGGAGCGCGGTGGGCAATGAATTCCTGCACTGCAATGAGCCCGGCACTCTCG 420
DB      361 ATCATCCAGGAGCGCGGTGGGCAATGAATTCCTGCACTGCAATGAGCCCGGCACTCTCG 420
QY      421 CACCTGGACTCAAGCCCGGGAACATCTGCTGATGTCCTACCTACAGTCAAGATTTCT 480
DB      421 CACCTGGACTCAAGCCCGGGAACATCTGCTGATGTCCTACCTACAGTCAAGATTTCT 480
QY      481 GATTTTGTGTGGCCAGTGCACGCGGCTGTCCACTGTGACATCTCAAGCATGGATGGC 540
DB      481 GATTTTGTGTGGCCAGTGCACGCGGCTGTCCACTGTGACATCTCAAGCATGGATGGC 540
QY      541 CTGTTTGGCAATTCCTACCTCCCTCAAGGCGCATCAAGAGAAAGCGGCTCTTC 600
DB      541 CTGTTTGGCAATTCCTACCTCCCTCAAGGCGCATCAAGAGAAAGCGGCTCTTC 600
QY      601 GACACCAAGCAGATGTATACAGCTTTGCGATCTGTGATCTGTGGGCTGTCTACAAGAG 660
DB      601 GACACCAAGCAGATGTATACAGCTTTGCGATCTGTGATCTGTGGGCTGTCTACAAGAG 660
QY      661 AAGCGTTTGCATGATGAGAAACAATCTTGCACATCATGTGAAAGTGTGAAGGGCCAC 720
DB      661 AAGCGTTTGCATGATGAGAAACAATCTTGCACATCATGTGAAAGTGTGAAGGGCCAC 720
QY      721 GCGCCCGAGCTGCGCGCGGTGTGCAAGAGCCGGCGCGGCGCTGAGGCACTGATAGC 780
DB      721 GCGCCCGAGCTGCGCGCGGTGTGCAAGAGCCGGCGCGGCGCTGAGGCACTGATAGC 780
QY      781 CTCATGACAGCGGTGTGCAAGGGGATCCGCGAGTTAGGCCCACTTCCAAAGAAATTACT 840
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DB      781 CTCATGACAGCGGTGTGCAAGGGGATCCGCGAGTTAGGCCCACTTCCAAAGAAATTACT 840
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DB      841 TCTGAAACCGAGACCTGTGTGAAAAGCCTGATGACGAAGTGAAGAAATCTGCTCATGAT 900
QY      901 CTGAGCGTGAAGAACCCCGGAGCCCAAGAGCGAGTGTGCTCGAGGCTCAAGCGG 960
DB      901 CTGAGCGTGAAGAACCCCGGAGCCCAAGAGCGAGTGTGCTCGAGGCTCAAGCGG 960
QY      961 GCCTTGCCCCCACTTGCATTAACGACTAAGCTTCTCCAGCTTCTCAAGCTTGAC 1020
DB      961 GCCTTGCCCCCACTTGCATTAACGACTAAGCTTCTCCAGCTTCTCAAGCTTGAC 1020
QY      1021 TCTGAGATTTCCAGAGCTGTGAGGGCCCGAGAGACTACGCGGAGCTCTTGAGTCC 1080
DB      1021 TCTGAGATTTCCAGAGCTGTGAGGGCCCGAGAGACTACGCGGAGCTCTTGAGTCC 1080
QY      1081 AAGCTGCATCGTCCGGCAGTGGGAAAGGCTCTCGGGGGTGTCTCGGTGACTCGGC 1140
DB      1081 AAGCTGCATCGTCCGGCAGTGGGAAAGGCTCTCGGGGGTGTCTCGGTGACTCGGC 1140
QY      1141 TTCTTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAACTTTCAACACGATCTG 1200
DB      1141 TTCTTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAACTTTCAACACGATCTG 1200
QY      1201 GGTACCAAGAGCTCAAGAAAGAAAGCTTGTGAGTGCATGATGTGCC-GGAGACACAG 1259
DB      1201 GGTACCAAGAGCTCAAGAAAGAAAGCTTGTGAGTGCATGATGTGCC-GGAGACACAG 1259
QY      1260 CAAACTGATGAATCCTGACGCGGACGAGACGTTGACCTTGACACAGCGGTGCGAG 1319
DB      1260 CAAACTGATGAATCCTGACGCGGACGAGACGTTGACCTTGACACAGCGGTGCGAG 1319
QY      1320 CTTGTGCACTTGGCGGTGAGGCGCGGCAAGAGTGTGCGCAATGCTGCTCAA 1379
DB      1320 CTTGTGCACTTGGCGGTGAGGCGCGGCAAGAGTGTGCGCAATGCTGCTCAA 1379
QY      1380 CAATGCCAACCCCAACCTGAGCAACGTTAGGGGCTCAACCCGTTGCAATGCGTGA 1439
DB      1380 CAATGCCAACCCCAACCTGAGCAACGTTAGGGGCTCAACCCGTTGCAATGCGTGA 1439
QY      1440 GAGGAGGGTGTGGGGTGTCTGTGAGGCTCTGTGAGCAGAGATCAAGTGTCAACGCGCA 1499
DB      1440 GAGGAGGGTGTGGGGTGTCTGTGAGGCTCTGTGAGGCTCTGTGAGTGTCAACGCGCA 1499
QY      1500 GATGAGGACCAAGTGCACAGCCCTTCCAATTGCAAGCCAGAACGCGGATGATGTAGCAC 1559
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QY      1560 ACGGCTGCTTTTGAAGAAAGACCCCTCGGTCAACGAGTGTGAACCTTTGAGGGCGGAGCGCC 1619
DB      1560 ACGGCTGCTTTTGAAGAAAGACCCCTCGGTCAACGAGTGTGAACCTTTGAGGGCGGAGCGCC 1619
QY      1620 CATGCAAGTGGCTGCGACGAGCCGAGAAATATGTGTGCGATCTGTGGCGGAGG 1679
DB      1620 CATGCAAGTGGCTGCGACGAGCCGAGAAATATGTGTGCGATCTGTGGCGGAGG 1679
QY      1680 CGTGACGTGAGCCTGCAAGGCAAGATGCTGTGCTGCACTGCACTACCTGTGCGCA 1739
DB      1680 CGTGACGTGAGCCTGCAAGGCAAGATGCTGTGCTGCACTGCACTACCTGTGCGCA 1739
QY      1740 GGGGCAACCTGCCCATGCTCAAGCTGCGGCAAGAGCGGGGGTGAAGTGAACGCCCA 1799
DB      1740 GGGGCAACCTGCCCATGCTCAAGCTGCGGCAAGAGCGGGGGTGAAGTGAACGCCCA 1799
QY      1800 GACGCTGATGAGGAGAGCGCATTTGCACTTGGCGGCAACGCGGCGGCACTAACGCGTGGC 1859
DB      1800 GACGCTGATGAGGAGAGCGCATTTGCACTTGGCGGCAACGCGGCGGCACTAACGCGTGGC 1859
QY      1860 CCGCATCTCATGACCTGTGTCTCCAGCTCAAGTGTGACGCTGTGGCAAGACACC 1919
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Db	1860	CCGATCTCTATCGAAGCTGTGTCCGAGGTCAAGCTCTGAGCTGTGGACAAGACAC	1919
QY	1920	CCTGCAAGTGGCCCGGAGAGCGGGGACACAGACATGCTCAGGCTGTCTTGCATCGGGG	1979
Db	1920	CCTGCAAGTGGCCCGGAGAGCGGGGACACAGACATGCTCAGGCTGTCTTGCATCGGGG	1979
QY	1980	CGCTGGCAAGAGGCGCTGACCTTCAAGAGGCTACACCGCTCTGCACTTGGGCTGCCCGCA	2039
Db	1980	CGCTGGCAAGAGGCGCTGACCTTCAAGAGGCTACACCGCTCTGCACTTGGGCTGCCCGCA	2039
QY	2040	CGGACACCTGGCCACTGTCAAGCTGCTTGTGAGGAGAGGCGGATGTGCTGGCCCGGGG	2099
Db	2040	CGGACACCTGGCCACTGTCAAGCTGCTTGTGAGGAGAGGCGGATGTGCTGGCCCGGGG	2099
QY	2100	ACCCCTGAACGAGCGGGGCTGACCTTGGCTGCGGCACTCGAGGTGTGA	2159
Db	2100	ACCCCTGAACGAGCGGGGCTGACCTTGGCTGCGGCACTCGAGGTGTGA	2159
QY	2160	GAGTGTGTCAAGCGGCGGATGTCAATTGACCTGTTCGACGAGCGGGCTCAAGCGGCTGCA	2219
Db	2160	GAGTGTGTCAAGCGGCGGATGTCAATTGACCTGTTCGACGAGCGGGCTCAAGCGGCTGCA	2219
QY	2220	CCTGGCCGCGGCGGAGCGGCAAGAGCGGTGAGACTGTCTCAGGCAATGGGCGCA	2279
Db	2220	CCTGGCCGCGGCGGAGCGGCAAGAGCGGTGAGACTGTCTCAGGCAATGGGCGCA	2279
QY	2280	CATCAACCTGCAAGCCTCAAGTTTCAAGGGCGGCAATGGCCCGGCCACACTCTTGGG	2339
Db	2280	CATCAACCTGCAAGCCTCAAGTTTCAAGGGCGGCAATGGCCCGGCCACACTCTTGGG	2339
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Search completed: September 17, 2005, 02:19:15
 Job time : 5370.39 secs

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Qy 481 GATTTTGGTCTGGCCAAATGCAAGGGTGTCCCACTGCACTGACATCTGAGATGATGGC 540
Db 481 GATTTTGGTCTGGCCAAATGCAAGGGTGTCCCACTGCACTGACATCTGAGATGATGGC 540
Qy 541 CTGTTTGGCAATCGCCTTACCTCCCTCCAGAGGCACTAGAGAAAGCGGCTCTTC 600
Db 541 CTGTTTGGCAATCGCCTTACCTCCCTCCAGAGGCACTAGAGAAAGCGGCTCTTC 600
Qy 601 GACAACAAGCAGATGATATACAGCTTTGCGATCGTCACTTGGGGCGTGTCAACAAG 660
Db 601 GACAACAAGCAGATGATATACAGCTTTGCGATCGTCACTTGGGGCGTGTCAACAAG 660
Qy 661 AAGCGTTTGCAGATGAGAAACAATCTGCAATCATGTGAAAGTGTGAAGGCGAC 720
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Qy 1681 GTGAGCTGAGCTTGCAGAGGCAAGATGCTGTGCTGCACTGCACTACGCTGTGCGAG 1740
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Qy 2341 CGAAGCAAGACTAG 2355
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RESULT 2
US-09-781-882-1
; Sequence 1, Application US/09781882
; Patent No. 6630335
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 14171 Protein Kinase and Uses Thereof
; FILE REFERENCE: 035800-209014(5800-6
; CURRENT APPLICATION NUMBER: US/09/781,882

; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: U.S. 60/182,096
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3860
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (17)..(2371)
 ; OTHER INFORMATION:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(3860)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-781-882-1

Query Match 100.0%; Score 2355; DB 4; Length 3860;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	77	GAGTTCACGGGCTGGGAGAGGTGGGCTTGGGGCGCTTCGGGCAAGTGTACAAAGTTCGC	136
QY	121	CATGTCCTCATGGAAGCTGGGCTGGCATCAAGTGTCTCCGCAAGCTTCGACCTTCGACGAC	180
DB	137	CATGTCCTCATGGAAGCTGGGCTGGCATCAAGTGTCTCCGCAAGCTTCGACCTTCGACGAC	196
QY	181	AGGAGCGCATGGAGCTTTTGGAGAGGCAAGAGATGAGATGGGCAAGTTTCGCTAC	240
DB	197	AGGAGCGCATGGAGCTTTTGGAGAGGCAAGAGATGAGATGGGCAAGTTTCGCTAC	256
QY	241	ATCTGCGCTGTGTATGGCATCTGCGCGAACCCTGTGCGCTGTGTCATGAGTACATGAG	300
DB	257	ATCTGCGCTGTGTATGGCATCTGCGCGAACCCTGTGCGCTGTGTCATGAGTACATGAG	316
QY	301	ACGGGCTCCCTGGAAAAAGCTGCTGGCTTGGAGACCATTTGCAATGGATTCCTGGTTCCGA	360
DB	317	ACGGGCTCCCTGGAAAAAGCTGCTGGCTTGGAGACCATTTGCAATGGATTCCTGGTTCCGA	376
QY	361	ATCATCCAGAGACGGCGGTGGGCAATGAACTTCTGTCAGTCGATGGGCGCGCACTCTG	420
DB	377	ATCATCCAGAGACGGCGGTGGGCAATGAACTTCTGTCAGTCGATGGGCGCGCACTCTG	436
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DB	437	CACCTGGAACCTCAAGCCCGGAGACATCTGCTGGATGCCCACTACAGCTCAAGATTCT	496
QY	481	GATTTGTGCTGGCCAAAGTGCACCGGCTGTCCCATCTCGCATGAACTTCAAGATGAGC	540
DB	497	GATTTGTGCTGGCCAAAGTGCACCGGCTGTCCCATCTCGCATGAACTTCAAGATGAGC	556
QY	541	CTGTTTGGGCAATGGCTTACCTCCCTCCAGAGCGCATGAGGAGAAAGCGGCTCTTC	600
DB	557	CTGTTTGGGCAATGGCTTACCTCCCTCCAGAGCGCATGAGGAGAAAGCGGCTCTTC	616
QY	601	GACACCAAGACGATGATATACAGCTTTCGATGTCATCTGGGGCGTGTCAACAGAA	660
DB	617	GACACCAAGACGATGATATACAGCTTTCGATGTCATCTGGGGCGTGTCAACAGAA	676
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DB	677	AAGCGCTTTGCAATGAGAAACATCTCTGCAATCATGATGAAAGTGTGAAAGGGCGAC	736
QY	721	CGCGCCGAGCTGCGCGCGGTGTGAGAGCCCGGCGCGGCTGACAGCCACTGATACCG	780
DB	737	CGCGCCGAGCTGCGCGCGGTGTGAGAGCCCGGCGCGGCTGACAGCCACTGATACCG	796

QY	781	CTCATGAGCGGTCTGGACAGGGGATCCGCAAGTTAGGCCCACTTCCAGAAATTACT	840
DB	797	CTCATGAGCGGTCTGGACAGGGGATCCGCAAGTTAGGCCCACTTCCAGAAATTACT	856
QY	841	TCTGAAACCGAGGACCTGTGTGAAAGCTGTATGACGAGTGAAGAAACTGCTCATGAT	900
DB	857	TCTGAAACCGAGGACCTGTGTGAAAGCTGTATGACGAGTGAAGAAACTGCTCATGAT	916
QY	901	CTGACCTGAAAGACCCCCCGAGGCCAGAGAGCGAGGTGTGCTGGAGGCTCAAGCGG	960
DB	917	CTGACCTGAAAGACCCCCCGAGGCCAGAGAGCGAGGTGTGCTGGAGGCTCAAGCGG	976
QY	961	GCTCTGCCCCCACTTGCATTAACGATCAAGCTCTCCAGCTTCTCTCAAGCTGAGC	1020
DB	977	GCTCTGCCCCCACTTGCATTAACGATCAAGCTCTCTCCAGCTTCTCTCAAGCTGAGC	1036
QY	1021	TCTGAGATTTCCAGGCTGTGAGAGGCCCGAGAGGCTCAGCCGCAAGCTCTCTGAGTCC	1080
DB	1037	TCTGAGATTTCCAGGCTGTGAGAGGCCCGAGAGGCTCAGCCGCAAGCTCTCTGAGTCC	1096
QY	1081	AAGCTGCATGTCTCCGAGTGGGAGAGGCTCTCGGGGGTGTCTCGTGGACCTCGGCC	1140
DB	1097	AAGCTGCATGTCTCCGAGTGGGAGAGGCTCTCGGGGGTGTCTCGTGGACCTCGGCC	1156
QY	1141	TTCTCTCCAGAGATCATGTGTGCTGCTTTGAGCGGAACTTCAACAGAGATCTG	1200
DB	1157	TTCTCTCCAGAGATCATGTGTGCTGCTTTGAGCGGAACTTCAACAGAGATCTG	1216
QY	1201	GATACCAAGACGTCCAGAAAGAAAGCTTGTGATGTCATGCTGTCCGAGACACAGC	1260
DB	1217	GATACCAAGACGTCCAGAAAGAAAGCTTGTGATGTCATGCTGTCCGAGACACAGC	1276
QY	1261	AAACTGATGAAGATCTTACAGCCCGCAAGACCTGTGACCTGTGACAGGGGTGCCAGC	1320
DB	1277	AAACTGATGAAGATCTTACAGCCCGCAAGACCTGTGACCTGTGACAGGGGTGCCAGC	1336
QY	1321	CTGCTGCACTGGGCGGTGAGAGCGCGGCAAGAGAGTGCAGAACTGCTCTGCTCAAC	1380
DB	1337	CTGCTGCACTGGGCGGTGAGAGCGCGGCAAGAGAGTGCAGAACTGCTCTGCTCAAC	1396
QY	1381	AATGCCAACCCCAACTTGAAGCAACCGTAGGGGCTTCAACCCGTTGACATGGCGGTGAG	1440
DB	1397	AATGCCAACCCCAACTTGAAGCAACCGTAGGGGCTTCAACCCGTTGACATGGCGGTGAG	1456
QY	1441	AGAGGGTGGGGGTGTGTGTGAGCTCTGCTGGGACGAAAGATGATGATACCCCAAG	1500
DB	1457	AGAGGGTGGGGGTGTGTGTGAGCTCTGCTGGGACGAAAGATGATGATACCCCAAG	1516
QY	1501	GATGAGGACCAATGAGCAGCCCTCCATTGAGCCGAGAAACGGGATGATGCTAGACAA	1560
DB	1517	GATGAGGACCAATGAGCAGCCCTCCATTGAGCCGAGAAAGATGATGATGCTAGACAA	1576
QY	1561	CGGCTGCTGTGGAAGAAAGCTCTCGGTCAACGAGTGAAGCTTGAAGGGCGGACGCC	1620
DB	1577	CGGCTGCTGTGGAAGAAAGCTCTCGGTCAACGAGTGAAGCTTGAAGGGCGGACGCC	1636
QY	1621	ATGCACTGGCTTCCAGACAGGGGAGAAATATCTGTGCGCATCTCTGCGCGGAGGC	1680
DB	1637	ATGCACTGGCTTCCAGACAGGGGAGAAATATCTGTGCGCATCTCTGCGCGGAGGC	1696
QY	1681	GTTGAGCGTGAAGCTTCCAGAGGAGAAATGCTGGGCTGCACTGCACTACCTCTGCGAG	1740
DB	1697	GTTGAGCGTGAAGCTTCCAGAGGAGAAATGCTGGGCTGCACTGCACTACCTCTGCGAG	1756
QY	1741	GGCACCTGCCCATGTCAAGCTGTGCGCAAGCAGCGGGGTGATGTGAACCCCGAG	1800
DB	1757	GGCACCTGCCCATGTCAAGCTGTGCGCAAGCAGCGGGGTGATGTGAACCCCGAG	1816
QY	1801	ACGCTGATGGAGAGACGCAATTGCACTGTGCGCAAGCGGGGCACTAACCGCGTGGCC	1860
DB	1817	ACGCTGATGGAGAGACGCAATTGCACTGTGCGCAAGCGGGGCACTAACCGCGTGGCC	1876

QY	1861	UGCATCTCATTCGACCTTGCTCCGACGTCAACGTCTGACCTCTGAGCAACAACACC	1920
Db	1877	CGCATCTCATTCGACCTTGCTCCGACGTCAACGTCTGACCTCTGAGCAACAACACC	1936
QY	1921	CTGCACGTGGCCGCGAGAACCGGAGCAACGAGCACTGGCAGGCTTCTTCATCCGGAGC	1980
Db	1937	CTGCACGTGGCCGCGAGAACCGGAGCAACGAGCACTGGCAGGCTTCTTCATCCGGAGC	1996
QY	1991	GCTGGCAAGAGAGCCGTGACCTTCAGACGGCTTACACCGCTCTGGACCTGGGCTGCCCGAAC	2040
Db	1997	GCTGGCAAGAGAGCCGTGACCTTCAGACGGCTTACACCGCTCTGGACCTGGGCTGCCCGAAC	2056
QY	2041	GGAACACTGGGCACTGTCTAGCTGCTTTCGAGAGAGAGGCCGATGTGCTTGCCCGGAGA	2100
Db	2057	GGAACACTGGGCACTGTCTAGCTGCTTTCGAGAGAGAGGCCGATGTGCTTGCCCGGAGA	2116
QY	2101	CCCTTGAAACAGACGGCCCTGCACTGGCTGCCGCCACCGGGCACTGAGAGTGTGTGAG	2160
Db	2117	CCCTTGAAACAGACGGCCCTGCACTGGCTGCCGCCACCGGGCACTGAGAGTGTGTGAG	2176
QY	2161	GAGTTGTGCAGGCGCGATGTCAATTGAACCTGTTCGACGAGCAGGGGCTCAGCGCCTGCAC	2220
Db	2177	GAGTTGTGCAGGCGCGATGTCAATTGAACCTGTTCGACGAGGAGGGGCTCAGCGCCTGCAC	2236
QY	2221	CTGGCCGCCAAGGCGCGGACGCAACAGCGGTGAGACTTGTCTCAGGCATGGGACCAC	2280
Db	2237	CTGGCCGCCAAGGCGCGGACGCAACAGCGGTGAGACTTGTCTCAGGCATGGGACCAC	2296
QY	2281	ATCAACCTGCAGAGGCTCAAGTTCAGAGGGCGGCATGGCCCGCGCGCAACTCTCTGGG	2340
Db	2297	ATCAACCTGCAGAGGCTCAAGTTCAGAGGGCGGCATGGCCCGCGCGCAACTCTCTGGG	2356
QY	2341	CGAAGCAAGACCTTAG	2355
Db	2357	CGAAGCAAGACCTTAG	2371

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RESULT 3
US-09-949-016-1103
; Sequence 1103, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1103
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1103

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	Query Match	Similarity	99.9%	Score 2330.4	DB 4	Length 3879
	Best Local	Similarity	99.9%	Pred. No. 0		
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Qy	1	ATGAGGCGCAGCGCGSACCCATG93GCTCTGCGCGACCTTGACGCG39C	60			
Db	49	ATGAGGCGCAGCGCGGACCCCATG93GCTCTGCGCGACCTTGACGCG39C	108			
Qy	61	GAGTTCA CGGCGTGGAGAGAGTGGGCTCGGCGCGCTTCGGGAGGTGTA CAAAGTTCGC	120			
Db	109	GAGTTCA CGGCGTGGAGAGAGTGGGCTCGGCGCGCTTCGGGAGGTGTA CAAAGTTCGC	168			

QY	121	CATGTCGACTGGAAGACCTGCTGCGCCATCAAGTGTCTGCGCCAGCTTGACGTTCGACGAC	180
Db	169	CATGTCCACTGGAAGACCTGTGCTGGCCATCAAGTGCTCGCCACGCTGCACGTTCGAGAC	228
QY	181	AGGAGCGGCATGAGAGCTTTTGGAGGAAGCCAAAGAAATGAGATGAGGCGCAAGTTTCGCTAC	240
Db	229	AGGAGCGGCATGAGAGCTTTTGGAGGAAGCCAAAGAAATGAGATGAGGCGCAAGTTTCGCTAC	288
QY	241	ATCTGCTGTGTATGTGACATCTGCTCGCGAACCTGTCTGACTGTATGAGTACATGAG	300
Db	289	ATCTGCTGTGTATGTGACATCTGCTCGCGAACCTGTCTGACTGTATGAGTACATGAG	348
QY	301	ACGGGCTCCCTGGAAAAGCTGTGAGGCTTTGGAGGCATTGGCCATGGGAAATCTCCGGTTCCGA	360
Db	349	ACGGGCTCCCTGGAAAAGCTGTGAGGCTTTGGAGGCATTGGCCATGGGAAATCTCCGGTTCCGA	408
QY	361	ATCATCCACGAGACGGCGGTGGGAGATGAACTTCTTGCACTGCAATGAGGCCCGCCCACTCTG	420
Db	409	ATCATCCACGAGACGGCGGTGGGAGATGAACTTCTTGCACTGCAATGAGGCCCGCCCACTCTG	468
QY	421	CACCTGGAACCTGAAAGCCCGCGAATATCTGTGTGATGCGCACTACACGTCAAGATTTCT	480
Db	469	CACCTGGAACCTGAAAGCCCGCGAATATCTGTGTGATGCGCACTACACGTCAAGATTTCT	528
QY	481	GATTTTGGTCTGGCAAGTGTGACGGGCTGTCCCACTCGCATGACCTCAGCATGATGATGCG	540
Db	529	GATTTTGGTCTGGCAAGTGTGACGGGCTGTCCCACTCGCATGACCTCAGCATGATGATGCG	588
QY	541	CTGTTTGGCAATATCGCCTTACTCTCCCTTCAGAGCGCATCAGGAGAAAGCCGCTCTTC	600
Db	589	CTGTTTGGCAATATCGCCTTACTCTCCCTTCAGAGCGCATCAGGAGAAAGCCGCTCTTC	648
QY	601	GACACCAAGCAAGATGTATACAGCTTTGGCATGTCTCATGTGGGGCGGTCTCACACAAAG	660
Db	649	GACACCAAGCAAGATGTATACAGCTTTGGCATGTCTCATGTGGGGCGGTCTCACACAAAG	708
QY	661	AAGCGTTTGGCATGGAAGAAACATCTGTCACTCATGTGTGAAGGTGTGAAGGGCCAC	720
Db	709	AAGCGTTTGGCATGGAAGAAACATCTGTCACTCATGTGTGAAGGTGTGAAGGGCCAC	768
QY	721	CGCCCGGAGCTGCGCCCGCTGTGAGAGCCCGGCGCGGCTCTGACACCACTGTATACG	780
Db	769	CGCCCGGAGCTGCGCCCGCTGTGAGAGCCCGGCGCGGCTCTGACACCACTGTATACG	828
QY	781	CTCATGACGCGGTCTGTGACGAGGAGATCCGCGAATTAGGCCCACTTCCAAGAAATTA	840
Db	829	CTCATGACGCGGTCTGTGACGAGGAGATCCGCGAATTAGGCCCACTTCCAAGAAATTA	888
QY	841	TCTGAAACCGAGGACCTGTGTGAAGAGCTGTATGACGAATGAAAGAACTGCTCATGAT	900
Db	889	TCTGAAACCGAGGACCTGTGTGAAGAGCTGTATGACGAATGAAAGAACTGCTCATGAT	948
QY	901	CTGACGCGGAAAAGCCCCCGGAGCCCAAGAGCGAGGCGGTGCTGTGAGGCTCAACGG	960
Db	949	CTGACGCGGAAAAGCCCCCGGAGCCCAAGAGCGAGGCGGTGCTGTGAGGCTCAACGG	1008
QY	961	GCTCTGCGCCCACTTGTGATTAAGACTTCTCGAGCTTCTCTCAACAGCTTGAC	1020
Db	1009	GCTCTGCGCCCACTTGTGATTAAGACTTCTCGAGCTTCTCTCAACAGCTTGAC	1068
QY	1021	TCTGGAATTTCCCAAGGCTGTGTGAGGGCCCGAGGAGCTCAGCCGCACTCTCTGATGTC	1080
Db	1069	TCTGGAATTTCCCAAGGCTGTGTGAGGGCCCGAGGAGCTCAGCCGCACTCTCTGATGTC	1128
QY	1081	AAGCTGCATGCTCGGCAATGTGGGAAAGAGCTCTCGGAGGAGTCTCGGTGACATTCGCGC	1140
Db	1129	AAGCTGCATGCTCGGCAATGTGGGAAAGAGCTCTCGGAGGAGTCTCGGTGACATTCGCGC	1188
QY	1141	TTCTCTTTCAGAGATCACTGTGCTGTCTTTGAGCGGAAACTTTCACCAAGCATCTG	1200
Db	1189	TTCTCTTTCAGAGATCACTGTGCTGTCTTTGAGCGGAAACTTTCACCAAGCATCTG	1248

QY 541 CTGTTGGCAACATGCGCTACCTCCCTCCAGAGCGCATCAGGGAGAAAGCCGGCTCTTC 600
Db 589 CTGTTGGCAACATGCGCTACCTCCCTCCAGAGCGCATCAGGGAGAAAGCCGGCTCTTC 648
QY 601 GACACCAAGCAAGATGATATACAGCTTTGCGATCGTCACTCTGCGGCGTGTCCACAGAAAG 660
Db 649 GACACCAAGCAAGATGATATACAGCTTTGCGATCGTCACTCTGCGGCGTGTCCACAGAAAG 708
QY 661 AAGCGCTTTGCAAGATGAGAAACAATCTTGCAATCATGTGTGAAGGTGTGTAAAGGGCAC 720
Db 709 AAGCGCTTTGCAAGATGAGAAACAATCTTGCAATCATGTGTGAAGGTGTGTAAAGGGCAC 768
QY 721 CGCCCCGAGCTGCGCCCGGTGTGAGAGCCGCGCGCGCTGCAAGCCCTGATAGCG 780
Db 769 CGCCCCGAGCTGCGCCCGGTGTGAGAGCCGCGCGCGCTGCAAGCCCTGATAGCG 828
QY 781 CTATGCAAGCGGTGCTGCGAGAGGGGATCCGAGATTAGGCCACCTTCCAAAGAAATTACT 840
Db 829 CTATGCAAGCGGTGCTGCGAGAGGGGATCCGAGATTAGGCCACCTTCCAAAGAAATTACT 888
QY 841 TCTGAAACCGAGGACCTGTGTGAAAAGCTGTATGACGAAGTGAAGAAAGAACTGTCTATGAT 900
Db 889 TCTGAAACCGAGGACCTGTGTGAAAAGCTGTATGACGAAGTGAAGAAAGAACTGTCTATGAT 948
QY 901 CTGAGCGTGAAGAAAGCCCCCGAGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Db 949 CTGAGCGTGAAGAAAGCCCCCGAGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 1008
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Db 1009 GCCTCTGCCCCACCTTGATTAACGATTAAGCCTCTCCAGCTTCTCTCAACAGCTGAGC 1068
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Db 1069 TCTGGAAGTTTCCAGGCTGTGTGAGAGGGCCCGAGAGCTCAAGCCGATCTCTGAGTCC 1128
QY 1081 AAGCTGCATGTCGCGAGTGTGGAGAGAGGCTCTTGCGGGGTGTCTCGTGTGAATCCGCC 1140
Db 1129 AAGCTGCATGTCGCGAGTGTGGAGAGAGGCTCTTGCGGGGTGTCTCGTGTGAATCCGCC 1188
QY 1141 TTCTCTTCCAGAGGATCACTGTGCTGTCTTTGAGCGGAACTTCAACAGCGATCTG 1200
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QY 1201 GGTACCAAGAACCTTCCAGAGAGAGAGCTTCTGCGGGGTGTCTCGTGTGAATCCGCC 1259
Db 1249 GGTACCAAGAACCTTCCAGAGAGAGAGCTTCTGCGGGGTGTCTCGTGTGAATCCGCC 1307
QY 1260 CAAACTGATGAAGATCTGCAAGCCGAGAGAGTGTGCACTGGAACAGCGGTGCAG 1319
Db 1308 CAAACTGATGAAGATCTGCAAGCCGAGAGAGTGTGCACTGGAACAGCGGTGCAG 1367
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Db 1368 CCTGCTGCACTGCGGTGTGAGAGCCGGGCAAGAGAGTGCCTCAAGTGGCTGTCTCA 1427
QY 1380 CAATGCCAACCCCAACCTGAGAACCTGTAGGGGCTCCACCCGTTGSCACATGCGGTGGA 1439
Db 1428 CAATGCCAACCCCAACCTGAGAACCTGTAGGGGCTCCACCCGTTGSCACATGCGGTGGA 1487
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Db 1488 GAGAGAGGTGCGGGGTGTGTGTGAGAGCTCTGTGCGCAAGAAAGTCAAGTGTCAAGCCAA 1547
QY 1500 GGATGAGAGCAAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGACGGGGATGAGTCTAGAC 1559
Db 1548 GGATGAGAGCAAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGACGGGGATGAGTCTAGAC 1607
QY 1560 ACGGTGTGTGTGTGAGAGAGAGCTTGTGCTGCAAGAGTGTGACTTTGAGGGCGGAGCC 1619
Db 1608 ACGGTGTGTGTGTGAGAGAGAGCTTGTGCTGCAAGAGTGTGACTTTGAGGGCGGAGCC 1667
QY 1620 CATGCAAGTGGCTGCTCAGCAAGGAGAGAGATATCTGTGGCATCTGTGCGCGGAGG 1679

Db 1668 CATGCAAGTGGCTGCTCAGCAAGGAGAGAGATATCTGTGGCATCTGTGCGCGGAGG 1727
QY 1680 CTGTGACGTGAGCTTGTGAGAGGCAAGATGCTGTGGCTGCCACTGTCACTACGCTGTGCA 1739
Db 1728 CTGTGACGTGAGCTTGTGAGAGGCAAGATGCTGTGGCTGCCACTGTCACTACGCTGTGCA 1787
QY 1740 GGGGCACTGTGCGCATGTGTCAAGCTGTGTGGCCAGAGAGCCGGGGGTGAGTGTGAAGCCCA 1799
Db 1788 GGGGCACTGTGCGCATGTGTCAAGCTGTGTGGCCAGAGAGCCGGGGGTGAGTGTGAAGCCCA 1847
QY 1800 GAGCGTGTGATGAGAGAGAGCCGATTTGCACTGTGCGCGCAAGAGCGGGCACTACGCTGTG 1859
Db 1848 GAGCGTGTGATGAGAGAGAGCCGATTTGCACTGTGCGCGCAAGAGCGGGCACTACGCTGTG 1907
QY 1860 CCGCATCTTATGACCTGTGTCTCCAGCTGCAAGTGTGAGAGCTGTGCGCAAGAGCACC 1919
Db 1908 CCGCATCTTATGACCTGTGTCTCCAGCTGCAAGTGTGAGAGCTGTGCGCAAGAGCACC 1967
QY 1920 CTTGCAAGTGGCGCGGAGAGAGGGGCAACAGAGCACTGCGAGGCTGCTCTGTGATCGAGG 1979
Db 1968 CTTGCAAGTGGCGCGGAGAGAGGGGCAACAGAGCACTGCGAGGCTGCTCTGTGATCGAGG 2027
QY 1980 CGCTGGCAAGAGAGCGCTGACCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAG 2039
Db 2028 CGCTGGCAAGAGAGCGCTGACCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAG 2087
QY 2040 CGGACACTTGTGCGCACTGTCAAGCTGTGTGAGAGAGAGCGGATGTGTGCGCGGG 2099
Db 2088 CGGACACTTGTGCGCACTGTCAAGCTGTGTGAGAGAGAGCGGATGTGTGCGCGGG 2147
QY 2100 ACCGCTGAACCAAGCGGCGCTGCACTGTGCGCGCCCAAGGCACTCGAGGTGTGTGA 2159
Db 2148 ACCGCTGAACCAAGCGGCGCTGCACTGTGCGCGCCCAAGGCACTCGAGGTGTGTGA 2207
QY 2160 GAGATTGTGACGCGCGCATGTGATCTGTGTGAGAGAGAGCGGCTCAAGCGGCTGTGCA 2219
Db 2208 GAGATTGTGACGCGCGCATGTGATCTGTGTGAGAGAGAGCGGCTCAAGCGGCTGTGCA 2267
QY 2220 CTTGCGCGCCCAAGGCGCGGCAAGAGAGAGAGAGCTGTGCTGAGAGATGGGGGCCA 2279
Db 2268 CTTGCGCGCCCAAGGCGCGGCAAGAGAGAGAGAGCTGTGCTGAGAGATGGGGGCCA 2327
QY 2280 CATCAACTGTGAGAGCTTCAAGTTTCCAGAGGCGGCAATGCGCGGCACTGCTGTGCG 2339
Db 2328 CATCAACTGTGAGAGCTTCAAGTTTCCAGAGGCGGCAATGCGCGGCACTGCTGTGCG 2387
QY 2340 GCGAAGCAAGACTTGA 2355
Db 2388 GCGAAGCAAGACTTGA 2403

RESULT 5
US-09-799-451-905
; Sequence 905, Application us/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Duntui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom

APPLICANT: Ghosh, Reena
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. 678396e1 Nucleic Acids and
 FILE REFERENCE: 803
 CURRENT APPLICATION NUMBER: US/09/799,451
 NUMBER OF SEQ ID NOS: 948
 SOFTWARE: pc_fl_genes Version 2.0
 SEQ ID NO 905
 LENGTH: 3981
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1) .. (2496)
 US-09-799-451-905

Query Match 92.1%; Score 2170; DB 4; Length 3981;
 Best Local Similarity 94.0%; Pred. No. 0;
 Matches 2349; Conservative 0; Mismatches 5; Indels 146; Gaps 3;

QY 1 ATGAGGCGGACGCGGCGGAGCCCATGGGCGCTGGCGCTGTCGCACTTCGACGCGGCG 60
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 QY 361 ATCATCCAGAGAGCGCGGTGGAGATGAACTTCTGCACTGATGAGGCGCGGCACTCTCG 420
 DB 361 ATCATCCAGAGAGCGCGGTGGAGATGAACTTCTGCACTGATGAGGCGCGGCACTCTCG 420
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 DB 721 GCGCCGAGAGCTGCGCGGTGTGAGAGCGCGGCGCGGCGCTGACGCACTGATACGC 780

QY 781 CTGATGAGCGGTGCTGGCAGGCGGATCCGAGATTAGGCCCACTTC----- 828
 DB 781 CTGATGAGCGGTGCTGGCAGGCGGATCCGAGATTAGGCCCACTTCGAGAGAACGG 840
 QY 829 ----- 828
 DB 841 CTGAATGGGAGCTCATCCGCAAGTCTGGCAGCTCTGCTCCCTGTGACTGCGAGGTGG 900
 QY 829 ----- 828
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 DB 961 CTTTCTTCCCAAGAAATTACTTTGAAACCGAGGACCTGTGTGAAAAGCTGATGAC 1020
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 DB 1021 GAAATGAAAGAACTGTCTCATGATCTGGAAGTGAAGAGCCCGGAGGCCAGAGCGAG 1080
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 DB 1081 GTGTGCTTGGAGGCTCAAGCGGCGCTTGTCCCACTTTGATTAAGTCAAGCTC 1140
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 DB 1141 TCCGAGCTTCTCAAGCTTGAAGTTCGAGGCTGTCCAGGCGGCGAGAG 1200
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 DB 1380 TGCCATGTGTCTGCGGAGACACAGCAAACTGATGAACTCTGACGCGCAGAGCTGGA 1439
 QY 1296 CTTGCACTGGAACAGCGGTGCACTGTGCACTCTGCGGTGAGAGGCTCGGCAAGAGGA 1355
 DB 1440 CTTGCACTGGAACAGCGGTGCACTGTGCACTCTGCGGTGAGAGGCTCGGCAAGAGGA 1499
 QY 1356 GTGGCCCAAGTGTGTGCTCAACATGCCAACCCCAACTGAGCAACGTTAGGGGCTC 1415
 DB 1500 GTGGCCCAAGTGTGTGCTCAACATGCCAACCCCAACTGAGCAACGTTAGGGGCTC 1559
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 DB 1560 CACCCGTTTGCATATGAGCGCTGAGAGAGGAGTGTGTGAGAGCTCTGCTGGC 1619
 QY 1476 AGCAAGATCAAGTGTCAACGCTCAAGATGAGAACCACTGCAAGCTCTTGTGAGC 1535
 DB 1620 AGCAAGATCAAGTGTCAACGCTCAAGATGAGAACCACTGCAAGCTCTTGTGAGC 1679
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 DB 1680 CCAAGACGGGATATAGTCTTACCAACAGCGCTGTTGAGAGAGAGCGCTGGTCAACGA 1739
 QY 1596 GATGACCTTTAGAGGCGGAGCGCCATGCAAGTGTGCTGCGCAGCAAGAGATAT 1655
 DB 1740 GATGACCTTTAGAGGCGGAGCGCCATGCAAGTGTGCTGCGCAGCAAGAGATAT 1799
 QY 1656 GTGTGCACTCTGCTGCGCGAGAGGCTGAGAGTGTGAGGCTGCAAGAGATATGCTGCT 1715
 DB 1800 GTGTGCACTCTGCTGCGCGAGAGGCTGAGAGTGTGAGGCTGCAAGAGATATGCTGCT 1859

Qy	1716	GCCACTGCACTAGCGCTGCTGGGAGGGCCACCTGCGCCATCTGTCAACACTCTGGCCAAAGA	1775
Db	1860	GCCACTGCACTAGCGCTGCTGGGAGGGCCACCTGCGCCATCTGTCAACACTCTGGCCAAAGA	1919
Qy	1776	GCCGAGGGGTGAAGTGTGAACGCGCCAGACGCTGGAATGGAGAGGACGCAATTGCACTTGGCGCG	1835
Db	1920	GCCGAGGGGTGAAGTGTGAACGCGCCAGACGCTGGAATGGAGAGGACGCAATTGCACTTGGCGCG	1979
Qy	1836	ACAGCGCGGACCACTACCGCGTGGCCCGCATCTTCATGACCTGTGCTCGACGTCACGCT	1895
Db	1980	ACAGCGCGGACCACTACCGCGTGGCCCGCATCTTCATGACCTGTGCTCGACGTCACGCT	2039
Qy	1896	CTGCAAGCTCTGTGGCAACAACCCCTGCACTGGTCCGCGAGACGCGGCGCAACAAGCAC	1955
Db	2040	CTGCAAGCTCTGTGGCAACAACCCCTGCACTGGTCCGCGAGACGCGGCGCAACAAGCAC	2099
Qy	1956	TGCGAAGCTCTCTCTGCAATGGGGCGGTGGCAAGAGGCGCTGACCTTCAGACGCGCTACAC	2015
Db	2100	TGCGAAGCTCTCTCTGCAATGGGGCGGTGGCAAGAGGCGCTGACCTTCAGACGCGCTACAC	2159
Qy	2016	CGCTCTGCACTCGGCTGCTCCCGCAACGCGACACTGTCGCACTGTCAAGCTCTGTGAGAGA	2075
Db	2160	CGCTCTGCACTCGGCTGCTCCCGCAACGCGACACTGTCGCACTGTCAAGCTCTGTGAGAGA	2219
Qy	2076	GAAAGCCGATGTGTGTGGCCCGGAGACCCCTGAAACAGACGCGCGTGCACCTGTGCGCGC	2135
Db	2220	GAAAGCCGATGTGTGTGGCCCGGAGACCCCTGAAACAGACGCGCGTGCACCTGTGCGCGC	2279
Qy	2136	CCACGGGCACTCGGAGGTGTGAGAGAGTTGTGACGCGCGGATGTGACCTGTTCGA	2195
Db	2280	CCACGGGCACTCGGAGGTGTGAGAGAGTTGTGACGCGCGGATGTGACCTGTTCGA	2339
Qy	2196	CGACCAAGGGGTGACGCGCGTGCACCTGGCGCGCCGAGGCGCGGCAAGACGAGCGGTGGA	2255
Db	2340	CGACCAAGGGGTGACGCGCGTGCACCTGGCGCGCCGAGGCGCGGCAAGACGAGCGGTGGA	2399
Qy	2256	GACTCTGCTCAGGAGTGGGGCCCAATCAACTGTGAGAGGCTCAAGTTCAGAGGCGGCA	2315
Db	2400	GACTCTGCTCAGGAGTGGGGCCCAATCAACTGTGAGAGGCTCAAGTTCAGAGGCGGCA	2459
Qy	2316	TGGCCCCGCGCGCACTCTGTGGCGGAGGAGAACTTAG	2355
Db	2460	TGGCCCCGCGCGCACTCTGTGGCGGAGGAGAACTTAG	2499
RESULT 6			
US-09-509-802-1			
: Sequence 1, Application US/09509802			
: Patent No. 6489130			
: GENERAL INFORMATION:			
: APPLICANT: Immunex Corp.			
: APPLICANT: Bird, Timothy			
: APPLICANT: Vitco, G.D.			
: TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)			
: FILE REFERENCE: 2889-US			
: CURRENT APPLICATION NUMBER: US/09/509,802			
: CURRENT FILING DATE: 2000-06-02			
: NUMBER OF SEQ ID NOS: 5			
: SOFTWARE: Patent version 3.0			
: SEQ ID NO 1			
: LENGTH: 2370			
: TYPE: DNA			
: ORGANISM: Mus sp.			
: US-09-509-802-1			

Query Match	74.1%;	Score 1745.4;	DB 4;	Length 2370;
Best Local Similarity	84.6%;	Pred. No. 0;		
Matches 1997;	Conservative	0;	Mismatches 356;	Indels 8; Gaps 3;

QY 2 TGGAGGCGACGCGGGAACCCATGGGCCCTGACGTGCACAATTGACGCGGGCG 61
Db 11 TGGAGGCGAGGCGCGGGGCGGGTGGCTCTGGGGCTGTTCGCACTTGACGCGGGCG 70			

QY	62	AGTTCA	CGGGCTGG	GAAGAAGT	GTGGGCTCTGGGCGGGCTTCTGGGCA	AGGTATCA	AAAGTGGCC	121
Db	71	AATTGCA	AGGCTGGG	AAAGTGGGCTCGGGCGGGCTTCTGGGCA	AGGTATCA	AAAGTGGCC	130	
QY	122	ATTGCA	CTGAAGAACC	TGGCTGGCCATCA	AGTGTCTGGCCAGGCTTCA	CGTGCAGCA	181	
Db	131	ATTGCA	CTGAAGAACC	TGGCTGGCCATCA	AGTGTCTGGCCAGGCTTCA	CGTGCAGCA	190	
QY	182	GGAGCGCA	TGAGACTTTT	GGAAAGAACCA	GAAGATGAGATGGCCAA	GTTTGGCTTACA	241	
Db	191	GGAAACGA	ATGAGACTCT	GGAGAGGAAGCTAA	GAAGATGAGATGGCCAA	GTTTGGCTTACA	250	
QY	242	TCTGCGCT	GTGTATG	GCATCTGCGGCA	ACTCTGTGGGCTGTGTATG	AGTATCATG	301	
Db	251	TTCTACCT	GTGTATG	CGCATATG	CCAGGAACCTGTGGCTGTGTATG	AGTATCATG	310	
QY	302	CGGGCTCC	CTGGAAAGCT	GTGGCTTGGAGCA	TTGGCATGGGATCTCGGGTCC	GAA	361	
Db	311	CAGGCTCC	CTGGAAAGCT	GTGGCTTGGAGCA	TTGGCATGGGATCTCGGGTCC	GAA	370	
QY	362	TCATCCA	CGAGCGGCGGTGGGCA	TGAACTTCTGCA	CTGCATGGAAGCCCGCA	CTCTGCG	421	
Db	371	TGATGCA	CGAGCAAGCGGTGGGCA	TGAACTTCTGCA	CTGCATGGAAGCCCGCA	CTCTGCG	430	
QY	422	ACTGGA	CTCAAGCCCGGCA	CATCTGTGTGATG	CCCACTACAGTCA	AGATTTCTG	481	
Db	431	ACTGGA	CTCAAGCCCGGCA	CATCTGTGTGATG	CCCACTACAGTCA	AGATTTCTG	490	
QY	482	ATTTTGGT	CTGGCCAAATG	GCAAGGGGCTGTC	CCATCGCATGAC	CTGAGATGGA	541	
Db	491	ACTTTGGG	CTGGCCAAATG	GCAATGGCATGTC	CCATCTCATGAC	CTGAGATGGA	550	
QY	542	TGTTTGGCA	CATCGCTACCTCCCTC	CAAGCGCATCA	GGGAGAAAGCCGGCTCTTG		601	
Db	551	TGTTTGGCA	CATCGCTACCTCCCTC	CAAGCGCATCA	GGGAGAAAGCCGGCTCTTG		610	
QY	602	ACACCA	AGCACATG	ATACAGCTTTGGCAT	CTGTCATCTGGGCGGTCTC	CACAGAGA	661	
Db	611	ACACCA	AGCACATG	ATACAGCTTTGGCAT	CTGTCATCTGGGCGGTCTC	CACAGAGA	670	
QY	662	AGCGTTT	GCAATGAGAAGAA	CATCTCGCA	CATATGTGAAGTGTGA	AGGGCCACC	721	
Db	671	AGCATTT	GCAATGAGAAGAA	CATCTCGCA	CATATGTGAAGTGTGA	AGGGCCACC	730	
QY	722	GCCCCG	AGCTGCGGCCGTGTG	CAAGAGCCCGGCGCGCGCT	TCAGGCA	CCTGTATAC	781	
Db	731	GCCCCG	AGCTGCGGCCGTGTG	CAAGAGCCCGGCGCGCGCT	TCAGGCA	CCTGTATAC	790	
QY	782	TCATGCA	CGGCTGTGGCAGGGGAGAT	CCGCGATTA	GGCCCATCTTCCAGAA	ATTATCT	841	
Db	791	TCATGCA	CGGCTGTGGCAGGGGAGAT	CCGCGATTA	GGCCCATCTTCCAGAA	ATTATCT	850	
QY	842	CTGAA	ACCGAGACCTGTGTGA	AAAGCTGTATG	CAAGTGAAGAA	AACTGTATATC	901	
Db	851	CTGAA	ACCGAGACCTGTGTGA	AAAGCTGTATG	CAAGTGAAGAA	AACTGTATATC	910	
QY	902	TGGA	CGTGAAGAGCCGCCG	AGCCAGAGCGAGTGTGTGCTG	-----CGAGGCTCA		955	
Db	911	CAGCG	GAAGAAAGCTCTTAT	AGTCCAGAGTGAAGGCCAGGCGCTCA	AGGCTCA		970	
QY	956	AGCGGG	CTGTGCCCCCATCTT	GCATTA	CGATCTCTCGAGCTTCTCA	CAGC	1015	
Db	971	AGCGGG	CTGTGTCTCCCCCTT	GCATTA	CGATCTCTCGAGTGTCTCA	CAGT	1030	
QY	1016	TGGA	CTCTGAAGTTTCC	AGGCTGTCA	AGGGCCCCGAGAGTCA	AGCGAGCTCTCTG	1075	
Db	1031	TGGA	CTCTGAAGTTTCC	AGGCTGTCA	AGGGCCCCGAGAGTCA	AGCGAGCTCTCTG	1090	
QY	1076	AGTCA	AGCTGCATCTGTC	CGGAGTGGAA	AGAGCTCTCGGAGGCTGTCTC	CGTGA	1135	
Db	1091	AATGCA	AGCTGCCATCTGTCC	AGAGTGGCA	AGAGGCTCTCGGAGGCTGTCTC	CAATGA	1150	
QY	1136	CGCGCTTCTT	CCAGAGATCA	CTGTGCTGTCTT	TGAAGGGAACTTCA	CAAGC	1195	

Db	1151	CAGCCTTTTCTCCAGAGGATCGCTGTCATGTCTTTTGAAGCGGAAAGCTTCAACAGGCG	1210
Oy	1196	ATTCGGGTACCAACAAGAGCTCCAGAGAAGAGCTTGTGATGATCATCGTGC-CGGAGC	1254
Db	1211	ACCTGGGCCCCAC-AGACATCCAGAGAAGAGCTAGTAGTCATCATATCAGGGAC	1269
Oy	1255	ACAGCAAACTGATGAAGATCTTGCAGCGCAGGACGTGACCTTGACACTGACACGGT	1314
Db	1270	ACAGCAGGCTGATGAAGATCTTACAGCGCCCAATGTGGACTTGGTTTACACAGCAGT	1329
Oy	1315	GCCAGCCTGCTGCACTCGCGGTGGAAGGCGGGGCAAGAGGTGCGCAATGGCTGCTG	1374
Db	1330	GCCAGCCTGCTGCACTCGGCTGTGAGGCGCGAAGAGAGGTGTGTCATAGTGGCTCTG	1389
Oy	1375	CTCAACAATGCAACCCCACTTGACCAACGTATGGGGCTTCAACCCGCTTGCAATGGCC	1434
Db	1390	CTTAACAATGCAACCCCACTTGACCAACAAGAGGGCTTTACACACTGCAATATGGCT	1449
Oy	1435	GTGAGAGAGAGGTGCGGGGTGTGCTGAGCTCTGCTGCGACGGAAGATCATGTCTAC	1494
Db	1450	GTGAGCGGGAAGGGAAGTGAATTTGTGAGCTACTGCTAGCCCGGAAACCAAGTGTCAAT	1509
Oy	1495	GCCAAAGATGAGAACCAATGACAGCCCTTCACTTTGAGGCCCAAGACGGGATGAGCT	1554
Db	1510	GCCAAAGATGAGAACCAATGACTGCGCTTGACCTTTGAGGCCCAAGATGGGGAATGAGCC	1569
Oy	1555	AGCACACGGCTGTGTTGAGAGAAGACGCTCGGTCAACGAGGTGGACTTTGAGGGCGG	1614
Db	1570	AGCACAGGCTGTCTGCTAGAGAAGATCTTGTGCATAGAGTGAATTGAGGGCGGA	1629
Oy	1615	ACGCCCATGACAGTGGCCTGCACAGACGGGACAGAAATATGTCGCATCTGCTGCGC	1674
Db	1630	ACACCCATGACATGTATGCTTGCACAGACTGAACAGAGAAATATGTATGTCGCACTCTGCGC	1689
Oy	1675	CGAGGCTGTGACGTGAGGCTTGCAGGGGCAAGATGCTCGGCTGCGACCTGACCTGAGC	1734
Db	1690	CGTGTGTGTGATGTGTGGGCTCTGACAGGAAGATGTCTGTGGCTCTGCACTATGTGCGC	1749
Oy	1735	TGGCAGGGGCAACTTGCCTCCATCGTCAAGGCTGTGGCAAGCAGCGGGGGTGAAGTGAAC	1794
Db	1750	TGGCAGGGGCAACTTCCATTGTTATGCTGTGACGACAGCGCTCGGGGTATGATGTAAT	1809
Oy	1795	GCCCAAGACGTGATGGAGAGACCGCCATTTGCACTTGGCGGACAGCGCGGCACTACCGC	1854
Db	1810	GCCCAAGACATTAAGACGGGAGGACACCCCTGCACTGGCTGCTAGAGGGGGCAATTACCGT	1869
Oy	1855	GTTGGCCCGCATCTCATGACCTTGTGCTCCACGTCAACGTCTGAGAGCTGTGTGGCAAG	1914
Db	1870	GTTGGCTGCAATCTCATTTGACCTTGTGCTCTGATGTTTAACTCTGAGGCTTACAGGCAAG	1929
Oy	1915	ACACCCCTGCAAGTGGCGCGGAGACGGGGGCAACGACACTGGCAGGCTGCTCGTCAAT	1974
Db	1930	ACACCTCTGCAAGTGTGTGTCAGAGACTGACACTATATATCTGCCAGGCTACTCTTGAT	1989
Oy	1975	CGGGGCGCTGGCAAGAGGCGGTGAACCTTCAAGCGGCTACACCGCTCTGCACTTGCTGCG	2034
Db	1990	CGTGGGTGCTGGCAAGAGGCTTTGAACCTTCAAGGGCTTATCTGCTTGCACCTGGCAGCC	2049
Oy	2035	CGCAACGCAACTTGGCCCATGTCAAGCTGTCTTGTCCAGAGAGAAAGCCGATGTGTGGCC	2094
Db	2050	CGAAATGGAACACTGGCTTACTGTCAAGGCTCATATGAGAGAAAGCTGATGTGATGCT	2109
Oy	2095	CGGGGACCCCTGAACCAAGCGGCGCTGCACTTGGCTGCGGCGCAAGGGCACTCGAGGTTG	2154
Db	2110	CGGGGTCTCCCTTAATACAGACACTGCACTGTGGCTGTGCGCCGTGACACTCAGAGGTTG	2169
Oy	2155	GTTGAGAGATGTGTACGCGCGATGTCAATTGAACCTGTTGCAGACAGAGGCTCAGCGCG	2214
Db	2170	GTTAGAGAGACTGATGATGCTGACCTCATTTGAACCTGTGATGACAGGGGCTCAGCGCA	2229
Oy	2215	CTGCACCTGGCGGCGGCGGCAAGACAGAGGTGTGAACTCTGCTCAGGCAATGGG	2274

Db	Query Match	Best Local Similarity	84.1%; Score 1745.4; DB 3; Length 3516;	Matches 1997; Conservative	84.6%; Pred. No. 0;	Mismatches 356; Indels 8; Gaps 3
Db	2230 CTGACCTGGCTGCTCAGGGCAGGCACTTCAACGCTGTGGAGACACTGTCAACATGGA	2288				
Qy	2275 GCCCACTCAACCTGCAAGCCTTCAAGTTCAGGGCGGCAATGGCCCCGCCCACTC	2334				
Db	2290 GCACACATCACTTGACAGATCTCAAGTTCAGAGGCAAGGCAAGCTCTGTCCACGTTG	2349				
Qy	2335 CTGGCGGAGCAAGACTAG	2355				
Db	2350 CTCGACGACGACAGACTAG	2370				
RESULT 7						
US-09-188-930-257						
Sequence 257, Application US/09188930A						
Patent No. 6150502						
GENERAL INFORMATION:						
APPLICANT: Watson, James D.						
APPLICANT: Strachan, Lorna						
APPLICANT: Sleeman, Matthew						
APPLICANT: Onrust, Rene						
APPLICANT: Mulison, James Greg						
TITLE OF INVENTION: Compositions Isolated From Skin Cells						
FILE REFERENCE: 11000.1011c1						
CURRENT APPLICATION NUMBER: US/09/188,930A						
CURRENT FILING DATE: 1998-11-09						
NUMBER OF SEQ ID NOS: 348						
SOFTWARE: FastSeq for Windows Version 3.0						
SEQ ID NO 257						
LENGTH: 3516						
TYPE: DNA						
ORGANISM: Mouse						
US-09-188-930-257						
Qy	2 TGAAGGCGACGCGCGGAGACCCCATGAGCGCTCTGCGCTCTGCGCACTTTCAGCGGGCG	61				
Db	5 TGAAGGCGAGGGCGCGGGCGGCTGTGGGCTCTGGGGCTGTCCGCACTTCGACCGCGCG	64				
Qy	62 AGTTCACGGGCTGGGAGAGAGGTGGGCTCGGGCGGCTTCGGGCAAGGTACAGGTGCGCC	121				
Db	65 AATTGCGAGGCTGGGAGAGGTGGGCTCGGGCGGCTTCGGGCAAGGTACAGGTGCGCC	124				
Qy	122 ATGTCCACTGGAAGACTGTGGCTGCGCATCAAGTGTGCGCCAGCCTGCAAGCTGACGACA	181				
Db	125 ATGTGCACTGGAAGACTGTGGCTGCGCATCAAGTGTGCGCCAGCTGCAAGCTGACGACA	184				
Qy	182 GGGAGCGCATGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGGCCCAAGTTTCCGTACA	241				
Db	185 GGGAGCGATGAGCTCTCGAGAGAGCTTAAAGAGATGAGATGGCCCAAGTTTCCGTACA	244				
Qy	242 TCCGCGCTGTGATATGGCATCTGCGCGGAAACCTGTGGGCTGATGAGTACATGAGAGA	301				
Db	245 TTTCACTGTGTACGGCATATGCAAGAACTGTGGCTTGTGTATGAGATGATGAGAGA	304				
Qy	302 CGGGCTCCCTGGAAAAGCTGTGGCTTTCGAGCCATTGCAATGGGATCTTCGGTTCCGAA	361				
Db	305 CAGGCTCCCTGGAGAAAGCTGTGGCTTCAGAGCCATTGCGGAACTCTGGGAACTCTTGCA	364				
Qy	362 TCATCCAGAGACGGCGGTTGGGCATGAACCTTCTGCACTGCAATGGCCCCGCCACTCTCG	421				
Db	365 TCGTCAAGAGACACCGGTGGGCATGAACCTTCTGCAATGATGATCTTCGGCCACTGCTTC	424				
Qy	422 ACCTGGACCTCAAGCCCGGAAACATCTGTGAGATGGCCCACTACACGTCAGAAATTTCTG	481				
Db	425 ACCTAGACCTGAAGCCAGGAAACATCTGTGAGATGGCCCACTACACATGCAAGATTTCTG	484				
Qy	482 ATTTTGTCTGGCCAAAGTGCACAGGGCTGTCCCACTGCGATGACCTTCAGCATGATGGCC	541				
Db	485 ACTTTGGGCTGGCCAAAGTGCATGCGATGTCCCACTTCATGACCTTCAGCATGATGGCC	544				

TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-257
Query Match 74.1%; Score 1745.4; DB 4; Length 3516;
Beat Local Similarity 84.6%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 356; Indels 8; Gaps 3;
QY 2 TGGAGGCGACGCGGAGCCCATGAGGCTGCTGCGCACTTTCAGCGCGGCG 61
DB 5 TGGAGGCGAGGCGCGGCGCGTGGGCTGCGCTGCGCACTTTCAGCGCGGCG 64
QY 62 AGTTCAACGGGCTGGGAGAGGTTGGGCTGGGCGGCTTGGGAGGTTGACAAAGGCGCC 121
DB 65 AATTGCGAGGCTGGGAGAGGTTGGGCTGGGCGGCTTGGGAGGTTGACAAAGGCGCC 124
QY 122 ATGTCCACTGGAAGACTGGCTGGCCATCAATGTCGCGCCAGCTTGACGTGACGACA 181
DB 125 ATGTGCACTGGAAGAGCTGGCTGGCGATCAAGTCTCGCCCACTGCGACGTGACGACA 184
QY 182 GGGAGCGCATGAGGCTTTTGGAGAGGCCAGAGAGATGAGATGAGCCAAAGTTTGGCTACA 241
DB 185 GGGAGCGATGAGGCTCTGCGAGAGGCTTACAGAGATGAGATGAGCCAAAGTTCCGATACA 244
QY 242 TCCTGCTGTGTATGAGCATCTGCGCGAACCCTGTGGGCTGGTCAATGAGATCATGAGGA 301
DB 245 TTCTTACTGTGTACGCGCATATGCCAGAGAACTGTGGGCTTGTGATGAGATCATGAGGA 304
QY 302 CGGGCTCCCTGGAGAAAGCTGTGGCTTGGAGCCATGTCATGGGATCTCCGGTTCCGAA 361
DB 305 CAGGCTCTCTGGAGAAAGCTGTGGCTTGGAGCCATGTCATGGGATCTCCGGTTCCGCA 364
QY 362 TCATCCAGAGACGCGCGGTGGCATGAATTTCTGTCATGTCATGAGCCCGCCGCACTCTGCG 421
DB 365 TCGTCACAGACAGCGCGGTGGCATGAATTTCTGTCATGTCATGAGCCCGCCGCACTCTGCG 424
QY 422 AGCTGAGCTTCAAGCCCGGAAATCTGCTGGAGTCCCACTACACGCTCAAGATTTCTG 481
DB 425 AGCTGAGCTTCAAGCCCGGAAATCTGCTGGAGTCCCACTACACGCTCAAGATTTCTG 484
QY 482 ATTTTGTCTGAGCAAGTCAAGGCTGTCCCACTGCGATGACCTCAGCATGATGAGCC 541
DB 485 ACTTTGGGTGGCGCAAGTGCATATGCGATCTCCACTCATATGACTCAGCATGATGAGCC 544
QY 542 TGTTTGGCAATTCGCTTACCTCTCCAGAGCGCATGAGGAGAAAGACCGGCTTTCTG 601
DB 545 TGTTTGGTATCATTCGCTTACCTCTCCAGAGCGAATTTGTGAGAAAGACCGGCTTTCTG 604
QY 602 AACAACAGACATGATATACAGCTTTGCGATGTCATCTGGGCGGTGCTCAACAGAGAA 661
DB 605 AACAACAGACATGATATACAGCTTTGCGATGTCATCTGGGCGGTGCTTACACAGAGAA 664
QY 662 AACCGTTTGCATGAGAGAGAAATCTGCGACATCATGATGAGGAGGAGGCGCAC 721
DB 665 AACCGTTTGCATGAGAGAGAAATCTGCGACATCATGATGAGGAGGAGGCGCAC 724
QY 722 GCCCGAGGCTGCGCGCGGTGTCAGAGCCCGCGCGCTGTCAGGCCACTGATAGCGC 781
DB 725 GCCCGAGGCTGCGCACCATCTGAGAGCCCGCGCGGTGTCAGGCCACTGATAGGCGC 784
QY 782 TCATGCAAGGTTGCTGAGGAGGAGATCCGCGAGTTAGGCCCACTTTCCAAAGAAATTAATT 841
DB 785 TCATGCAAGGTTGCTGAGGAGGAGATCCGCGAGTTAGGCCCACTTTCCAAAGAAATTAATT 844
QY 842 CTGAAACCGAGGACTGTGTAAGAAAGCTGATGACGAGTGAAGAAATGTGCTCATGATC 901
DB 845 CTGAAACCGAGGACTGTGTAAGAAAGCTGATGAGAGGTTGAAGAAATGTGCTCATGAGC 904
QY 902 TGGACGTGAAAGCCCGCGAGCCCGAGAGCGAGGTGTGCTG-----CGAGGCTCA 955
DB 905 CAGGCGAGAAAGCTCTTGAAGTCCAGAGTGAAGGCCCGAGGCTCTCAAGCCTCA 964
QY 956 AGCGGCGCTCTGCGCCCACTTTCGATACGATACAGCTCTTCGAGCTTCTCTACAGC 1015

DB 965 AGCGGCGCTCTGCTGCGCCCGCTTCGATACGATGCACTGCTCTCGAGTGTGTCACAGT 1024
QY 1016 TGAACCTTGAAGTTTCCAGAGGCTGTGAGAGGCCCGAGAGGCTTACGCCGAGCTCTCTG 1075
DB 1025 TGAACCTTGAAGTTTCCAGAGGCTGTGAGAGGCCCGAGAGGCTTACGCCGAGCTCTCTG 1084
QY 1076 AGTCAAGCTTCCATTCGTCGCGGAGTGGAGAGGCTCTGCGGAGGTTCTCGGTGAGACT 1135
DB 1085 AATTCAGGCTTCCATTCGTCGCGGAGTGGAGAGGCTCTGCGGAGGTTCTCGGTGAGACT 1144
QY 1136 CGGCTTCTCTTCCAGAGGATTCATCTGTGCTCTTTCCTTTGAGCGGAACTTTCACACAGC 1195
DB 1145 CAGGCTTCTCTTCCAGAGGATTCGTCATCTGTCTTTTGAAGCGGAGAGCTTTCACAGGCG 1204
QY 1196 ATCTGGGTTCCACAGAGCTTCAGAGAGAAAGTTGATGATGCTATGCTGTG-C-GGGAC 1254
DB 1205 ACTTGGGCGCCAC-AGACATTCAGAGAGAAAGCTTGTGATGCTATCATACAGGGGAC 1263
QY 1255 ACCAGCAATGATGAATTCCTGCAAGCCGAGAGCGTGGACCTTGGACATGAGAGCGGT 1314
DB 1264 ACCAGCAAGCTGATGAAGATTCACAGCCCGAGATGAGCTTGTGTTAGACAGAGT 1323
QY 1315 GCCAGCTTGTGCACTGTGCGGTGAGAGCGCGGAGAGAGAGTGGCCAAAGTGTGCTGTG 1374
DB 1324 GCCAGCTTGTGCACTGTGCTGTGAGAGCGCGAGAGAGAGTGTGCAAGTGTGCTGTG 1383
QY 1375 CTCAACATGTCACCCCAACTGAGCAACCGTAGGAGGCTTTCACCCGTTTGCATATGAGCC 1434
DB 1384 CTTAACATGTCACCCCAACTGAGCAACAGAGAGGCTTTCACCACTCATATATGCT 1443
QY 1435 GTGAGAGAGAGGTTGCGGAGTGTGTGAGAGCTCTGCTGCGACGGAAGATGAGTCAAC 1494
DB 1444 GTGAGAGAGAGGAGCTGTGAATTTGTGAGCTTGTGCTGAGCCGGAAGACAGTGTCAAT 1503
QY 1495 GCCAAGATGAGAGCAAGTGGACAGCCCTCCACTTTCAGCGCCAGAAAGCGGAGTGAATCT 1554
DB 1504 GCCAAGATGAGAGCAAGTGGACAGCCCTCCACTTTCAGCGCCAGAAATGGAGATGAGGCC 1563
QY 1555 AGCAACAGGCTGTGTTGAGAGAGAAAGCTCTGCTCAACGAGTGTGACTTTGAGGCGCG 1614
DB 1564 AGCAACAGGCTGTGTTGAGAGAGAAATGCTTCTCATATGAGTGTGACTTTGAGGCGCG 1623
QY 1615 ACGCCATGCAAGTGGCTGTGCAAGCGGAGAGAGAAATTCGTCGATCTGTGCGC 1674
DB 1624 ACGCCATGCAAGTGGCTGTGCAAGCGGAGAGAGAAATTCGTCGATCTGTGCGC 1683
QY 1675 CGAGGCGTGAAGTGAAGCTTGCAGAGGCAAGATGCTGTGCTGCACTGACTAGCTGCGC 1734
DB 1684 CGTGTGTGATGTGGCTGTGAGAGAGAAAGATGCTGTGCTGCTGTGCACTATGCTGCGC 1743
QY 1735 TGGAGAGGCGCACTGCGCATGCTGCAAGCTGTGCGCAAGCGCGGAGTGTGTAAC 1794
DB 1744 TGGAGAGGCGCACTTCCCATTTTAAGTGTGTACCAAGCAGCTGAGGAGTGTGTAAT 1803
QY 1795 GCCCAAGCTGTGATGAGAGAGAGCGCATTTGCACTGTGCGCGCAAGCGCGGCACTAACCGC 1854
DB 1804 GCCCAAGCTGTGATGAGAGAGAGCGCGCATTTGCACTGTGCGCGCGCACTTAACCGT 1863
QY 1855 GTGGCGGCACTCTCATGCACTGTGCTCGACGCTCAACGTCGTGCAAGCTGTGCGCAG 1914
DB 1864 GTGGCGGCACTCTCATGCACTGTGCTCGACGCTCAACGTCGTGCAAGCTGTGCGCAG 1923
QY 1915 AACCCCTGCAAGTGGCGCGGAGAGCGGAGCAACAGACATGCGCAGGCTGCTCTGCTCAT 1974
DB 1924 AACCCCTGCAAGTGGCTGCGAGAGCTGAGACACTGTGTAATGCGCAGGCTACTCTTTCAT 1983
QY 1975 CGGGCGGTGAGAGAGAGCGGTGACCTTCAGACGCTTACACCGCTTTCAGCTGCGCGC 2034
DB 1984 CGTGTGTGCAAGAGAGGCTTTGACCTTCAGAGGCTTATATCTGCTTGCACCTGCGAGCC 2043
QY 2035 CGCAACGACACCTGTGCAAGCTGTGCAAGCTTGTGAGAGAGGCGGATGTGCTGCGC 2094

Db 2044 CAGAAATGGAACACCTGCTACTGTCAAGCTGCTCATAGAGAGAAAGCTGATGTATGAGCT 2103
Qy 2095 CGGGGACCCCTTGAACCAAGCGGCGCTGACCTGGCTGCGCCCAAGGCAATCGGAAGTG 2154
Db 2104 CGGGGATCCCTGGAATCAGACAGCACTGCACTGGCTGCTGCGCTGAGCACTCAGAGAGTG 2163
Qy 2155 GTGAGAGAGTTGTTCAGCGCCGATGTCAATTGACCTGTGTCAGAGAGAGGGCTCAGGCGC 2214
Db 2164 GTAAAGAGCTGTGTCAAGTGTCACTTCACTTGTCTGTATGAGCAGAGGCTCAGGCGCA 2223
Qy 2215 CTGCACTGGCGCGCCCAAGGCGCGCAAGCAAGCTGTGAGAGACTTGTCTCAGGCAATGG 2274
Db 2224 CTGCACTGGCTGTCTCAGAGGCGAGGCAATTCAGACTGTGAGAGACACTGTCAAACTGGA 2283
Qy 2275 GCCCAATCAACCTGCGAGAGGCTCAAGTTCCAGAGGCGGCGCTAGGCGCCCACTC 2334
Db 2284 GCACACATCAACTTGCAGAGAGCTCAAGTTCCAGAGAGCGCAGAGCTGTGCGACGTTG 2343
Qy 2335 CTGCGGCGAAGCAAGACCTAG 2355
Db 2344 CTCGAGCGCAGCAAGACCTAG 2364

RESULT 9
US-09-312-283C-403
Sequence 403, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 403
LENGTH: 1774
TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-403

Query Match 55.6%; Score 1310.2; DB 4; Length 1774;
Best Local Similarity 85.0%; Pred. No. 1.3e-293;
Matches 1503; Conservative 0; Mismatches 258; Indels 8; Gaps 3;

Qy 2 TGAAGGCGACGCGGAGAGCCCATAGGCGCTGCGCTGCTGCGCACTTGCAGCGGCGG 61
Db 7 TGAAGGCGGAGAGGCGCGGCGCTGCGCTGCGGCTGCTGCGCACTTGCAGCGGCGG 66
Qy 62 AGTTCACGCGGCTGGAAGAGGAGGCTGCGGCGCTTCCGAGAGTGAAGAGGAGGCGC 121
Db 67 AATTGAGGCTGGAAGAGGAGGCTGCGGCGCTTCCGAGAGTGAAGAGGAGGCGC 126
Qy 122 ATGTCACTGGAAGACTGTGCGCATCAAGTGTGCGCCAGGCTGCGCACTGCGAGCA 181
Db 127 ATGTGCACTGGAAGACTGTGCGCATCAAGTGTGCGCCAGGCTGCGCACTGCGAGCA 186
Qy 182 GGAAGCGCATGAGGCTTTTGAAGAGCAAGAAAGATGAGATGGCCAAATTTGGCTACA 241
Db 187 GGAAGCGAATGAGGCTCTGGAAGAGCTTAAGAAAGATGAGATGGCCAAATTTCCGATACA 246
Qy 242 TCCGCGCTGTGATGAGGACTTGCAGCGCAAGCTGTGCGCTGTATGAGAGTACATGAGA 301
Db 247 TTCTACCTGTGTAGCGCATATGCGAGAACTGTGCGCTGTGTATGAGAGTACATGAGA 306
Qy 302 CGGAGCTCCCTGAGAAAGCTGTGCTTCCGAGGCAATTCGAGATCTCCGATTCCGAA 361

Db 307 CAGGCTCCCTGAGAAAGCTGTGAGCTCAGAGCAATTCCTTGGGACCTTGCGCTTTCGCA 366
Qy 362 TCATTCACGAGAGCGGCTGGGATGAACCTTCTGCACTGCAAGGCGCGGCACTCTGCG 421
Db 367 TCGTGCAGAGACGCGGTGGGATGAACCTTCTGCACTGCAAGGCGCGGCACTCTGCG 426
Qy 422 ACCTGACCTCAAGCCCGGCAATCCTGCTGATGCGCCACTACAGATCAAGATTTCTG 481
Db 427 ACCTGACCTCAAGCCCGGCAATCCTGCTGATGCGCCACTACAGATCAAGATTTCTG 486
Qy 482 AATTGGTCTGGCCAAAGTGAACGAGCTGTCCCACTTCGATGACCTCAGATGATGCC 541
Db 487 ACTTGGGCTGGCCAAAGTGAACGAGCTGTCCCACTTCGATGACCTCAGATGATGCC 546
Qy 542 TGTTTGGCAAAATCGCTTACTCTCTCCAAAGGCAATCAGGAGAAAGCGGCTCTTG 601
Db 547 TGTTTGGTAAATCGCTTACTCTCTCCAAAGGAAATCGTGAAGAAAGCGGCTTGTG 606
Qy 602 ACACCAAGCAGATGATPACAGCTTTGCGATCGTCAATCTGGGCGTGTCCACAGAGA 661
Db 607 ACACCAAACTGATGTATACAGCTTGGCATTTGTGATCTGGGCTGTCTTACACAGAGA 666
Qy 662 AGCGTTTGCAGATGAGAGAAACATCTGCAATCATGTGAAGTGTGAAGGCGCAC 721
Db 667 AGCCATTGCAATGAGAAAGAAATCTTACATCATGATGAAGAGTGAAGGCGCAC 726
Qy 722 GCCCGGAGCTGCGCGCGGTGTGAGAGCGCGCGCGCGCTGACGCACTGATACGCC 781
Db 727 GCCCAGGCTGCCACCATCTGAGAGCCCGCGCGGTGTGCGCTGTGCGCTGATGAGGA 786
Qy 782 TCATGACGCGGTCTGCGAGGAGATCCGAGATTAGGCCCACTTCCAAAGAAATTAATT 841
Db 787 TAATGCAACGCTGTCTGCGACATGCAAGCCCAAGGTGCGGCCACTTCCAGAAATTAAT 846
Qy 842 CTGAACCGAGAGCTGTGTGAAGCTGTATGACGAAGTGAAGAAATCTGTATGATC 901
Db 847 CTGAACCGAGAGCTGTGTGAAGCTGTATGAGAGGTGAAGAAATCTGTATGATGAGC 906
Qy 902 TGAAGTGAAGAGCGCGCGGAGCGCGAGCGAGAGGTGTGCGTGTG-----CGAGGCTCA 955
Db 907 CAGGCGGAAAGAGCTCTAGAGTCCAGAGTGAAGGCGCGAGGCTCCTCAGGCTCA 966
Qy 956 AGCGGCGCTGTGCG 1015
Db 967 AGCGGCGCTGTGCG 1026
Qy 1016 TGAAGTGAAGTTCCTCAGGCTGTGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCT 1075
Db 1027 TGAAGTGAAGTTCCTCAGAGCTTGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1086
Qy 1076 AGTTCAGCTGCAATCGTCCGCGAGTGAAGAGGCTCTGCGGAGTGTCTCTCGGTGCA 1135
Db 1087 AATGCAAGCTCCATCTCTCAGAGAGTGAAGAGGCTCTGCGGAGTGTCTCTCAGTGA 1146
Qy 1136 CGCGCTTCTCTTCCAGAGGATCACTGTGCTGTCTTGAAGCGGAACTTCAACAGCG 1195
Db 1147 CAGGCTTTTCTTCCAGAGGATCGTGTCACTGTCTTTTGAAGCGGAACTTCAACAGCG 1206
Qy 1196 AATGAGGTACCAAGAGCTGTCAAGAGAGAGCTGTGATGATCGTGTCT- CGGAGC 1254
Db 1207 ACCTGGGCGCCAC- AGACATCTCAGAGAGAAAGCTAGTGAATCCATATCAAGGAGC 1265
Qy 1255 ACCAGCAAACTGATGAAGATCTGCGAGCGCGCAAGAGCTGTGCACTGCGCAAGCGGT 1314
Db 1266 ACCAGCAAGGTGATGAAGATCTCAGCGCCCAAGATGTGAAGCTTGTGAAGAGAGT 1325
Qy 1315 GCCAGCTGTGCACTGCGGCTGAGAGCGCGCGCAAGAGAGTGTGCGCAAGTGTGCTG 1374
Db 1326 GCCAGCTGTGCACTGCGGCTGAGAGCGCGCGCAAGAGAGTGTGTCAAGTGTGCTG 1385
Qy 1375 CTCAACATGCAACCCCAACTGAGCAACCTGAGCAACCTGAGGAGCTTCAACCCGTTTGA 1434
Db 1386 CTTAACATGCAACCCCAACTGAGCAACCTGAGCAACCTGAGGAGCTTCAACCACTGATGCT 1445

NOT A RESEARCH REPORT

Db	185	GGGAAACGAAAGGAGCTCTGGAGAGAGCTTAAGAGATGGACATGGCCAAATTCCGATAC	244
OY	242	TCCGACCTGTGTATGGCATCTGCGCGAACCCTGTGCGCTGTATGAGTACATGGAGA	301
Db	245	TTTCTACTGTGTATGCGCATATGCCAGAAACCTGTGCGCTTGTGTATGAGTACATGGAGA	304
OY	302	CGGCGCTCCCTGGAAAGCTGTGGCTTGGAGCCATTGCCATGGGATCTCCGTTCCGAA	361
Db	305	CAGGCTCCCTGGAAAGCTGTGGCTTGGAGCCATTGCCATGGGATCTCCGTTCCGAA	364
OY	362	TCATCCACGAGCGGCGGTGGGCATGAATTCTCTGCACTGCAATGGCCCGGCACTCCGAC	421
Db	365	TCGCGACACGAGCGGCGGTGGGCATGAATTCTCTGCACTGCAATGGCCCGGCACTCCGAC	424
OY	422	ACCTGACCTCAAGCCCGGAAACATCTGTGCTGATGTCCTACAC--ACGTCAAGATTTTC	479
Db	425	ACCTGACCTGAAACCGGAAACATCTGTGCTGATGTCCTACACATGTCAGATTTTC	484
OY	480	-TGATTTTGTCTGGCCAAGTGCAACGGGCTGTCCACTGGCATGACTTCAGCATGGATG	538
Db	485	TTGACTTTGGGCTGGCCAAGTGCAATGGCATGTGTCCACTGCATGACCTCAGCATGGATG	544
OY	539	GCCGTGTTGGCACAATGGCTTACCTCCCTCAGAGGCGCATCAGGAGAAAGCGCGCTCT	598
Db	545	GCCGTGTTGGCACAATGGCTTACCTCCCTCAGAGGCGCAATTCGTAAGAGAGCGCGCTTGT	604
OY	599	TCGACACCAAGCAGATGTATACAGCTTGGCATGTCACTCTGGGCGGTGCTCACAGA	658
Db	605	TTGACACCAACATGATGTATACAGCTTGGCATGTGATCTGGGCGGTGCTTACAGA	664
OY	659	AGAAACCGTTTGCAATGAGAAAGACATCTTGCAATCATGTGTGAAGGTGTGAAGGCC	718
Db	665	ATAATTCATTTGCAATGAGAAAGACATCTTGCAATCATGTGTGAAGGTGTGAAGGCC	724
OY	719	ACCGCCCCGAGCTGCGCGCGTGTGCAAGCGCCGCGCGCTTGCAAGCCACCTGATAC	778
Db	725	ACCGCCCCGAGCTGCGCACCCATCTGCAAGACCCGCGCGCGCTGTGCAAGCTGATAG	784
OY	779	GCTCATGTCAGCGGCTGGCAGGAGGATCCGCAAGTTAAGGCCACCTTCCAGAAATTA	838
Db	785	GACTCATGTCAGCGGCTGGCAGTGCACACCCAGTGTGCGGCCACCTTCCAGAAATTA	844
OY	839	CTTCTGAAACCGAGGACCTGTGTGAAAAAGCTGTGACGAAGTGAAGAAATCTGCTCATG	898
Db	845	CCTCTGAAACCGAGGACCTTTGTGTGAAGGCTGTGAGAGGTGAAGAAATCTGCTCATG	904
OY	899	ATCTGAGCTGAAAAAGCCCCCGGAGCCACAGAGCGAGTGTGTGCTGCG-----AAGC	952
Db	905	AGCCAGCGGAAAGAGCTCTTAAGTGCAGAGTGAAGGAGCCAGGCTCCAGTCTCAAGCC	964
OY	953	TCAGCGGAGCTCTGAGCCCCCACTTGCATTAACAAGTACAGGCTCTCCAGCTTCTCTGAC	1012
Db	965	TCAGCGGAGCTCTGAGCCCCCACTTGCATTAACAAGTACAGTGTCTCCAGTGTGCTGTAC	1022
OY	1013	AGCTGACCTGTGAAGTTTCCAGGCTGTG--GAGGAGCCCGAGAGGCTCAGCGCAGCT	1066
Db	1025	AGTTGACCTGTGGAGTCTTCCCAAGACTTGAAGAGGCCCGAAGAGCTCAGCCAGAGTT	1082
OY	1070	CCTCTGAGTCCAAGTGGCATATGTTCGGGCAATGGGAAAGAGCTCTCGGGGGGTGCTGGG	1122
Db	1085	CCTCTGAGTCCAAGTGGCATATGTTCGGGCAATGGGAAAGAGCTCTCGGGGGGTGCTTCA	1144
OY	1130	TGGAATCGGCTTCTCTTCAAGAGATCACTGTGCTGTCTCTTTGAGCGGAAACCTTCA	1188
Db	1145	TGGAATCAGGCTTCTCTCTCAAGAGATGTGTCTGTCTCTTTTGAAGGGGAAAGCTTCA	1200
OY	1190	CCAGGATCTGGGTACCAAGAGCTCCAGAAAGAAAGCTTGTGTGATGCCATGTGTTC-	1244
Db	1205	CAGGAGACTGGGCCCCAC-AGACATCCAGAAAGAAAGCTTGTGTGATGCCATGTATCA	1262
OY	1249	CGGACACCGAGAACTGTGAAGTCTTGCAGCCGCGAGACGTGGACCTGGACCTGGAC	1306

Db 1264 GGGGACACGAGCTGATGAAATCTCTACAGCCCAAGATGTGACTTGTGTTCTAGAC 1323
QY 1309 AGCGGTGCGAGCTGTGCTGCACTTGGCGGTGGAGGCGGGCAAGAGAGTGGCCCAAGTGG 1368
Db 1324 AGCAGTGCACGCTGTGCTGCACTTGGCGGTGGAGGCGGGCAAGAGAGTGTGTCAAGTGG 1383
QY 1369 CTGCTGCTCAACATGAGCCCAACCTGAGCAACCGGTAGGGGTCCACCCGTTGGAC 1428
Db 1384 CTGCTGCTTAACATGAGCCCAACCTGAGCAACCGGTAGGGGTCCACCACTGCAAT 1443
QY 1429 ATGCGCGTGGAGAGGAGTGGCGGGTGTCTGTGAGCTCTGTGCTGCAAGAGATCAAT 1488
Db 1444 ATGCGTGTGAGCGGAGAGAGAGATGTGTGAGCTACTGTAGCCCGAGAGCCAGT 1503
QY 1489 GTCAACGCGCAAGATGAGAGCAAGTGGACAGCTCTCCACTTTGCAAGCCCAAGCGGGAT 1548
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QY 1549 G-AGTCTAGCAACAGGCTGTGTTGGAGAGAGACGCTCGGTCAACGAGGTGACTTTGA 1607
Db 1564 GAGGCGCAGCAACAGAGCTGTGCTGCTAGAGAGAGATCTTCTCAATGAGTGGACTTTGA 1623
QY 1608 GGGCGCGAGCGCCCAATGCACTGTGCTGTGCAAGCGGAGAGAGATATCTGTGCGCATCT 1667
Db 1624 GGGCGCGAGCACCAATGCACTGTGCTGTGCAAGCGGAGAGATATCTGTGCGCATCT 1683
QY 1668 GCTGCGCGGAGCGCTGTGCACTGTGCTGTGCAAGCGGAGAGATATCTGTGCGCATCT 1727
Db 1684 GCTGCGCGGAGCGCTGTGCACTGTGCTGTGCAAGCGGAGAGATATCTGTGCGCATCT 1743
QY 1728 GCGTGCCTGTGAGAGGCGCACTGTGCTGTGCAAGCGGAGAGATATCTGTGCGCATCT 1787
Db 1744 TGTGCTCT-GCAGGCGCACTTCCCATTTGATGCTGTGCAAGCGGAGAGATATCTGTGCGCATCT 1802
QY 1788 TGTGACCGCGCAGAGCTGTGATGAGAGAGCGCCATTTGCACTGTGCGCGAGCGGAGCA 1847
Db 1803 TGTGATGCGCGCAGAGCTGTGATGAGAGAGCGCCATTTGCACTGTGCGCGAGCGGAGCA 1857
QY 1848 CTACCGCGCTGTGCGCGCATCTCTCATGTGACTGT 1878
Db 1858 TTTACGCTGTGCTGTGCGCATCTCTCATGTGACTGT 1888

RESULT 11
US-09-312-283C-66
; Sequence 66, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) --(1888)
; OTHER INFORMATION: n = A,T,C or G
US-09-312-283C-66

Query Match 54.5%; Score 1284; DB 4; Length 1888;
Best Local Similarity 83.1%; Pred. No. 1.5e-287;

Matches 1572; Conservative 0; Mismatches 298; Indels 21; Gaps 9;
QY 2 TGGAGGCGCACGCGCGGAGACCCCATGTGGCCCTGTGGCGCTGTGCGCACCTTGTGAGCGGGCG 61
Db 5 TGGAGGCGCGAGGCGCGGCGCGGTGTGGGCTGTGGGCTGTGCGCACCTTGTGAGCGGGCG 64
QY 62 AGTTTCAAGGCGCTGGAGAAAGTGGGCTGTGGGCGGCTTGTGGGAGGTGTACAAAGTGTGGCC 121
Db 65 AATTTCGAGGCTGGAGAAAGTGGGCTGTGGGCGGCTTGTGGGAGGTGTACAAAGTGTGGCC 124
QY 122 ATGTTCACGTGAAAGACTGTGCTG3CCATCAAGTGTGTGCGCCAGCTGTGACGTGTGAGACA 181
Db 125 ATGTGACTGTGAAAGACTGTGCTGCGCATCAAGTGTGTGCGCCAGTGTGTGACGTGTGAGACA 184
QY 182 GGGAGCGCAATGAGAGCTTTTGGAGAGAGCCAAAGAGTGGAGTGGGCAAGTTTGGCTACA 241
Db 185 GGGAGCAATGAGAGCTTCTGAGAGAGCTTAAGAGAGTGGAGTGGGCAAGTTTGGATACA 244
QY 242 TCTGCTGTGTATGAGACTGTGCGGAGACCTGTGCGCTGTGTATGTAGATATGAGAGA 301
Db 245 TTCTACTGTGTACGGCATATGCAAGAGACTGTGCGCTGTGTATGTAGATATGAGAGA 304
QY 302 CGGCTCTCTGGAAGACTGTGCTG3CTTGGAGCAATTTGCCATGTGGATCTCGGTTCCGAA 361
Db 305 CAGGCTCTCTGGAAGACTGTGCGCTGCAAGAGCAATTTGCCATGTGGATCTCGGTTCCGCA 364
QY 362 TCAATCCAGAGAGCGGCGGTGGGATGAACTTCTGCACTGTGATGGGCGCGCACTCTGCG 421
Db 365 TGTGCACTGAGAGAGCGGCGGTGGGATGAACTTCTGCACTGTGATGGGCGCGCACTCTGCG 424
QY 422 ACCTGAGCTCAAGCCCGCGCAACATCTGTGTGATGCGCCACTAC--ACGTCAAGATTTTC 479
Db 425 ACCTGAGCTCAAGCCCGCGCAACATCTGTGTGATGCGCCACTAC--ACGTCAAGATTTTC 484
QY 480 -TGATTTTGTGTGTGCGCAATGCAAGCGGCTGTGCTTCCATCTGTGATGACTTGTGAGATG 538
Db 485 TTTGACTTTTGGGCTGTGCGCAATGCAATGCGATGTGCTTCCATCTGTGATGACTTGTGAGATG 544
QY 539 GCGTGTGTGCAACATGCGCTTACCTGCTGAGAGGCGCATCAGGAGAGAGCGGCTGT 598
Db 545 GCGTGTGTGCAACATGCGCTTACCTGCTGAGAGGCGCATCAGGAGAGAGCGGCTGT 604
QY 599 TCGACACCAAGCAGATGTATACAGCTTTTGCATCTGTGAGGCGGTCTCAACAGA 658
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QY 659 AGAAGCGCTTTGCAATGAGAGAAACATCTGTGCACTATGAGTGTGAGAGGCGG 718
Db 665 ATATTCATTTTGCAGATGAGAGAAACATCTGTGCACTATGAGTGTGAGAGGCGG 724
QY 719 ACCGCGCGGAGCTGCGCGCTGTGAGAGCGCGCGCGCGCTGTGAGCACTGTATAC 778
Db 725 ACCGCGCGGAGCTGCGCGCATCTGTGAGAGCGCGCGCGCGCTGTGTGCGCACTGTATAG 784
QY 779 GCTCATGAGCGGTGTGCGAGGAGGATTCGCGAGTTAG3CCCACTTTCAGAGAAATTA 838
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QY 839 CTTTGTGAACCGAGAGACTGTGTGAAAGCTGTATGACGAAGTGAAGAAAGTGTCTATG 898
Db 845 CCTGTGAAGCAAGAGACTTGTGTGAAAGCTGTATGAGAGTGAAGAAAGTGTGTATG 904
QY 899 ATCTGAGCGTGAAGAAAGCGCGCGGAGCGCGAGAGCGAGTGTGTGCGG-----AGGC 952
Db 905 AGCGAGCGAGAGAAAGCTTCTTGAAGTTCGAAGAGTGAAGCGCAAGCGCGAGTCTTCAAGCC 964
QY 953 TCAAGCGGCGCTTGTGCGCGCACTTGTGATTAAGACTACAGCTTCTCGAGCTTCTTAC 1012
Db 965 TCAAGCGGCGCTTGTGCGCGCGCTTGTGATTAAGACTACAGCTTCTCGAGTGTGTAC 1024
QY 1013 AGCTGAGCTGTGAGTTTCCAGGCTGTG---GAGGCGCGCGAGAGACTCAGCGGAGCT 1069
Db 1025 AGTTGAGCTGTGGATCTTCCAGACTTGTGAAGGCGCGCGAGAGACTCAGCGGAGTT 1084

QY 1070 CCTCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1129
DB CCTCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1144
QY 1130 TGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1189
DB TGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1204
QY 1190 CCAGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1248
DB CCAGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1263
QY 1205 CAGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1263
DB CAGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1323
QY 1249 CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1308
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QY 1309 AGCGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1368
DB AGCGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1383
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QY 1429 ATGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1488
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DB GTCAAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1563
QY 1504 GTCAAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1563
DB GTCAAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1607
QY 1549 G-AGTCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1607
DB G-AGTCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1623
QY 1608 GGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1667
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QY 1668 GTTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1727
DB GTTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1743
QY 1728 CCTGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1787
DB CCTGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1802
QY 1744 TGTGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1802
DB TGTGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1847
QY 1788 TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1847
DB TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1857
QY 1803 TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1857
DB TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1878
QY 1848 CTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1878
DB CTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1888
QY 1858 TTTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1888
DB TTTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1888

RESULT 12
US-09-949-016-12845
Sequence 12845, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12845
LENGTH: 31718
TYPE: DNA
ORGANISM: Human
US-09-949-016-12845

Query Match 48.1%; Score 1131.6; DB 4; Length 31718;
Best Local Similarity 99.5%; Pred. No. 8.2e-252;
Matches 1156; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1195 GATCTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1253
DB GATCTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1253
QY 1205 CAGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1263
DB CAGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1263
QY 1249 CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1308
DB CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1313
QY 1309 AGCGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1368
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QY 1369 CTGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1428
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DB ATGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1493
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QY 1504 GTCAAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1563
DB GTCAAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1563
QY 1549 G-AGTCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1607
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DB GTTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1733
QY 1728 CCTGCTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1787
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QY 1788 TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1847
DB TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1847
QY 1803 TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1857
DB TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1857
QY 1848 CTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1878
DB CTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1878
QY 1858 TTTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1888
DB TTTACGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1888

QY 1854 CGTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1913
DB CGTGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1913
QY 1914 GACAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1973
DB GACAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 1973
QY 1974 TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 2033
DB TGTGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 2033
QY 2034 CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 2093
DB CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 2093
QY 2093 CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 2153
DB CGGAGTCCAGAGCTGCTCCAGAGTGGAGAGAGCTCTCGGGGGTGTCTCGG 2153

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RESULT 13
US-09-949-016-16947
; Sequence 16947, Application US/09949016
; Patent No. 681339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16947
; LENGTH: 31720
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16947

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Query Match	Similarity	48.1%	Pred. No.	8.2e-252	DB 4	Length	31720											
Best Local	Similarity	99.5%	Pred.	No.	8.2e-252	DB 4	Length											
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							Gaps											
QY	1195	GATCTGGGTA	CCA	CMA	CGTCC	GAGA	GAA	GAA	GCTTGTGTGATGTCATCGTCC-GGGA	1253								
Db	27095	GATCTGGGGCA	CAC	A	ACGCTC	GAGA	GAA	GAA	GCTTGTGTGATGTCATCGTCCGGGGA	27153								
QY	1254	CACCA	GCAAA	CTGAT	TGA	AGAT	CCT	CGAC	CGCGCA	AGAC	CTGTGCA	CAC	CGG	1313				
Db	27154	CACCA	GCAAA	CTGAT	TGA	AGAT	CCT	CGAC	CGCGCA	AGAC	CTGTGCA	CAC	CGG	27213				
QY	1314	TG	CAC	GCCTG	CTG	CA	CT	CG	CGGTG	AG	CGCGG	CA	AG	AGATG	TGGCG	CTG	CT	1373
Db	27214	TG	CAC	GCCTG	CTG	CA	CT	CG	CGGTG	AG	CGCGG	CA	AG	AGATG	TGGCG	CTG	CT	27273
QY	1374	GCT	CA	CA	CAT	TGCC	CA	CC	CT	GA	CA	CC	CT	GA	CA	TGGC	1433	
Db	27274	GCT	CA	CA	CAT	TGCC	CA	CC	CT	GA	CA	CC	CT	GA	CA	TGGC	27333	
QY	1434	CG	TGA	G	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	1493	
Db	27334	CG	TGA	G	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	27393	
QY	1494	CG	CA	AG	AT	GA	GC	CA	GC	CT	CA	CT	TG	CA	CC	CA	AG	1553

Db	27394	CGCCAGAGATGAGAGACCACTGAGCAACGCCCTTCCACTTTGGACGCCAAGAACGGGGAGCAAGTCC	27455
QY	1554	TAGACACCGGCTCTGTTGGAGAGAAAGCGCTCGGTCAAAGAGTGAACCTTTGAGGGCCG	1613
Db	27454	TAGACACCGGCTCTGTTGGAGAGAAAGCGCTCGGTCAAAGAGTGAACCTTTGAGGGCCG	27513
QY	1614	GAGCCCATATCAGCTGGCCCTGACAGACGGGCGAGAGAAATATCTGTCGATCCTGCTGG	1673
Db	27514	GAGCCCATCAGCTGGCCCTGACAGACGGGCGAGAGAAATATCTGTCGATCCTGCTGG	27573
QY	1674	CCGAGGCGTGAAGCTGAGCCTTGACAGGGGCAAGATATGCTGGCTGCCACTGCATCACTGCTGC	1733
Db	27574	CCGAGGCGTGAAGCTGAGCCTTGACAGGGGCAAGATATGCTGGCTGCCACTGCATCACTGCTGC	27633
QY	1734	CTGGCAGGGGCAACTGCTCCATCGTCAAAGCTGCTGGCCAAAGCAGCCGGGGGTGAGTGTGAA	1793
Db	27634	CTGGCAGGGGCAACTGCTCCATCGTCAAAGCTGCTGGCCAAAGCAGCCGGGGGTGAGTGTGAA	27693
QY	1794	CGCCCAACGCTGGATGGAGGAGCGGCATTGGACCTGGGCGGCAAGCGGGGGGACCTAACCG	1853
Db	27694	CGCCCAACGCTGGATGGAGGAGCGGCATTGGACCTGGGCGGCAAGCGGGGGGACCTAACCG	27755
QY	1854	CGTGGCCCGGATCCTCATTCGACCTGTGCTTCCAGCGTCAAAGTCTGAGGCTGTGTGGCACA	1913
Db	27755	CGTGGCCCGGATCCTCATTCGACCTGTGCTTCCAGCGTCAAAGTCTGAGGCTGTGTGGCACA	27813
QY	1914	GACACCCCTTCACAGTGGCCGCGGGAGACGGGGGCAACAGACACTGGCAGGCTGCTCTGCA	1973
Db	27814	GACACCCCTTCACAGTGGCCGCGGGAGACGGGGGCAACAGACACTGGCAGGCTGCTCTGCA	27873
QY	1974	TCCGGGCGCTGGAGAGAGGCGCTGACCTTCAGACCGGCTAACCCGCTCTGCACTTGCTGC	2033
Db	27874	TCCGGGCGCTGGAGAGAGGCGCTGACCTTCAGACCGGCTAACCCGCTCTGCACTTGCTGC	27933
QY	2034	CCGCAACGGAACCTTGGCCACTGTCAAAGCTGCTTGTGAGAGAGAGGCCGATGTGCTGCG	2093
Db	27934	CCGCAACGGAACCTTGGCCACTGTCAAAGCTGCTTGTGAGAGAGAGGCCGATGTGCTGCG	27993
QY	2094	CCGGGGAGCCCTTGAAACGAGCGGCGGTGCAACCTGGCTGGCGGCAACGGGCACTCGGAGGT	2153
Db	27994	CCGGGGAGCCCTTGAAACGAGCGGCGGTGCAACCTGGCTGGCGGCAACGGGCACTCGGAGGT	28053
QY	2154	GATTGAGAGATTGATGACGCGCCGATGTCAATTGAACCTTTCGACAGACAGGGGCTCAGCGC	2213
Db	28054	GATTGAGAGATTGATGACGCGCCGATGTCAATTGAACCTTTCGACAGACAGGGGCTCAGCGC	28113
QY	2214	GCTGCACCTTGGCCGGCCCAAGGGCCGGCAACGACAGAGGTGAGAACTTCTCTCAGGGCATGG	2273
Db	28114	GCTGCACCTTGGCCGGCCCAAGGGCCGGCAACGACAGAGGTGAGAACTTCTCTCAGGGCATGG	28173
QY	2274	GGCCCAATCAACCTTGACAGGCTTCAAAGTTCCAGGGCGGCGCAATGGCCCGCGCCCAACT	2333
Db	28174	GGCCCAATCAACCTTGACAGGCTTCAAAGTTCCAGGGCGGCGCAATGGCCCGCGCCCAACT	28233
QY	2334	CTTGCGGCGAAGCAAGACTTAG	2355
Db	28234	CTTGCGGCGAAGCAAGACTTAG	28255

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1 RESULT 14
2 US-09-949-016-39628/C
3 ; Sequence 39628, Application US/09949016
4 ; Patent No. 6812339
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: VENTER, J. Craig et al.
8 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
9 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
10 ;
11 ; FILE REFERENCE: CL001307
12 ;
13 ; CURRENT APPLICATION NUMBER: US/09/949,016
14 ;
15 ; CURRENT FILING DATE: 2000-04-14
16 ;
17 ; PRIOR APPLICATION NUMBER: 60/241,755
18 ;
19 ; PRIOR FILING DATE: 2000-10-20
20 ;
21 ; PRIOR APPLICATION NUMBER: 60/237,768
22 ;

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;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 39628
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-39628

Query Match 23.6%; Score 555.4; DB 4; Length 601;
Best Local Similarity 99.1%; Pred. No. Se-119; Indels 2; Gaps 2;
Matches 578; Conservative 1; Mismatches 2;

QY 1195 GATCTGGGTACCAACAAGCTCCAGAGAAGAGCTTGTGATGTCATCGTGTCC-GGGA 1253
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QY 1254 CACCAAGAACTGATGAAGATCTTCAGCCGCGAGAGCTGGAAGCTGGACCTGGACAGCGG 1313
DB 523 CACCAAGAACTGATGAAGATCTTCAGCCGCGAGAGCTGGAAGCTGGACCTGGACAGCGG 464
QY 1314 TGCAGGCTGTGCACTTGGCGGTGAGAGCGCGGCAAGAGAGTGGCGCAAGTGGCTCT 1373
DB 463 TGCAGGCTGTGCACTTGGCGGTGAGAGCGCGGCAAGAGAGTGGCGCAAGTGGCTCT 404
QY 1374 GCTCAACAATGCAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCTTGGACATGGC 1433
DB 403 GCTCAACAATGCAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCTTGGACATGGC 344
QY 1434 CGTGAAGAGAGGGGTGCGGGGTGTCTGTGAGAGCTCTGTGCAAGAGATCAAGTGTCAA 1493
DB 343 CGTGAAGAGAGGGGTGCGGGGTGTCTGTGAGAGCTCTGTGCAAGAGATCAAGTGTCAA 284
QY 1494 CGCCAAAGATGAGAGCAAGTGGACAGCCCTCCACTTTGAGGCCAAGACGGGAGTAGTC 1553
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QY 1554 TAGCACAAGGCTGTGTTGAGAGAGAGCTCTCGGTCAACGAGGTGGAATTTGAGGGCGG 1613
DB 223 TAGCACAAGGCTGTGTTGAGAGAGAGCTCTCGGTCAACGAGGTGGAATTTGAGGGCGG 164
QY 1614 GACGCCCATGACAGTGGCTGTGCAAGACGGGCAAGAGAAATATCGTGGCATCTGCTGG 1673
DB 163 GACGCCCATGACAGTGGCTGTGCAAGACGGGCAAGAGAAATATCGTGGCATCTGCTGG 104
QY 1674 CCGAGGCGTGGACGTGAGCTTCAGAGGGCAAGAGATCTCGGCTGCACTAGAGCTGC 1733
DB 103 CCGAGGCGTGGACGTGAGCTTCAGAGGGCAAGAGATCTCGGCTGCACTAGAGCTGC 44
QY 1734 CTGGCAAGGGCACTGGCCCATGTCAGTCAAGTGTGGCCAAAGCAG 1776
DB 43 CTGGCAAGGGCACTGGCCCATGTCAGTCAAGTGTGGCCAAAGCAG 1

RESULT 15
US-09-949-016-181231/c
; Sequence 181231. Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 181231
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-181231

Query Match 23.6%; Score 555.4; DB 4; Length 601;
Best Local Similarity 99.1%; Pred. No. Se-119; Indels 2; Gaps 2;
Matches 578; Conservative 1; Mismatches 2;

QY 1195 GATCTGGGTACCAACAAGCTCCAGAGAAGAGCTTGTGATGTCATCGTGTCC-GGGA 1253
DB 582 GATCTGGGTACCAACAAGCTCCAGAGAAGAGCTTGTGATGTCATCGTGTCCGGGA 524
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DB 523 CACCAAGAACTGATGAAGATCTTCAGCCGCGAGAGCTGGAAGCTGGACCTGGACAGCGG 464
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QY 1374 GCTCAACAATGCAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCTTGGACATGGC 1433
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QY 1434 CGTGAAGAGAGGGGTGCGGGGTGTCTGTGAGAGCTCTGTGCAAGAGATCAAGTGTCAA 1493
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QY 1614 GACGCCCATGACAGTGGCTGTGCAAGACGGGCAAGAGAAATATCGTGGCATCTGCTGG 1673
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QY 1674 CCGAGGCGTGGACGTGAGCTTCAGAGGGCAAGAGATCTCGGCTGCACTAGAGCTGC 1733
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DB 43 CTGGCAAGGGCACTGGCCCATGTCAGTCAAGTGTGGCCAAAGCAG 1

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Job time : 1155.4 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
13358.712 Million cell updates/sec

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Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_esc1:*
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7: gb_esc6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2138.8	90.8	2173	9	AY419490	Homo sapi
2	1637.2	69.5	1901	9	AY419491	Pan trogl
3	1604.4	68.1	2173	9	AY419492	AY419492 Mus muscu
4	1571.8	66.7	3741	3	AK077233	AK077233 Homo sapi
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6	843.4	35.8	1119	5	BM924233	BM924233 AGENCOURT
7	691.6	29.4	731	7	CN308493	CN308493 170004241
8	651.2	27.7	830	4	BG031653	BG031653 602300806
9	647.2	27.5	924	5	BU151784	BU151784 AGENCOURT
10	567.4	24.1	768	4	B1558987	B1558987 603241351
11	545	23.1	583	5	BP132709	BP132709 BP132709
12	544	23.1	583	5	BP248960	BP248960 BP248960
13	543.4	23.1	583	5	BP314864	BP314864 BP314864
14	542.4	23.0	582	5	BP248808	BP248808 BP248808
15	537.6	22.8	580	5	BP277059	BP277059 BP277059
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18	529	22.5	588	5	BP246741	BP246741 BP246741
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21	509.8	21.6	789	4	B1689810	B1689810 603316024
22	493.2	20.9	642	7	CN715008	CN715008 E0644G01-
23	485.8	20.6	719	7	CN529728	CN529728 UT-M-H00-
24	469.6	19.9	908	5	BQ957957	BQ957957 AGENCOURT

25	462.2	19.6	928	6	CA787797	CA787797 AGENCOURT
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28	436.8	18.5	544	7	CP163286	CP163286 B0723H08-
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30	433.6	18.4	544	7	CK338360	CK338360 C0629C05-
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32	425.6	18.1	938	4	BG242784	BG242784 602355424
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35	405.6	17.0	508	7	CP161687	CP161687 B0700F02-
36	399.8	17.0	499	7	CN673475	CN673475 A0934H11-
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38	386	16.4	644	2	BF102436	BF102436 601751858
39	373.2	15.8	640	1	AI862829	AI862829 AL862929
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45	353.2	15.0	885	6	CA792904	CA792904 AGENCOURT

ALIGNMENTS

RESULT 1	AY419490	2173 bp	DNA	linear	GSS 17-DEC-2003
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DEFINITION	Homo sapiens ANKRD3 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY419490.1	GI:39775447			
VERSION	AY419490.1	GI:39775447			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2173)				
AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Fertiera,S., Wang,G., Zheng,X.H., White,T.D., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCES	2 (bases 1 to 2173)				
AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Fertiera,S., Wang,G., Zheng,X.H., White,T.D., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submision				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.				
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source	1..2173				
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>2173 /gene="ANKRD3" /locus_tag="HCM6908"				
ORIGIN	90.8%; Score 2138.8; DB 9; Length 2173; Best Local Similarity 99.6%; Pred. No. 0; Matches 2165; Conservative 0; Mismatches 7; Indels 2; Gaps 2;				
QY	183 GGAGGCGATGAGCTTTGGAAGAGCAAGAGATGAGATGCGCAATTTCGTACAT 242				

Dh 1 GGAAGCATGGAAGCTTTTGGAGAAGCCAAAGAAATGGAATGGCCAAAGTTTGCTACAT 60
Qy 243 CCGGCTGTGTATGCAATCTGGCCGGAACCTGTGGCCTGTGATGGAATACATGGAGAC 302
Db 61 CCGGCTGTGTATGCAATCTGGCCGGAACCTGTGGCCTGTGATGGAATACATGGAGAC 120
Qy 303 GGGGCTCCCTGGAAAAGCTGGCTTGGAGCCATTGCAATGGGATCTCCGGTTCCGAAT 362
Db 121 GGGGCTCCCTGGAAAAGCTGGCTTGGAGCCATTGCAATGGGATCTCCGGTTCCGAAT 180
Qy 363 CATCCAGAGACGGCGGTGGCATGAACCTTCTGCACTGATGAGCCCGGCACCTCTGCA 422
Db 181 CATCCAGAGACGGCGGTGGCATGAACCTTCTGCACTGATGAGCCCGGCACCTCTGCA 240
Qy 423 CTTGGACCTCAAGCCCGGAACATCTGCTGGATGCCCACTACAGCTCAAGATTTCTGA 482
Db 241 CTTGGACCTCAAGCCCGGAACATCTGCTGGATGCCCACTACAGCTCAAGATTTCTGA 300
Qy 483 TTTTGGCTGGCCGAAGTGCACAGGGGCTGTCCCACTGGATGACCTCAAGCATGATGGCT 542
Db 301 TTTTGGCTGGCCGAAGTGCACAGGGGCTGTCCCACTGGATGACCTCAAGCATGATGGCT 360
Qy 543 GTTTGGCAATCGCCTACCTCCCTCCAGAGCGCATCAAGGAGAAGCCGGCTCTTCA 602
Db 361 GTTTGGCAATCGCCTACCTCCCTCCAGAGCGCATCAAGGAGAAGCCGGCTCTTCA 420
Qy 603 CACCAAGCAAGATGTATACAGCTTTGGATGTGTATCTGGGGCGTGTCAACAGAA 662
Db 421 CACCAAGCAAGATGTATACAGCTTTGGATGTGTATCTGGGGCGTGTCAACAGAA 480
Qy 663 GCGCTTGGCAGATGAGAAGACATCTGCAATCATGATGATGAGGTGTAAGGGCCACG 722
Db 481 GCGCTTGGCAGATGAGAAGACATCTGCAATCATGATGATGAGGTGTAAGGGCCACG 540
Qy 723 CCGGAGCTGGCCGCTGTGTCAGAGCCGGCGCGGCTGTGAGCCACCTGATACGCT 782
Db 541 CCGGAGCTGGCCGCTGTGTCAGAGCCGGCGCGGCTGTGAGCCACCTGATACGCT 600
Qy 783 CATGCAAGGTGTGGCAGGGGGATCCGCGATTAAGCCCACTTCCAAAGAAATTAATTC 842
Db 601 CATGCAAGGTGTGGCAGGGGGATCCGCGATTAAGCCCACTTCCAAAGAAATTAATTC 660
Qy 843 TGAACCGAGGACCTGTGTGAAAAAGCTGATGACGAAGTGAAGAAATCTGCTCATGATCT 902
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Db 1080 AACTGATGAAGATCTTGAGCCGCAAGACGTGGAACCTTGACAAGCGGTGCCAGCC 1139

Qy 1322 TGCTGACCTGGCGGTGGAGGGCCGGCAAGAGAGTGGCCAAAGTGGCTGTCAACA 1381
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Qy 1382 ATGCCAACCCCAACCTGAGCAACCGTAAGGGCTCCACCCCGTTGCAATAGCCGTGAGA 1441
Db 1200 ATGCCAACCCCAACCTGAGCAACCGTAAGGGCTCCACCCCGTTGCAATAGCCGTGAGA 1259
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Db 1260 GGAAGGTGGGGGTGTGTGTAGAGCTCTGTGGCGGGAAGATCAATGTTCACGCCAAG 1319
Qy 1502 ATGAGGACAGTGGACAGCCCTCCACTTTGGACGCCAGAACGGGGATGAGTTAGACAC 1561
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Qy 1562 GGTGTGTGTGAGAAAGAACGCTTCGTGCAACGAGGTGAACCTTTGAGGGCCGGAAGCCCA 1621
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Qy 1682 TGGACGTGAGCTTGCAAGGGCAAGATGCTGGCTGCACTGCACTACGCTGCTGCAAG 1741
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genomic survey sequence.
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VERSION AY419491.1 GI:39775448
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1901)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tenenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
gene titlos
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1901)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tenenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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location/Qualifiers
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VERSION	AY419492.1	
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2173)

Clark, A.G., Głanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

TITLE
Interferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL
Science 302 (5652), 1960-1963 (2003)

PUBMED
REFERENCE
AUTHORS
14671302
2 (bases 1 to 2173)
Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejarival,A.,

TITLE
JOURNAL
COMMENT

Tanembalum, D.M., Ciavella, D.R., Lu, F., Murphy, B.,
Todd, M.A., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J.,
Ferreira, S., Adams, M.D. and Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.

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source	location/Qualifiers
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 HTC; CAP trapper.
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 1
 Carninci, P., and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Mech. Enzymol. 303, 19-44 (1999)
 99279253
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 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
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 3
 Shibata, K., Itoh, M., Aizawa, K., Nagata, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, U., Nishi, K., Kitamura, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, K., Kizawa, A., and Hayashizaki, Y.
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kizawa, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multichipillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3741)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
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 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
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 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 Direct Submission
 Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

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 REFERENCE 1 (bases 1 to 2691)
 Bloeker, H., Boecker, M., Brandt, P., Mewes, H.W., Weill, B., Amid, C., Obanger, A., Podo, G., Han, M. and Wiemann, S.
 The German CDNA Consortium
 Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
 COMMENT
 CONSRM Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
 TITLE Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 JOURNAL Braunschweig/Germany) within the CDNA sequencing consortium of the
 German Genome Project.
 This clone (DKFZp434B2328) is available at the RZPD Deutsches
 Ressourcentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp434B2328
 Further information about the clone and the sequencing project is
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 RRVAVSLIQGDVALPLHYAMQSHLPLVYKILAAQPVSVVAQTLDRTPHLAAQRG
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 Query Match 48.3%; Score 1138; DB 3; Length 2691;
 Best Local Similarity 99.8%; Pred. No. 9.8e-234;
 Matches 1160; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1195 GATCTGGGTATCCACAAGACCTCCAGAGAGAAAGAACTTGTGATGCACTGCTCC-GGGA 1253
 Db 36 GATCTGGGTATCCAC-AGACGTCAGAGAGAAAGAACTTGTGATGCACTGCTCCGGGA 94
 QY 1254 CACGAGAACTGATGAGATCTCTGAGCGCGGACAGAGACTGTGACCTGGAACAGCGG 1313
 Db 95 CACGAGAACTGATGAGATCTCTGAGCGCGGACAGAGACTGTGACCTGGAACAGCGG 154
 QY 1314 TGGCAGCTGTGCACTGCGCGGTGAGAGCGCGGAGAGAGAGATGTCGCTGCT 1373
 Db 155 TGGCAGCTGTGCACTGCGCGGTGAGAGCGCGGAGAGAGATGTCGCTGCT 214
 QY 1374 GCTCAACAATGCCAACCCCACTGAGAGAACCTGATGGGGCTCCACCCGGTGCACATGGC 1433
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 Db 395 TAGCACAGGCTGCTGTTGAGAGAGAACGCTTCGGTCAACAGAGTGAAGCTTTGAGGGCGG 454
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 Db 455 GACGCGCAATGACAGTGGCGCTGACAGACGAGGAGAGAAATATCGGCATCTCTGCG 514
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 Db 635 CGCCAGAGCGCTGATGAGAGAGAGCGCAATGCACTGCGCGGACAGCGCGGCACTACCG 694
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QY 1914 GACACCCCTGACAGTGGCCCGGAGACGAGGACACAGACACTGGCAGGCTGCTCCGCA 1973
DB 755 GACACCCCTGACAGTGGCCCGGAGACGAGGACACAGACACTGGCAGGCTGCTCCGCA 814
QY 1974 TCGGGGCGCTGGCAAGAGAGCGCTGACCTGACAGCGGCTACACCGCTGACCTGAGCTGC 2033
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DB 935 CCGGGGACCCCTGAAACGAGACGCGCTGACCTGCTGCGCCCAACCGGCGACTGAGAGT 994
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DB 995 GGTGAGAGAGTGTGTCAGCGCCGATGTCTATTGACCTGTTGACGAGCGAGGCTCAGCGC 1054
QY 2214 GCTGCACTGGCCCGCCGAGGCGCGGACGACACAGACGCTGAGACTGTGCTCAGGCAATGG 2273
DB 1055 GCTGCACTGGCCCGCCGAGGCGCGGACGACACAGACGCTGAGACTGTGCTCAGGCAATGG 1114
QY 2274 GCGCCACATCAACCTGACGAGACCTCAAGTTCCAGGCGCGGCGCCGCGCACACT 2333
DB 1115 GCGCCACATCAACCTGACGAGACCTCAAGTTCCAGGCGCGGCGCCGCGCACACT 1174
QY 2334 CTTGCGGCGAAGCAAGACTAG 2355
DB 1175 CTTGCGGCGAAGCAAGACTAG 1196

RESULT 6 1119 bp mRNA linear EST 12-MAR-2002
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DEFINITION AGENCOURT 6630417 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760485
ACCESSION BM924233
VERSION 1 GI:19374612
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1119)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M12807 row: j column: 06
High quality sequence stop: 664.
Location/Qualifiers
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/clone_id="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sports; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon, 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.8%; Score 843.4; DB 5; Length 1119;
Best Local Similarity 94.1%; Pred. No. 1.8e-170;
Matches 987; Conservative 0; Mismatches 46; Indels 16; Gaps 10;

QY 1 ATGAGAGGCGACCGCGGAGACCCCATATGGCCCTGGCGCTGCTGCGACACTTGCAGCGGCG 60
DB 12 ATGAGAGGCGACCGCGGAGACCCCATATGGCCCTGGCGCTGCTGCGACACTTGCAGCGGCG 71
QY 61 GAGTTCAAGGAGCTGGGAGAGAGTGGCTCGGAGCGCTTCCGAGAGTGTACAAAGTGGCG 120
DB 72 GAGTTCAAGGAGCTGGGAGAGAGTGGCTCGGAGCGCTTCCGAGAGTGTACAAAGTGGCG 131
QY 121 CATGTCACTGAAAGACCTGGCTGGCATCAAGTGTGCTGCCAGCTGCAAGTGCAGAC 180
DB 132 CATGTCACTGAAAGACCTGGCTGGCATCAAGTGTGCTGCCAGCTGCAAGTGCAGAC 191
QY 181 AGGAGAGGCGATGAGACTTTTGAAGAGCAAGAGATGAGATGAGCAAGTTTCGCTAC 240
DB 192 AGGAGAGGCGATGAGACTTTTGAAGAGCAAGAGATGAGATGAGCAAGTTTCGCTAC 251
QY 241 ATCTGCTGCTGTATGACATCTGCGCGAACTGTTCGAGCTGTGTATGATGATGATGAG 300
DB 252 ATCTGCTGCTGTATGACATCTGCGCGAACTGTTCGAGCTGTGTATGATGATGATGAG 311
QY 301 ACGGAGCTCCCTGAGAAAGCTGGCTTGGAGAGCATTTGCGATGGATTCCTGGTTCCGA 360
DB 312 ACGGAGCTCCCTGAGAAAGCTGGCTTGGAGAGCATTTGCGATGGATTCCTGGTTCCGA 371
QY 361 ATCATTCACAGAGACGCGGCGTGGGATGAACCTTCTGTGACAGTACAGTGGCCGCACTCTG 420
DB 372 ATCATTCACAGAGACGCGGCGTGGGATGAACCTTCTGTGACAGTACAGTGGCCGCACTCTG 431
QY 421 CACCTGACCTCAAGCCCGGAAACATCTCTGTGATGCCCATCAACGTCAGATTTCT 480
DB 432 CACCTGACCTCAAGCCCGGAAACATCTCTGTGATGCCCATCAACGTCAGATTTCT 491
QY 481 GATTTTGTCTGGCAAGTGAACGAGGCTGTCCATCTGCAATGACCTCAGATGATGATGAG 540
DB 492 GATTTTGTCTGGCAAGTGAACGAGGCTGTCCATCTGCAATGACCTCAGATGATGATGAG 551
QY 541 CTGTTTGGCAAAATCGGCTTACCTCCCAAGAGCGATCAAGGAGAGAGCGGCTCTTC 600
DB 552 CTGTTTGGCAAAATCGGCTTACCTCCCAAGAGCGATCAAGGAGAGAGCGGCTCTTC 611
QY 601 GACACCAAGACAGATGTATACAGCTTTCGATCTGATCTGAGGCGCTGTACACAGAG 660
DB 612 GACACCAAGACAGATGTATACAGCTTTCGATCTGATCTGAGGCGCTGTACACAGAG 671
QY 661 AAGCGTTTGGCAATGAGAGAAACATCTGTGACATCATGTGAAAGGT-GGTGAAAGGCGCA 719
DB 672 AAGCGTTTGGCAATGAGAGAAACATCTGTGACATCATGTGAAAGGT-GGTGAAAGGCGCA 731
QY 720 CCGGCGCGAGCTGCGCGCGCTGTGCAAGGCGGCGCGGCGCTGCGACCACTGATACG 779
DB 732 CCGGCGCGAGCTGCGCGCGCTGTGCAAGGCGGCGCGGCGCTGCGACCACTGATACG 791
QY 780 CTTGATGACAGGCTGTGCAAG-GGGGAGTCCGCGAGTTAGGCCCACTTCCAG-AAATT 837
DB 792 CTTGATGACAGGCTGTGCAAG-GGGGAGTCCGCGAGTTAGGCCCACTTCCAG-AAATT 851
QY 838 ACTTCTGAAACCGAGACCTGTGTG-AAAGCTGTGAGAGAGT-GAAGAAACTGTCTC 895
DB 852 ATTTCTGAAACCGAGACCTGTGTGAAAGCTGTGAGAGAGT-GAAGAAACTGTCTC 911

Qy	896	ATGAT-CTGACGCTGAAAAGCCCCCGAGGCC--AGAGGAGAGTGTG--CCTGCGAG	950		
Db	912	ATGATCTTGACGGGAAAAGCCCCCGGAGACCCGAGAACCAAGTGTGCTGGAG	971		
Qy	951	GCTCAGCGGGGCTCTGCCCCCA--CCTTGATNACGACTACAGCTTCC----	GAGCT 1004		
Db	972	GCTCAGGGGGGCTTGTGCCCCCACCCTTGAAAACGAAATTATAGGCTTTTCCGAA	GTTGT 1031		
Qy	1005	TCTCTCAGACTGACCTTGAGTTTCCC	1033		
Db	1032	TCTTAAGATTGACCTCGAGTTTCC	1060		
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DEFINITION	17000424186811 GRN_EB Homo sapiens CDNA 5', mRNA sequence.				
ACCESSION	CN308493				
VERSION	CN308493.1	GI:47324907			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	BukariOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 731) Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Ro, M. S., Mandalam, R., Lebowksi, J. and Stanton, L. M. Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 731 Std Error: 0.00. Location/Qualifiers 1..731 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_11b="GRN_EB" /note="Oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."				
FEATURES					
source					
ORIGIN					
Query Match	29.4%	Score 691.6;	DB 7;	Length 731;	
Best Local Similarity	99.2%;	Pred. No. 7.1e-138;			
Matches 716; Conservative	0;	Mismatches 4;	Indels 2;	Gaps 2;	
Qy	681	GAACTCTTGCACTCATCATGTGTGAAGTGTGAAGGCCACCGCCCCGAGCTGCGGCGCT	740		
Db	11	GGAAATCTTGCACTCATCATGTGTGAAGTGTGAAGGCCACCGCCCCGAGCTGCGGCGCT	70		
Qy	741	GGCAGAGGCCGCGCGCGCGCTGCGAGCACACTGATACGCTCATGACAGCGGTGCTGCA	800		
Db	71	GTGCGAGAGCCCGGCGCGCGCTGCGAGCACACTGATACGCTCATGACAGCGGTGCTGCA	130		
Qy	801	GGGGGATCCGCGAGTTAGGCCCACTTCCAGAAATTACTTGTGAAACCGAGACTGTG	860		
Db	131	GGGGGATCCGCGAGTTAGGCCCACTTCCAGAAATTACTTGTGAAACCGAGACTGTG	190		
Qy	861	TGAAAAGCCTGATGACGAAGTGAAAAGAACTGCTCATGATCTGAGACGTGAAAAGCCCC	920		
Db	191	TGAAAAGCCTGATGACGAAGTGAAAAGAACTGCTCATGATCTGAGACGTGAAAAGCCCC	250		

QY	921	GAAGCCCAAGAGAGAGGTGTGTGCTGTGGAGAGCTCAAGCGGAGCCCTGTGCCCACTTCGA	980
Db	251	GGAGCCCAAGAGAGAGGTGTGTGCTGTGGAGAGCTCAAGCGGAGCCCTGTGCCCACTTCGA	310
QY	981	TTAAGCACTAAGCCTCTCCAGCTTCTCTCAAGCTGGACTCTGAGTTTCCAGAGCTGT	1040
Db	311	TTAAGCACTAAGCCTCTCCAGCTGCTCTCAAGCTGGACTCTGAGTTTCCAGAGCTGT	370
QY	1041	CGAGGGCCCGCAGAGAGCTCAAGCGCAGACTCTCTGAGTCCAACTGTCATGTTCGGCAG	1100
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QY	1101	TGGGAAAGAGCTCTCGGGGGGTGTCTCTGTGTGAACTCGGCTTCTCTTCCAGAGATCACT	1160
Db	431	TGGGAAAGAGCTCTCGGGGGGTGTCTCTGTGTGAACTCGGCTTCTCTTCCAGAGATCACT	490
QY	1161	GTCCCTGTCTTTGAGCGGGGAACCTTCAACCAAGGATCTGGGTACCAAGAAGTCGAGA	1220
Db	491	GTCCCTGTCTTTGAGCGGGGAACCTTCAACCAAGGATCTGGGCACACACAGACTCCAGA	549
QY	1221	AGAGGAAGCTTGTGTGATGTGCATCGTGTCC-GGGACACCAACAACTGATGAAGATCTGTGC	1279
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QY	1280	AGCGCAGAGACGTGTGAACCTGTGCACTGTGACAGCGGTGCAAGCTGTGCACCTGTGGCGGTGG	1339
Db	610	AGCGCAGAGACGTGTGAACCTGTGCACTGTGACAGCGGTGCAAGCTGTGTGCACCTGTGGCGGTGG	669
QY	1340	AGGCGCGGCAAGAGAGTGTGGCCCAAGTGTGTCTGTCTCAACATGTGCCAATCCCAACTTGA	1399
Db	670	AGGCGCGGCAAGAGAGTGTGGCCCAAGTGTGTCTGTCTCAACATGTGCCAATCCCAACTTGA	729
QY	1400	GC 1401	
Db	730	GC 731	
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RESULT 8
LOCUS      BG031653
DEFINITION  BG031653      830 bp      mRNA      linear      EST 24-JAN-2001
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ACCESSION  BG031653
VERSION    BG031653.1  GI:12422155
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1  (bases 1 to 830)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgsabers@mai.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L14M10110 row: 1 column: 01
            High quality sequence stop: 646.

Location/Qualifiers
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FEATURES
Source

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ORIGIN

/note="Organ: breast; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

Query Match 27.7%; Score 651.2; DB 4; Length 830;
Best Local Similarity 93.8%; Pred. No. 3.5e-129;
Matches 765; Conservative 0; Mismatches 43; Indels 8; Gaps 8;

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1239 GGCACCTGACA-GCGGTGCCAGCTCTGACCTTGCGCGGTGAGAGCGCGGACAGAGAGT 1357
61 GGCACCTGACAAGCGCGGTGCCAGCTCTGACCTTGCGCGGTGAGAGCGCGGACAGAGAGT 120
1358 GCGCAACTGGCTGCTGCTCAACAAATGCAACCCCACTGAGCAACGCTGAGGCGCTCA 1417
121 GCGCAACTGGCTGCTGCTCAACAAATGCAACCCCACTGAGCAACGCTGAGGCGCTCA 180
1418 CCCCCTTGACATGGCCGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1477
181 CCCCCTTGACATGGCCGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
1478 GGAAGATCATGTCTCAAGCCCAAGATGAGAGCAAGCTGAGCAAGCCCTGCACTTTGAGCC 1537
241 GGAAGATCATGTCTCAAGCCCAAGATGAGAGCAAGCTGAGCAAGCCCTGCACTTTGAGCC 300
1538 AGAAGCGGGATGAGCTGAGCAACGCGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1597
301 AGAAGCGGGATGAGCTGAGCAACGCGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
1598 TGGAATTGAGAGGCGGACGCGCATGACAGTGGCTTGCAGAGCAGGAGAGAGAGATATCG 1657
361 TGGAATTGAGAGGCGGACGCGCATGACAGTGGCTTGCAGAGCAGGAGAGAGAGATATCG 420
1658 TGCGCATCTGCTGCGCGGAGCGGTGAGAGCTTGCAGAGGCAAGAGATGCTGGCTGC 1717
421 TGCGCATCTGCTGCGCGGAGCGGTGAGAGCTTGCAGAGGCAAGAGATGCTGGCTGC 480
1718 CACTGCATCAAGCGCTGAGAGAGGCGCACTGCGCATGAGTGCATGAGCTGAGCAAGCAGC 1777
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1778 CCGGGGATGAGTGAAGCCCGCAGAGCTGAGTGAAGAGAGCGC-ATTGCACCTGGCGCA 1836
539 CCGGGGATGAGTGAAGCCCGCAGAGCTGAGTGAAGAGAGAGCGCATTGCACTGGCGCA 598
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599 CAGCGCGGACATCAAGCGGTGAGCGCATCTGATGACCTGTGCTCCGACGTCACGTC 657
1897 -TGCAAGCTGCTGCG-CAGAGACAGCCCTG-CACGTGCGCGGAGAGAGCGGAGACAGAGC 1953
658 TTGCAAGCTGCTGCGCGCAGAGACCTCTGATCTGTTGCTCGGAGAGACGCGGCGCAAGC 717
1954 ACTGCAGAGCTGCTCTGATGAGAGGCGCTGAGCAAGAGCGCTGACCTGACAGCGCTAC 2013
718 ACTGCAGAGCTGCTCTGATGAGAGGCGCTGAGCAAGAGCGGAGAGAGGCGGAGAGCTCCGAAACCGGTT 777
2014 ACCGCTGACACTGAGCTGCGCGGCAAGAGACCTG 2049
778 ACCGCTGAGCTGAGCTGAGCTGAGCGGAGAGCGGCACTG 813

RESULT 9
BUI51784 924 bp mRNA linear EST 03-SEP-2002
LOCUS BUI51784
DEFINITION AGENCOURT 8753255 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6394286
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BUI51784
BUI51784.1 GI:22665316
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Mark Macdonald, Ph.D. and Nancy L. Freeman,
Ph.D.

FEATURES
source

CDNA Library Preparation: Resgen, Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LHAM1387 row: b column: 15
High quality sequence stop: 649.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH MGC 130"
/note="Organ: olocyats; Vector: PCMV-SPORT6.1; Site 1:
EcoRV, Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.95 kb. Constructed by
Resgen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.5%; Score 647.2; DB 5; Length 924;
Best Local Similarity 85.3%; Pred. No. 2.5e-128;
Matches 733; Conservative 0; Mismatches 124; Indels 2; Gaps 1;

10 GAGCGCGGAGACCCCATGAGGCGCTGCGCGCATGTCGACCTTCAAGCGGCGAGATTGACG 69
1 GAGCGCGGAGACCCCATGAGGCGCTGCGCGCATGTCGACCTTCAAGCGGCGAGATTGACG 60
70 GCGTGGAGAGAGTGGCTGCGGCGCTTGGGAGAGTGAAGAGTGGCGCATGTCAC 129
61 GCGTGGAGAGAGTGGCTGCGGCGCTTGGGAGAGTGAAGAGTGGCGCATGTCAC 120
130 TGGAAGACTGGGCTGAGCATCAAGTGTGCGCCAGCGTGCACGTCAGACAGAGGAGGCG 189
121 TGGAAGAGTGGCTGAGCATCAAGTGTGCGCCAGTGTGACGTCAGACAGAGGAGAGCA 180
190 ATGAGGCTTTTGAAGAAGCCCAAGAGATGAGATGAGCAAGTTGCTACATCTGCT 249
181 ATGAGGCTCTGAGAGAGAGCAAGTGAAGATGAGATGAGCAAGTTGCTACATCTGCT 240
250 GTGATGAGCATCTGCGGAGACCTGTGCGCTGCTGATGAGATGAGAGAGCGGCTCC 309
241 GTGATGAGCATCTGCGGAGACCTGTGCGCTGCTGATGAGATGAGAGAGCGGCTCC 300
310 CTGAAGAGCTGCTGCGCTGAGAGCAATGCAATGAGATGCTCGGATCCGAATATCAAC 369
301 CTGAAGAGCTGCTGCGCTGAGAGCAATGCAATGAGATGCTCGGATCCGAATATCAAC 360
370 GAGAGCGGAGTGGCATGAATCTTCTGACATGACAGCCCGCATCTGACAGCTGAGAC 429
361 GAGAGCGGAGTGGCATGAATCTTCTGACATGACAGCTTCTGACAGCTGAGACAGCTGAGAC 420
430 CTGAAGCCCGGAGACATCTGCTGAGATGCCCATGACAGTCAAGATTTCTGATTTGCT 489
421 CTGAAGCCCGGAGACATCTGCTGAGATGCCCATGACAGTCAAGATTTCTGATTTGCT 480

ORIGIN	and	Differentiation 7, 3-11 (1996)."
Query Match	24.1%;	Score 567.4; DB 4; Length 768;
Best Local Similarity	87.3%;	Pred. No. 3.5e-11;
Matches 633; Conservative	0; Mismatches 91;	Indels 1; Gaps 1;
QY	1	ATGGAGGGCGACGCGCGGACCCCAATGGAGCCCTGGCGCTGCTGCGCACCTTCGACGCGGGC 60
DB	20	ATGAGGGCGAGAGGGCCGGGGCCGGGTGGGCTCTGGGGGCTGCTGGCGCACCTTCGACGCGGGC 79
QY	61	GAGTTCACGGGCTGGAGAGAGTGGGCTTCGGGGCGGCTTCGGGGCAGGTGTACAA-GGTGCG 119
DB	80	GAATTCGACGAGCTGGAGAGAGTGGGCTTCGGGGCGGCTTCGGGGCAGGTGTACAAAGTGTGCG 139
QY	120	CCATGTCCATCTGGAGAGACCTGGGCTGGGCATCAATGCTCGGCCGACGCTGCAGCGTGCAGCA 179
DB	140	CCATGTGACATCGAGAGAGCTGGGCTGGGCATCAATGCTCGGCCGACGCTGCAGCGTGCAGCA 199
QY	180	CAGGAGAGCGCANTGAGAGCTTTTGGAGAGAGCCAAAGAGATGAGATGAGCCAAAGTTTCGCTA 239
DB	200	CAGGAGACGAATGAGAGCTCTCTGGAGAGAGCTCAAGAGATGAGATGAGCCAAAGTTCCGATA 259
QY	240	CATCTGCTGTGTATGAGCATCTGCCGGAACCTGTGGGCTGTGTCATGAGATCATGGA 299
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Db	350	GACAGGCTCCCTGGAGAGGCTGCTGGCTCAGAGCCATGCTTGGGACCTGGCCTTTG	579
Qy	360	AATATCCAGAGACGGGGGTGGGCATGAATCTTCTGCACTGCATGAGCCCGCACTCT	419
Db	380	CATGCTGCACAGACAGCCGTGGGCAATGAATTTCTGATGTCATGTCTCCGCCACTGT	439
Qy	420	GCACTGAGACTCAAGCCCGGAAATCTCTGATGGATGCCACTACACGTCMAATTTG	479
Db	440	GCACTTAGACTTGAAGCCAGGAACTCTCTGATGATGCCACTACATGTCAGATTTG	499
Qy	480	TGATTTTGGTGTGGCCAGTGCMAAGCGGCTGTCCACTCGATGATCCTCAGCATGGATGG	539
Db	500	TGACTTTGGGGTGGCCMAAGTGCATATGGATGTCCACTCTATGATCCTCAGATGGATGG	559
Qy	540	CCTGTTTGGCAATATCGCTTACTCTCTCCAGAGGCAATCAGGGAGAAAGCCGGCTCTT	599
Db	560	CCTGATGGGTACAAATCGCTTACTCTCTCCAGAGGAAATTCGTGAGGAAGACCGCTTGT	619
Qy	600	CGACACCAAGACGATGTATATACGTTTGGCATGTCTATCTGGGGCGGTCTCACACAGA	659
Db	620	TGACACGACAAATGATGTATACAGTTTCGCAATGTGATCTGGGGGTGTGCTTACACAGA	679
Qy	660	GAAAGCCGTTTCCAGATGAGAAAGAAATCTTCGCAATCATGTGGAGAAAGGTGTAAGGGCA	719
Db	680	GAAAGCAATTTGCAGATGAAAGAAACATCTTACACATCATGTATGAAGATGTGTACAGGGCA	739
Qy	720	CGGCC 724	

DB	/40	CGCC	/44
RESULT 11			
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LOCUS	BP312709 Sugano CDNA library, mammary gland	OCUB-F	linear
DEFINITION	CDNA clone OFR00893, mRNA sequence.		EST 17-SEP-2004
ACCESSION	BP312709		
VERSION	BP312709		
KEYWORDS	BP312709.1 GI:52241684		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 563)		

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mitsushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

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/clone_1lb="Sugano cDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"

ORIGIN
Query Match 23.1%; Score 545; DB 5; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.2e-106;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGAGGCGACAGCGGCGGACCCCATGGCCCTGCGCTGCGGACCTTGGACGCGGCG 60
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99 GAGTTACGCGGCTGGGAGAGAGTGGCTCGGCGCGCTTGGGAGGTATACAGGTGCGC 158
121 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTCTCGCCACGCTGACGACGAC 180
159 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTCTCGCCACGCTGACGACGAC 218
181 AGGAGGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGGCCAAAGTTTCGCTAC 240
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339 AGGAGGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGGCCAAAGTTTCGCTAC 398
361 ATCATCCACAGAGACGGCGGTGGGATGAACTTCCCTGCACTGATGAGCCCGGCACTCGTG 420
399 ATCATCCACAGAGACGGCGGTGGGATGAACTTCCCTGCACTGATGAGCCCGGCACTCGTG 458
421 CACCTGAGACTCAAGCCCGGGAACATCTGTGATGAGCCCACTACACAGTCAAGATTCT 480
459 CACCTGAGACTCAAGCCCGGGAACATCTGTGATGAGCCCACTACACAGTCAAGATTCT 518
481 GATTGTGATCTGGCCAAAGTGAACGGGCTGTCCCACTGCGATGACCTTCAAGATGAGTGC 540
519 GATTGTGATCTGGCCAAAGTGAACGGGCTGTCCCACTGCGATGACCTTCAAGATGAGTGC 578
541 CTGTT 545
579 CTGTT 583

RESULT 12
BP248960
LOCUS BP248960 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
DEFINITION HKR12328, mRNA sequence.
ACCESSION BP248960

VERSION BP248960.1 GI:52131239
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mitsushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/db_xref="taxon:9606"
/clone="HKR12328"
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ORIGIN
Query Match 23.1%; Score 544; DB 5; Length 583;
Best Local Similarity 99.8%; Pred. No. 3.6e-106;
Matches 544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGAGAGGCGACAGCGGCGGACCCCATGGCCCTGCGCTGCGGACCTTGGACGCGGCG 60
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99 GAGTTACGCGGCTGGGAGAGAGTGGCTCGGCGCGCTTGGGAGGTATACAGGTGCGC 158
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159 CATGTCCACTGGAAGACCTGGCTGGCCATCAAGTCTCGCCACGCTGACGACGAC 218
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339 AGGAGGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGGCCAAAGTTTCGCTAC 398
361 ATCATCCACAGAGACGGCGGTGGGATGAACTTCCCTGCACTGATGAGCCCGGCACTCGTG 420
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421 CACCTGAGACTCAAGCCCGGGAACATCTGTGATGAGCCCACTACACAGTCAAGATTCT 480
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481 GATTGTGATCTGGCCAAAGTGAACGGGCTGTCCCACTGCGATGACCTTCAAGATGAGTGC 540
519 GATTGTGATCTGGCCAAAGTGAACGGGCTGTCCCACTGCGATGACCTTCAAGATGAGTGC 578
541 CTGTT 545
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RESULT 13
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LOCUS         BP314864
DEFINITION    BP314864 Sugano cDNA library, mammary gland OCB-F Homo sapiens
               cDNA clone OR07268, mRNA sequence.
ACCESSION     BP314864
VERSION       BP314864.1
KEYWORDS      GI:52243839
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
               1 (bases 1 to 583)
               Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
               Mizushima-Sugano,J., Nakai,K. and Sugano,S.
               Sequence comparison of human and mouse genes reveals a homologous
               block structure in the promoter regions
               Genome Res. 14 (9), 1711-1718 (2004)
TITLE         JOURNAL
COMMENT       Contact: Yutaka Suzuki
               Department of Virology
               Institute of Medical Science, University of Tokyo
               4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
               Email: yusuzuki@ims.u-tokyo.ac.jp.
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 4.9e-106;
Matches 544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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39  ATGAGGGGCGACGGGGGACCCCATGGGCGCTGGCGCTGCGACCTTCGACCGGGGC 98
   |||
61  GAGTTCACGGGCTGGGAGAGAGTGAGGCTCGGGCGCTTCGGGCAAGGTGCGC 120
   |||
99  GAGTTCACGGGCTGGGAGAGAGTGAGGCTCGGGCGCTTCGGGCAAGGTGCGC 158
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121  CATGTCCACTGGAAGACCTGCTGGCCATCAAGTGTGCGCCAGCTTGACAGTGCAC 180
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159  CATGTCCACTGGAAGACCTGCTGGCCATCAAGTGTGCGCCAGCTTGACAGTGCAC 218
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181  AGGGAGCGCATGAGAGCTTTTGAAGAAGCAAGAAGATGAGATGAGCCAAAGTTTGCCTAC 240
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219  AGGGAGCGCATGAGAGCTTTTGAAGAAGCAAGAAGATGAGATGAGCCAAAGTTTGCCTAC 278
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279  ATCTGCTGCTGTATGAGCATCTGCGCGAAGCTGTGCGGCTGTGATCAATGAGTACATGAG 338
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301  ACGGGCTCCCTGGAAGAAAGCTGCTGGCTTGGAGCCATTGCGCATGGGATTCGCGTTCCGA 360
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339  ACGGGCTCCCTGGAAGAAAGCTGCTGGCTTGGAGCCATTGCGCATGGGATTCGCGTTCCGA 398
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361  ATTCATCAGAGAGCGGGGATGAGCAATTCCTGCACTGATGAGCCCGGCACTCTG 420
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421  CACTGGAAGCTCAAGCCCGGCAATCTGCTGATGAGCCCACTACCAAGTCAAGATTCT 480
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RESULT 14
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DEFINITION    BP248808 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
               HKR11917, mRNA sequence.
ACCESSION     BP248808
VERSION       BP248808.1
KEYWORDS      GI:52131087
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
               1 (bases 1 to 582)
               Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
               Mizushima-Sugano,J., Nakai,K. and Sugano,S.
               Sequence comparison of human and mouse genes reveals a homologous
               block structure in the promoter regions
               Genome Res. 14 (9), 1711-1718 (2004)
TITLE         JOURNAL
COMMENT       Contact: Yutaka Suzuki
               Department of Virology
               Institute of Medical Science, University of Tokyo
               4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
               Email: yusuzuki@ims.u-tokyo.ac.jp.
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Best Local Similarity 99.8%; Pred. No. 8e-106;
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DEFINITION KDN07909, mRNA sequence.
ACCESSION BP277059
VERSION BP277059.1 GI:52190791
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 580)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
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Query Match 22.8%; Score 537.6; DB 5; Length 580;
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Matches 546; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Db 552 CTGTTTGGCAAAATCACTACTCTCC 580

Search completed: September 16, 2005, 06:26:00
Job time : 6738.33 secs

PT New 14171 human protein kinase and nucleic acids encoding the protein,
PT useful for treating viral infections, cellular growth related disorders,
PT cancers, disorders related with programmed cell death, or autoimmune
PT disorders.

XX Claim 1; SEQ ID NO 3; 50pp; English.

CC This invention relates to a novel isolated nucleic acid sequence and the
CC novel kinase protein encoded by it. Protein kinases play critical roles
CC in the regulation of biochemical and morphological changes associated
CC with cellular growth and division. The sequences of the invention may be
CC useful for gene therapy. The protein kinase or the nucleic acid encoding
CC the protein is useful for modulating cellular growth, differentiation
CC and/or development, and for modulating cellular metabolic pathways,
CC particularly for regulating one or more proteins involved in growth and
CC metabolism. The invention may also be useful for development of
CC therapeutics for the treatment of viral infections (for example hepatitis
CC B), cellular growth related disorders (for example heart failure,
CC hypertension, atrial fibrillation, dilated and idiopathic cardiomyopathy
CC or angina), proliferative or differentiative disorders such as cancer
CC (for example liver, melanoma, prostate, cervical, breast, colon or
CC sarcoma), disorders related with programmed cell death (for example
CC Alzheimer's disease, Parkinson's disease or epilepsy), or autoimmune
CC disorders (for example systemic lupus erythematosus). The present
CC sequence is the novel human kinase protein 14171 gene coding sequence of
CC the invention.

XX Sequence 2355 BP; 464 A; 738 C; 759 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 2355; DB 10; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CATGTCACTGAGAGACCTGGCTGGCATCAAGTCTCGCCAGCTTCGACGTCGACGAC 180
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QY 1261 AAACGTAGTAAGAAATCTGCGAGCGCGCAGAGAGTGAACCTGCGACATGACAGCGGTCCAGC 1320
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QY 1321 CTGCTGACACTGGCGGTGAGAGGCGCGCAAGAGAGTGGCCCAAGTGGCTGTCTCAAC 1380
DB 1321 CTGCTGACACTGGCGGTGAGAGGCGCGCAAGAGAGTGGCCCAAGTGGCTGTCTCAAC 1380
QY 1381 AATGCCAACCCCAACTGAGCAACCTGAGGGGCTCCACCCGTTGCAATAGCGCTGAGAG 1440
DB 1381 AATGCCAACCCCAACTGAGCAACCTGAGGGGCTCCACCCGTTGCAATAGCGCTGAGAG 1440
QY 1441 AGAGGGGTGGGGGTGTGCTGAGACTCTGCTGGCAAGAAAGATCAATGTCAACGCGAAG 1500
DB 1441 AGAGGGGTGGGGGTGTGCTGAGACTCTGCTGGCAAGAAAGATCAATGTCAACGCGAAG 1500
QY 1501 GATGAGAGCAAGTGAACAGCCCTTCACTTTGACAGCCCAAGAACGGGAGTGAAGTGAACA 1560
DB 1501 GATGAGAGCAAGTGAACAGCCCTTCACTTTGACAGCCCAAGAACGGGAGTGAAGTGAACA 1560
QY 1561 CGGCTGTGTGAGAGAAAGCGCTCGGTCAACAGAGTGAACCTTTGAGGGCCGAGACGCC 1620
DB 1561 CGGCTGTGTGAGAGAAAGCGCTCGGTCAACAGAGTGAACCTTTGAGGGCCGAGACGCC 1620
QY 1621 ATGACAGTGGCTGGCGACAGCGGCAAGAAATATCTGTGCAATCTGTGCGCCGAGGCG 1680
DB 1621 ATGACAGTGGCTGGCGACAGCGGCAAGAAATATCTGTGCAATCTGTGCGCCGAGGCG 1680
QY 1681 GTGACGTGAGCTGACAGGCGCAAGAAATGCTGTGCTGCACTGACATACGCTGTGCGAG 1740

Db 1681 GTGACGTTGAGCTTCAGAGGCAAGATGCTGAGCTGCACTGCACTAGCTGCTGGAG 1740
Qy 1741 GGCACCTGCTCCATGTCAGAGTGTGTCGCAAGACGCGGGGTGATGTAAGCCGAG 1800
Db 1741 GGCACCTGCTCCATGTCAGAGTGTGTCGCAAGACGCGGGGTGATGTAAGCCGAG 1800
Qy 1801 ACGCTGATGAGGAGACGCTATGTCAGCTGCGGCAAGCGGGGCACTTACCGCTGGCC 1860
Db 1801 ACGCTGATGAGGAGACGCTATGTCAGCTGCGGCAAGCGGGGCACTTACCGCTGGCC 1860
Qy 1861 CGCATCTCATGACCTGTGTCGCAAGTGAAGTGTGACCTGTGCACTGAGCTGAGCC 1920
Db 1861 CGCATCTCATGACCTGTGTCGCAAGTGAAGTGTGACCTGTGCACTGAGCTGAGCC 1920
Qy 1921 CTGCACTGTCGCGCGGAGACGCGGCAAGCACTGCGAGGCTCTCTGATCGGGGC 1980
Db 1921 CTGCACTGTCGCGCGGAGACGCGGCAAGCACTGCGAGGCTCTCTGATCGGGGC 1980
Qy 1981 GCTGCGAAGAGGCGCTGACCTTCAGACGCTGACCTGCTGCTGCTGCTGCTGCTG 2040
Db 1981 GCTGCGAAGAGGCGCTGACCTTCAGACGCTGACCTGCTGCTGCTGCTGCTGCTG 2040
Qy 2041 GGAACACCTGCGGCACTGTCAGAGTGTGTCGAGGAGGAGGAGGAGGAGGAGGAGG 2100
Db 2041 GGAACACCTGCGGCACTGTCAGAGTGTGTCGAGGAGGAGGAGGAGGAGGAGGAGG 2100
Qy 2101 CCCCTGAACACGAGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 CCCCTGAACACGAGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Qy 2161 GAGTGTGTCAGCGCGGATGTCATGACCTGTTGACAGACGAGGAGGAGGAGGAGG 2220
Db 2161 GAGTGTGTCAGCGCGGATGTCATGACCTGTTGACAGACGAGGAGGAGGAGGAGG 2220
Qy 2221 CTGCGCGCGGAGGCGGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Db 2221 CTGCGCGCGGAGGCGGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Qy 2281 ATCAACCTGACAGGCTCAAGTTCCAGGCGGCGCATGCGCGGCACTCTCTGCGG 2340
Db 2281 ATCAACCTGACAGGCTCAAGTTCCAGGCGGCGCATGCGCGGCACTCTCTGCGG 2340
Qy 2341 CGAAGCAAGACCTAG 2355
Db 2341 CGAAGCAAGACCTAG 2355
RESULT 2
ADL67199
ID ADL67199 standard; DNA; 2355 BP.
XX
AC ADL67199;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human 14171 protein kinase coding region.
XX
XX Human; 14171 protein kinase; cancer; immunological disorder;
XX inflammation; heart failure; hypertension; atrial fibrillation;
XX viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
XX predictive medicine; forensic biology; gene; ss.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..2355
FT /tag= a
FT /product= "Human 14171 protein kinase"
XX
XX US2004048305-A1.
XX
PD 11-MAR-2004.

XX 10-SEP-2003; 2003US-00658904.
XX
XX 11-FEB-2000; 2000US-0182096P.
XX 12-FEB-2001; 2001US-00781882.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kapeller-Libermann R;
XX
XX WPI; 2004-226195/21.
XX P-PSDB; ADL67198.
XX
XX New 14171 protein kinase and nucleic acid, useful for diagnosing or
XX treating diseases with aberrant expression of the 14171 protein kinase,
XX PT such as cancer, an immunological disorder, inflammation, heart failure
XX and hypertension.
XX
XX Claim 1; SEQ ID NO 3; 62pp; English.
XX
XX The invention provides novel human 14171 protein kinase polypeptides and
XX CC polynucleotides. The methods and compositions of the present invention
XX CC are useful for the diagnosis and/or treatment of diseases or conditions
XX CC associated with aberrant expression or activity of a 14171 protein kinase
XX CC such as cancer, immunological disorder, inflammation, heart failure,
XX CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.
XX CC The invention can also be used in chromosome mapping, tissue typing,
XX CC predictive medicine, forensic biology and prognostic assays. The present
XX CC sequence is human 14171 protein kinase coding region.
XX
XX Sequence 2355 BP; 464 A; 738 C; 759 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 2355; DB 12; Length 2355;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGGCGAGCGGAGACCCATGAGGCGCTGCGCTGCTGCACTTGAAGCGGGC 60
Db 1 ATGAGAGGCGAGCGGAGACCCATGAGGCGCTGCGCTGCTGCACTTGAAGCGGGC 60
Qy 61 GAGTTACAGGCGCTGAGAGAGTGGCTCGGCGGCTTGGGCAAGTGTACAGGTGCGC 120
Db 61 GAGTTACAGGCGCTGAGAGAGTGGCTCGGCGGCTTGGGCAAGTGTACAGGTGCGC 120
Qy 121 CATGTCCATGGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 CATGTCCATGGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 181 AGGAGGCGCATGAGCTTTTGAAGAGCAAGAGATGAGATGAGGCAAGTTTGCCTAC 240
Db 181 AGGAGGCGCATGAGCTTTTGAAGAGCAAGAGATGAGATGAGGCAAGTTTGCCTAC 240
Qy 241 ATCTGCTGTGTATGAGCATGTCGCGCAACCTGCGCTGCTGATGAGATGAGAG 300
Db 241 ATCTGCTGTGTATGAGCATGTCGCGCAACCTGCGCTGCTGATGAGATGAGAG 300
Qy 301 ACGGCTCTCCCTGGAAGAAACCTGCTGCTGCGAGCATGTCGCTGCTGATGAGATGAGAG 360
Db 301 ACGGCTCTCCCTGGAAGAAACCTGCTGCTGCGAGCATGTCGCTGCTGATGAGATGAGAG 360
Qy 361 ATCATCAAGAGAGCGGCGGATGAGATGAACTTCTGCACTGATGAGCCCGCACTCTCG 420
Db 361 ATCATCAAGAGAGCGGCGGATGAGATGAACTTCTGCACTGATGAGCCCGCACTCTCG 420
Qy 421 CACCTGACCTCAAGCCCGGAGAACTCTGCTGATGAGCCCACTACAGTCAAGATTTCT 480
Db 421 CACCTGACCTCAAGCCCGGAGAACTCTGCTGATGAGCCCACTACAGTCAAGATTTCT 480
Qy 481 GATTTTGTGTCGCGCAAGTGAAGGAGGCTGTCCTGCACTGATGAGGAGGAGGAGGAG 540
Db 481 GATTTTGTGTCGCGCAAGTGAAGGAGGCTGTCCTGCACTGATGAGGAGGAGGAGGAG 540
Qy 541 CTGTTGCAAGATGCTACTCTCTCCAGAGCGCATCAGGAGAGAGAGCGGCTCTTC 600

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Db 541 CTGTTGGCACAATGCTTACCTCCCTCCAGAGGCGCATCAAGGAGAAAGCGCGCTTTC 600
Qy 601 GACACCAAGCAGCATGTATACAGCTTTGCGATCGTCACTCTGGGCGGTCTCAACACAGAG 660
Db 601 GACACCAAGCAGCATGTATACAGCTTTGCGATCGTCACTCTGGGCGGTCTCAACACAGAG 660
Qy 661 AAGCGTTTGAAGATGAAGAAGCATCTGCGACATCATGTGAAGGTGTGAAGGGCCAG 720
Db 661 AAGCGTTTGAAGATGAAGAAGCATCTGCGACATCATGTGAAGGTGTGAAGGGCCAG 720
Qy 721 CGCCCGAGCTGCGCGCGGTGTGAGAGCGCGCGCGCGCGCTGCGAGCCACTGATAGC 780
Db 721 CGCCCGAGCTGCGCGCGGTGTGAGAGCGCGCGCGCGCGCTGCGAGCCACTGATAGC 780
Qy 781 CTCAATGAGCGGTGTGAGAGGGGATCCGCGAGTTAGGCCCACTTTCAGAAATTAAT 840
Db 781 CTCAATGAGCGGTGTGAGAGGGGATCCGCGAGTTAGGCCCACTTTCAGAAATTAAT 840
Qy 841 TCTGAAACGAGGACCTGTGTGAAAGCTGATGACGAAGTGAAGAAAGAACTGCTATGAT 900
Db 841 TCTGAAACGAGGACCTGTGTGAAAGCTGATGACGAAGTGAAGAAAGAACTGCTATGAT 900
Qy 901 CTGAGCGTGAAGAGCCCGCGAGGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Db 901 CTGAGCGTGAAGAGCCCGCGAGGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Qy 961 GCTCTGCCCCCACTTTGATTAAGATCAAGCTCTCCAGCTTCTCAAGCTGAGC 1020
Db 961 GCTCTGCCCCCACTTTGATTAAGATCAAGCTCTCCAGCTTCTCAAGCTGAGC 1020
Qy 1021 TCTGAGTTTCCAGAGCTGTGAGAGGGCCCGAGAGGCTCAAGCGGAGCTCCCTGAGTCC 1080
Db 1021 TCTGAGTTTCCAGAGCTGTGAGAGGGCCCGAGAGGCTCAAGCGGAGCTCCCTGAGTCC 1080
Qy 1081 AAGCTGCATCGTCCGCGAGTGGAGAGGCTCTCGGGGGTGTCTCGTGGAGCTCCGCG 1140
Db 1081 AAGCTGCATCGTCCGCGAGTGGAGAGGCTCTCGGGGGTGTCTCGTGGAGCTCCGCG 1140
Qy 1141 TTTCTTTCCAGAGATCACTGTCTGTCTTTGAGCGGGAACTTCAACCAAGGATTTG 1200
Db 1141 TTTCTTTCCAGAGATCACTGTCTGTCTTTGAGCGGGAACTTCAACCAAGGATTTG 1200
Qy 1201 GGTACCAAGACGTCAGAGAGAGAGAGCTTGTGATGCCATCGTCCGGGACACAGC 1260
Db 1201 GGTACCAAGACGTCAGAGAGAGAGAGCTTGTGATGCCATCGTCCGGGACACAGC 1260
Qy 1261 AAACGTATGAAGATCTGCAAGCCGAGAGAGCTGGAAGCTGGAAGCGGTGCGAGC 1320
Db 1261 AAACGTATGAAGATCTGCAAGCCGAGAGAGCTGGAAGCTGGAAGCGGTGCGAGC 1320
Qy 1321 CTGCTGCACTGTGCGGTGAGAGCGCGGCAAGAGAGTGGCCCAAGTGGCTGTCTCAAC 1380
Db 1321 CTGCTGCACTGTGCGGTGAGAGCGCGGCAAGAGAGTGGCCCAAGTGGCTGTCTCAAC 1380
Qy 1381 AATGCCAACCCCAACCTGAGCAACGTAAGGGCTCAACCCGTTGCAATGAGCGGTGAG 1440
Db 1381 AATGCCAACCCCAACCTGAGCAACGTAAGGGCTCAACCCGTTGCAATGAGCGGTGAG 1440
Qy 1441 AGAGAGGTGCGGGGTGTGTGAGAGCTCTGTGCGAGCGAAAGATCATGTCACGCGCAG 1500
Db 1441 AGAGAGGTGCGGGGTGTGTGAGAGCTCTGTGCGAGCGAAAGATCATGTCACGCGCAG 1500
Qy 1501 GATGAGACCAATGAGACAGCTTCACTTTGAGCGCCAGAAAGGGGATGAGTCTTAGCA 1560
Db 1501 GATGAGACCAATGAGACAGCTTCACTTTGAGCGCCAGAAAGGGGATGAGTCTTAGCA 1560
Qy 1561 CGGCTGCTGTTGAGAGAGAGAGCTCGGTCAACAGAGTGGACTTTGAGGGCCGAGCGCC 1620
Db 1561 CGGCTGCTGTTGAGAGAGAGAGCTCGGTCAACAGAGTGGACTTTGAGGGCCGAGCGCC 1620
Qy 1621 ATGCACTGTGCTGCGAGCAGCGGAGAGAAATATCGTCCGATCTCTGCGCGGAGGC 1680
Db 1621 ATGCACTGTGCTGCGAGCAGCGGAGAGAAATATCGTCCGATCTCTGCGCGGAGGC 1680

Db 1621 ATGCACTGTGCTGCGAGCAGCGGAGAGAAATATCTGTGCGATCTCTGCGCGGAGGC 1680
Qy 1681 GTGAGCGTGAAGCTGTGAGAGGGGCAAGGATGCTGGCTGCACTGACATACGCTGCGCAG 1740
Db 1681 GTGAGCGTGAAGCTGTGAGAGGGGCAAGGATGCTGGCTGCACTGACATACGCTGCGCAG 1740
Qy 1741 GGCACCTGCGCATCTGCAAGCTGTGCGCAAGAGCGCGGGGTGATGTGAACGCCAG 1800
Db 1741 GGCACCTGCGCATCTGCAAGCTGTGCGCAAGAGCGCGGGGTGATGTGAACGCCAG 1800
Qy 1801 ACCTGATGAGAGAGAGCGCATTTGACCTGCGCGCAGAGCGCGGACATACCGGTGGCC 1860
Db 1801 ACCTGATGAGAGAGAGCGCATTTGACCTGCGCGCAGAGCGCGGACATACCGGTGGCC 1860
Qy 1861 CGCATCTCATCGACTGTGTGCGAGGTCAAGCTGTGAGAGCTGTGAGCAAGACCC 1920
Db 1861 CGCATCTCATCGACTGTGTGCGAGGTCAAGCTGTGAGAGCTGTGAGCAAGACCC 1920
Qy 1921 CTGACGCTGCGCGCGAGAGCGGGGCAACAGAGCACTGCGAGGCTGCTCTGATCGGGGC 1980
Db 1921 CTGACGCTGCGCGCGAGAGCGGGGCAACAGAGCACTGCGAGGCTGCTCTGATCGGGGC 1980
Qy 1981 GCTGCGAAGAGAGCTGTGACCTCAAGACGCTTCAACCGCTTGTGCACTGTGCTGCCAGC 2040
Db 1981 GCTGCGAAGAGAGCTGTGACCTCAAGACGCTTCAACCGCTTGTGCACTGTGCTGCCAGC 2040
Qy 2041 GGAACCTGCGCACTGTCAAGCTGTGTGAGAGAGAGCGATGTGCTGGCCCGGGGA 2100
Db 2041 GGAACCTGCGCACTGTCAAGCTGTGTGAGAGAGAGCGATGTGCTGGCCCGGGGA 2100
Qy 2101 CCCCTGAACAGAGAGCGGCTGCACTGTGCTGCGCGCCACCGGACCTCGAGGTGTGAG 2160
Db 2101 CCCCTGAACAGAGAGCGGCTGCACTGTGCTGCGCGCCACCGGACCTCGAGGTGTGAG 2160
Qy 2161 GAGTTGCTCAGCGCGCATTTGATTTGACTGCTTTGCAAGAGAGGGGCTCAAGCGCTGAC 2220
Db 2161 GAGTTGCTCAGCGCGCATTTGATTTGACTGCTTTGCAAGAGAGGGGCTCAAGCGCTGAC 2220
Qy 2221 CTGCGCGCCAGAGGCGGCGACGCGACAGACGCTGGAAGCTGTGCTCAGGCAATGGGGCCAC 2280
Db 2221 CTGCGCGCCAGAGGCGGCGACGCGACAGACGCTGGAAGCTGTGCTCAGGCAATGGGGCCAC 2280
Qy 2281 ATCAACCTGAGAGAGCTTCAAGTTTCAAGGCGGCGCATGAGCCCGCGCACACTTTCGG 2340
Db 2281 ATCAACCTGAGAGAGCTTCAAGTTTCAAGGCGGCGCATGAGCCCGCGCACACTTTCGG 2340
Qy 2341 CGAAGCAAGACTTG 2355
Db 2341 CGAAGCAAGACTTG 2355

RESULT 3
ADL67197
ID ADL67197 standard; cDNA; 3860 BP.
XX
XX ADL67197;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human 14171 protein kinase cDNA.
XX
XX Human ; 14171 protein kinase; cancer; immunological disorder;
XX inflammation; heart failure; hypertension; atrial fibrillation;
XX viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
XX predictive medicine; forensic biology ; gene; ss.
XX
XX Homo sapiens.
XX
XX OS
XX Key Location/Qualifiers
XX CDS 17..2371
XX FT /*tag= a
XX FT /product= "Human 14171 protein kinase"
XX
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QY	1681	GTGACGCTGACCTTGACAGGAGCAAGGATCTCTGGCTGGCCACTGACCTACGCTGGCGAG	1740
Db	1697	GTGACGCTGACCTTGACAGGAGCAAGGATCTCTGGCTGGCCACTGACCTACGCTGGCGAG	1756
QY	1741	GGCCACCTGGCCCATCTGTCAGAGCTGTGGCCAAAGACCCGGGGGTGAGTGTGAAGGCCCGAG	1800
Db	1757	GGCCACCTGGCCCATCTGTCAGAGCTGTGGCCAAAGACCCGGGGGTGAGTGTGAAGGCCCGAG	1816
QY	1801	AACGCTGATTTGGGAGAGGACGCCAATTGACCTTGGCCCGGACAGGCCCGGCACTACGCCGTGGCC	1860
Db	1817	AACGCTGATTTGGGAGAGGACGCCAATTGACCTTGGCCCGGACAGGCCCGGCACTACGCCGTGGCC	1876
QY	1861	CGCATCTCCATCTGACCTTGTGCTCCGACGTCACAGCTTCAGCTGCTGGTGGCAAGACATCC	1920
Db	1877	CGCATCTCCATCTGACCTTGTGCTCCGACGTCACAGCTTCAGAGCTGAGCTGTGGCAAGACATCC	1936
QY	1921	CTGCACGTGGCCGGCGGAGACGGGGCAACAGACACTGGCAAGCTGTCTCTGCATTTGGGGC	1980
Db	1937	CTGCACGTGGCCGGCGGAGACGGGGCAACAGACACTGGCAAGCTGTCTCTGCATTTGGGGC	1996
QY	1961	GCTGGCAAGAGAGGCGCGTGACCTTCACAGCGCTTACACCGCTTGGACCTGGCTGGCCCGGCAAC	2040
Db	1997	GCTGGCAAGAGAGGCGCGTGACCTTCACAGCGCTTACACCGCTTGGACCTGGCTGGCCCGGCAAC	2056
QY	2041	GGACACCTGGGACCTGTCAAGGTGCTTGTGAGAGAGAAAGGCCGATGTCTGGGCGGGGGA	2100
Db	2057	GGACACCTGGGACCTGTCAAGGTGCTTGTGAGAGAGAAAGGCCGATGTGTCTGGGCGGGGGA	2116
QY	2101	CCCCCTGAACACAGACGGGCGCTGACACTTGGCTGCGGCTCAACGGGCACTTGGAGGTGTGGAG	2160
Db	2117	CCCCCTGAACACAGACGGGCGCTGACACTTGGCTGCGGCTCAACGGGCACTTGGAGGTGTGTGGAG	2176
QY	2161	GAGTTGGTTCAGGCGCGGATGTCAATTGACTCTGTTCACAGACAGAGGGGCTCAGGCGGCTGGAC	2220
Db	2177	GAGTTGGTTCAGGCGCGGATGTCAATTGACTCTGTTCAGAGACAGAGGGGCTCAGGCGGCTGGAC	2236
QY	2221	CTGGGCGGCCCAAGGGCGGGACAGCAAGAGCGTGTGAGAGCTTGTCTCAGGCAATGGGGCCAC	2280
Db	2237	CTGGGCGGCCCAAGGGCGGGACAGCAAGAGCGTGTGAGAGCTTGTCTCAGGCAATGGGGCCAC	2296
QY	2281	ATCAACCTTGACAGAGCTTCAAGTTTCAAGGGCGGCAATGGCCCGGCGGCAACTTCTGTGGG	2340
Db	2297	ATCAACCTTGACAGAGCTTCAAGTTTCAAGGGCGGCAATGGCCCGGCGGCAACTTCTGTGGG	2356
QY	2341	CGAAGCAAGACTTAG 2355	
Db	2357	CGAAGCAAGACTTAG 2371	

AD38376	RESULT 4
ID	AD38376 standard; DNA; 3860 BP.
XX	
AC	AD38376;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human protein 14171 gene sequence.
XX	
KW	tumorigenic disorder; angiogenic disorder; aberrant gene expression;
KW	aberrant protein activity; cytoskeletal; antithyroid; antidiabetic;
KW	ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
KW	prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;
XX	protein 14171.
XX	
OS	Homo sapiens.
XX	
FN	Key Location/Qualifiers

FT	CDS		14..2371	
FT			/*tag= a	
FT			/product= "Human protein 14171"	
XX	PN	WO2003065006-A2.		
XX	PD	07-AUG-2003.		
XX	PF	30-JAN-2003; 2003MO-USO02588.		
XX	PR	31-JAN-2002; 2002US-0353600P.		
PR	PR	15-MAR-2002; 2002US-0364517P.		
PR	PR	09-APR-2002; 2002US-0371075P.		
PR	PR	10-APR-2002; 2002US-0371507P.		
PR	PR	16-APR-2002; 2002US-0372984P.		
PR	PR	19-APR-2002; 2002US-0374194P.		
PR	PR	24-MAY-2002; 2002US-0382995P.		
PR	PR	31-MAY-2002; 2002US-0385023P.		
PR	PR	14-JUN-2002; 2002US-038853P.		
PR	PR	17-JUN-2002; 2002US-0389395P.		
PR	PR	25-JUN-2002; 2002US-0391324P.		
PR	PR	15-JUL-2002; 2002US-0395944P.		
PR	PR	22-JUL-2002; 2002US-0397726P.		
PR	PR	13-AUG-2002; 2002US-0403046P.		
PR	PR	22-AUG-2002; 2002US-0405155P.		
PR	PR	27-AUG-2002; 2002US-0406361P.		
PR	PR	25-OCT-2002; 2002US-0421195P.		
PR	PR	12-NOV-2002; 2002US-0425456P.		
PR	PR	19-NOV-2002; 2002US-0427626P.		
PR	PR	10-DEC-2002; 2002US-0432122P.		
PA	(MTL-) MILLENNIUM PHARM INC.			
PI	Hunter JJ, Macbeth KU, Tsai F,	Lesoon A,	Lightcap ES;	
PI	Williamson MW, Rudolph-Owen LA;			
DR	P-PsDB; ADE38377.			
XX	WP1; 2003-646176/61.			
PT	Treating subject having tumorigenic disorder or angiogenic disorder			
PT	caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic			
PT	acid, by administering a modulator.			
PS	Disclosure; SEQ ID NO 37; 454pp; English.			
XX	This invention relates to a novel method of treating a human subject			
CC	having a tumorigenic disorder or angiogenic disorder, caused by aberrant			
CC	gene expression or activity of an isolated protein, by administering a			
CC	modulator. The modulator may have cytostatic, antithyroid, antidiabetic			
CC	or ophthalmological activity. The method is useful for treating a subject			
CC	having a tumorigenic or angiogenic disorder, in particular for treating			
CC	cancer (for example breast cancer, colon cancer, lung cancer or prostatic			
CC	cancer) and, for example, Grave's disease and diabetic retinopathy. The			
CC	present sequence is a DNA sequence which encodes the novel isolated human			
CC	protein 14171 of the invention.			
SQ	Sequence 3860 BP; 809 A; 1066 C; 1169 G; 816 T; 0 U; 0 Other;			
Query Match	99.0%; Score 2332; DB 10; Length 3860;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 2354; Conservative	0; Mismatches 0; Indels 2; Gaps			
Db	1 ATGGAGGCGCAGCGGCGGAGACCCCATGGGCCCTTGGGCGTGTCGCACCTTCGACGCGGAGC 60			
OY	ATGGAGGCGCAGCGGCGGAGACCGCCATGGGCCCTTGGGCGTGTCGCACCTTCGACGCGGAGC 76			
Dd	GAGTTCAACGGGCTGGGAGAAGGTGGGCTCGGAGCGCTTCGAGGACAGGTATACAAGGTGCGC 136			
OY	GAGTTCAACGGGCTGGGAGAAGGTGGGCTCGGAGCGCTTCGAGGACAGGTATACAAGGTGCGC 120			
Dd	GAGTTCAACGGGCTGGGAGAAGGTGGGCTCGGAGCGCTTCGAGGACAGGTATACAAGGTGCGC 180			
OY	CATGTCACCTGGAAGACTTGCTGGCCATCAAGGCTGCGCCACGCTGACAGTGAAGAC 180			
Dd	CATGTCACCTGGAAGACTTGCTGGCCATCAAGGCTGCGCCACGCTGACAGTGAAGAC 196			

Db 1308 CAAGCTGATGAAAGATCTCTGACACCGCAGACGTGACCTTGGACCTGGACACACGCGTGCAG 1367
 QY 1320 CCTGTGCACTGTGCGGTGAGAGCCGAGCAAGAGAGTGCAGGCTGCTGCTCA 1379
 Db 1368 CTTGTGCACTGTGCGGTGAGAGCCGAGCAAGAGAGTGCAGGCTGCTGCTCA 1427
 QY 1380 CAATGCCAACCCCAACTGAGCAACCTGATGAGGCTTCCACCCCGTTGGACATGAGCCGTGGA 1439
 Db 1428 CAATGCCAACCCCAACTGAGCAACCTGATGAGGCTTCCACCCCGTTGGACATGAGCCGTGGA 1487
 QY 1440 GAGGAGGGTGGGGGGTGTGCTGAGAGCTCTGCTGGCAGAGAAATCAAGTCAACGCCAA 1499
 Db 1488 GAGGAGGGTGGGGGGTGTGCTGAGAGCTCTGCTGGCAGAGAAATCAAGTCAACGCCAA 1547
 QY 1500 GGATGAGGACAGTGGAGAGCCCTCCACTTTGGACCCAGAAAGAGGAGTGAAGCTAGAC 1559
 Db 1548 GGATGAGGACAGTGGAGAGCCCTCCACTTTGGACCCAGAAAGAGGAGTGAAGCTAGAC 1607
 QY 1560 ACGGCTGCTGTTGGAGAGAGACGCTCGGTCAACGAGGTGGAATTGAGGGCCGAGACGC 1619
 Db 1608 ACGGCTGCTGTTGGAGAGAGACGCTCGGTCAACGAGGTGGAATTGAGGGCCGAGACGC 1667
 QY 1620 CATGACAGTGGCTGCTGCGCAGACAGGGCAGAGAAATATCGTGGCATCTGCTGCGCGAGG 1679
 Db 1668 CATGACAGTGGCTGCTGCGCAGACAGGGCAGAGAAATATCGTGGCATCTGCTGCGCGAGG 1727
 QY 1680 CGTGGACGTGAGCCCTGACAGGAGCAAGATGCTGTGCTGCACTGCACTACGCTCTGCA 1739
 Db 1728 CGTGGACGTGAGCCCTGACAGGAGCAAGATGCTGTGCTGCACTGCACTACGCTCTGCA 1787
 QY 1740 GGGGCCACCTGCCCATCTGTCAGAGCTGTGCGCAGACAGCCGGGGGTGATGTGAAGCCCA 1799
 Db 1788 GGGGCCACCTGCCCATCTGTCAGAGCTGTGCGCAGACAGCCGGGGGTGATGTGAAGCCCA 1847
 QY 1800 GACGCTGATGAGGAGAGAGCCATTGACCTGCGCGCAGACAGCGCGGAGCACTACCGGCTGAC 1859
 Db 1848 GACGCTGATGAGGAGAGAGCCATTGACCTGCGCGCAGACAGCGCGGAGCACTACCGGCTGAC 1907
 QY 1860 CCGCATCTCATGACCTGTGTCTCCGACGTCAACGTCTGACCTGTGCGCAGACAGCAAC 1919
 Db 1908 CCGCATCTCATGACCTGTGTCTCCGACGTCAACGTCTGACCTGTGCGCAGACAGCAAC 1967
 QY 1920 CCTGCACTGTGCGCGGAGAGCGGGGCAACAGACACTGCGAGGCTGTCTTGCATTCGGGG 1979
 Db 1968 CCTGCACTGTGCGCGGAGAGCGGGGCAACAGACACTGCGAGGCTGTCTTGCATTCGGGG 2027
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 Db 2028 CGCTGGCAAGAGAGCGCTGTACCTTCAACCGGCTACACCGGCTGTGACCTGTGCGCGGCA 2087
 QY 2040 CGGACACCTGGGCACTGTCAAGCTGTTGTGAGAGAGAGCGGATGTGCTGCGCGGGG 2099
 Db 2088 CGGACACCTGGGCACTGTCAAGCTGTTGTGAGAGAGAGCGGATGTGCTGCGCGGGG 2147
 QY 2100 ACCCTTGAACAGACGCGCGCTGCACTGTGCTGCGCGGCACTGCGAGGTGATGGA 2159
 Db 2148 ACCCTTGAACAGACGCGCGCTGCACTGTGCTGCGCGGCACTGCGAGGTGATGGA 2207
 QY 2160 GGAATTTGTGACAGCGCGGATGTATTTGACCTGTTTCAAGAGAGAGGGGCTTCAAGGCGCTGGA 2219
 Db 2208 GGAATTTGTGACAGCGCGGATGTATTTGACCTGTTTCAAGAGAGAGGGGCTTCAAGGCGCTGGA 2267
 QY 2220 CTTGGCGCGGCGGAGCGGCAAGCAAGACGAGTGAAGCTTGTCTTCAAGGATGAGGCCCA 2279
 Db 2268 CTTGGCGCGGCGGAGCGGCAAGCAAGACGAGTGAAGCTTGTCTTCAAGGATGAGGCCCA 2327
 QY 2280 CATCAACCTTGACAGAGCTTCAAGTTTCAAGGGCGGCGCATGAGCCCGCGCAACTCTTGGG 2339
 Db 2328 CATCAACCTTGACAGAGCTTCAAGTTTCAAGGGCGGCGCATGAGCCCGCGCAACTCTTGGG 2387
 QY 2340 GCGAAGCAAGACCTAG 2355

Db 2388 GCGAAGCAAGACCTAG 2403
 RESULT 6
 ADR25979
 ID ADR25979 standard; DNA, 3879 BP.
 XX
 AC ADR25979;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Breast cancer prognosis marker #1840.
 XX
 KW ds; breast cancer; prognosis; gene expression; diagnosis.
 OS Homo sapiens.
 PN W02004065545-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 15-JAN-2004; 2004WO-US001100.
 XX
 PR 15-JAN-2003; 2003US-00342887.
 XX
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 PI Van't Veer LJ, He Y;
 DR WPI, 2004-593473/57.
 XX
 PT Classifying a breast cancer patient according to prognosis comprises
 PT determining the similarity between the level of expression of each of
 PT five genes in a cell sample taken from patient, to control levels.
 XX
 PS Disclosure; SEQ ID NO 1840; 226bp; English.
 CC
 CC The invention relates to a method of classifying a breast cancer patient
 CC according to prognosis by determining the similarity between the level of
 CC expression of each of five genes for which markers are listed in the
 CC specification, in a cell sample taken from the breast cancer patient, to
 CC control levels of expression for each respective five genes to obtain a
 CC patient similarity value. The methods are useful for classifying a breast
 CC cancer patient according to prognosis. Kits and computer program products
 CC are useful for data analysis using the diagnostic, prognostic and
 CC statistical methods of the invention. This sequence corresponds to a
 CC marker used in the method of the invention.
 XX
 SQ Sequence 3879 BP; 807 A; 1074 C; 1178 G; 820 T; 0 U; 0 Other;
 Query Match 99.0%; Score 2330.4; DB 13; Length 3879;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2253; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 QY 1 ATGAGAGGCGACGGCGGGAACCCCATGGGCGCTGGCGCTGCGGCACTTGCAGCGGGG 60
 Db 49 ATGAGAGGCGACGGCGGGAACCCCATGGGCGCTGGCGCTGCGGCACTTGCAGCGGGG 108
 QY 61 GAGTTACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTTCGGGCAAGTGTACAAAGTGGGC 120
 Db 109 GAGTTACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTTCGGGCAAGTGTACAAAGTGGGC 168
 QY 121 CATGTCACTGGAAGACCTGTGCTGGCATCAAGTGTCTGCGGCAAGTGTGACGAC 180
 Db 169 CATGTCACTGGAAGACCTGTGCTGGCATCAAGTGTCTGCGGCAAGTGTGACGAC 228
 QY 181 AGGAGCGCATGAGAGCTTTTGAAGAAGCAAGAGATGAGATGAGGCAAGTTTGCTAC 240
 Db 229 AGGAGCGCATGAGAGCTTTTGAAGAAGCAAGAGATGAGATGAGGCAAGTTTGCTAC 288
 QY 241 ATCTGCTGTGTATGAGCATGCGCGCAACTGTGCGCTGTGTCATGAGATACATGAG 300

Db 289 ATCCGCTGTGTATGCAATCGCCGCGAGACCTGTGGGCTGTGTATGAGATACATGAG 348
Qy 301 ACCGGCTCCCTGGAAAAAGCTGTGGCTTTCGAGACCATTTGCCATTTGGGATCTCCGGTCCGA 360
Db 349 ACCGGCTCCCTGGAAAAAGCTGTGGCTTTCGAGACCATTTGGGATCTCCGGTCCGA 408
Qy 361 ATCATCCAGAGACGGCGGTGGGCAATGAATCTTCCGACCTGACATGAGCCCGCACTCCG 420
Db 409 ATCATCCAGAGACGGCGGTGGGCAATGAATCTTCCGACCTGACATGAGCCCGCACTCCG 468
Qy 421 CACCTGACCTCAAGCCCGGAAACCTCTGTGATGACCTCACTACACAGCATGATTTCT 480
Db 469 CACCTGACCTCAAGCCCGGAAACCTCTGTGATGACCTCACTACAGCATGATTTCT 528
Qy 481 GATTTGGTCTGGCCAAATGCAACGGGCTGTCCCATGGCATGACCTCAAGATGATGGC 540
Db 529 GATTTGGTCTGGCCAAATGCAACGGGCTGTCCCATGGCATGACCTCAAGATGATGGC 588
Qy 541 CTGTTGGCACAATCGCTACCTCCCTCCAGAGCGCATCAAGGAGAAAGCCGGCTTTC 600
Db 589 CTGTTGGCACAATCGCTACCTCCCTCCAGAGCGCATCAAGGAGAAAGCCGGCTTTC 648
Qy 601 GACAACAGACAAGATGATACAGCTTTTGCATTCGTCACTGAGGCGTGTCCACAAGAG 660
Db 649 GACAACAGACAAGATGATACAGCTTTTGCATTCGTCACTGAGGCGTGTCCACAAGAG 708
Qy 661 AAGCGTTTGCAGATGAGAAAGAACTCTGCACATCATGTGAAAGTGTGAAGGCCAC 720
Db 709 AAGCGTTTGCAGATGAGAAAGAACTCTGCACATCATGTGAAAGTGTGAAGGCCAC 768
Qy 721 CGCCCGAGCTGCGCCCGGTGTGACAGACCCGCGCGCGCTGACAGCACTGTATAGC 780
Db 769 CGCCCGAGCTGCGCCCGGTGTGACAGACCCGCGCGCGCTGACAGCACTGTATAGC 828
Qy 781 CTCAATGACGCGTGTGTCAGAGGAGATCGGAGATTAGGCCCACTTTCAGAAATTAAT 840
Db 829 CTCAATGACGCGTGTGTCAGAGGAGATCGGAGATTAGGCCCACTTTCAGAAATTAAT 888
Qy 841 TCTGAAACCGAGAGACCTGTGTAAGAAAGCTGATGACGAAAGTGAAGAACTGTATAT 900
Db 889 TCTGAAACCGAGAGACCTGTGTAAGAAAGCTGATGACGAAAGTGAAGAACTGTATAT 948
Qy 901 CTGGAAGTGAAGAGCCCGCGAGAGCCAGAGACGAGTGTGCTGCGAGGCTCAAGCGG 960
Db 949 CTGGAAGTGAAGAGCCCGCGAGAGCCAGAGACGAGTGTGCTGCGAGGCTCAAGCGG 1008
Qy 961 GCTCTGCCCCCACTTGTGATTAAGATCAAGCCTCTCCAGCTTCTCTCAAGCTGAC 1020
Db 1009 GCTCTGCCCCCACTTGTGATTAAGATCAAGCCTCTCCAGCTTCTCTCAAGCTGAC 1068
Qy 1021 TCTGAGTTTCCAGAGCTGTGAGAGGCGCCGAGAGCTCAAGCGAGCTCCTGAGTTC 1080
Db 1069 TCTGAGTTTCCAGAGCTGTGAGAGGCGCCGAGAGCTCAAGCGAGCTCCTGAGTTC 1128
Qy 1081 AAGCTGACATGTCGCGAGTGGAGAGAGCTCTGCGGGTGTCTCGGTGACCTCCGC 1140
Db 1129 AAGCTGACATGTCGCGAGTGGAGAGAGCTCTGCGGGTGTCTCGGTGACCTCCGC 1188
Qy 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTTCACACAGATGTG 1200
Db 1189 TTCTCTTCCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTTCACACAGATGTG 1248
Qy 1201 GGTACCAAGACGTTCAGAGAGAAAGACTTGTGATTCATTCGTTC -GGAGACAG 1259
Db 1249 GGTACCAAGACGTTCAGAGAGAAAGACTTGTGATTCATTCGTTC -GGAGACAG 1307
Qy 1260 CAAACTGATGAAGATCTGACAGCGCAGAGACGTGACCTTGACCTGACAGCGGTCCAG 1319
Db 1308 CAAACTGATGAAGATCTGACAGCGCAGAGACGTGACCTTGACCTGACAGCGGTCCAG 1367
Qy 1320 CCTGTGCACTGTGCGGTGAGAGCCGGGCAAGAGATGCGCAAGTGGCTGTCTCA 1379
Db 1368 CCTGTGCACTGTGCGGTGAGAGCCGGGCAAGAGATGCGCAAGTGGCTGTCTCA 1427

Qy 1380 CAATGCCAACCCTGAGCAACCGGTAGGGGTCCACCCCGTTGACATGGCCGTTGA 1439
Db 1428 CAATGCCAACCCTGAGCAACCGGTAGGGGTCCACCCCGTTGACATGGCCGTTGA 1487
Qy 1440 GAGAGGGGTGCGGGGTGTCTGTGAGAGCTCTGTGCGACGGAAGATCATGTCTCAAGCCAA 1499
Db 1488 GAGAGGGGTGCGGGGTGTCTGTGAGAGCTCTGTGCGACGGAAGATCATGTCTCAAGCCAA 1547
Qy 1500 GATGAGAGACATGAGACAGCCCTCCACTTTTGACGCCAAGACGGGATGAGTTACAC 1559
Db 1548 GATGAGAGACATGAGACAGCCCTCCACTTTTGACGCCAAGACGGGATGAGTTACAC 1607
Qy 1560 ACCGCTGTGTGAGAAAGAACGCTGATCAACGAGGTGATCTTTGAGGCGCGAGCC 1619
Db 1608 ACCGCTGTGTGAGAAAGAACGCTGATCAACGAGGTGATCTTTGAGGCGCGAGCC 1667
Qy 1620 CATGCACTGAGCTGCCAGACAGGGCAGAGAAATATGTGCGCATCTGTGCGCGAGG 1679
Db 1668 CATGCACTGAGCTGCCAGACAGGGCAGAGAAATATGTGCGCATCTGTGCGCGAGG 1727
Qy 1680 CTGTGACGTGAGCTGTGACAGGCAAGATGCTGTGCTGCACTGTGACATACGCTGTGCA 1739
Db 1728 CTGTGACGTGAGCTGTGACAGGCAAGATGCTGTGCTGCACTGTGACATACGCTGTGCA 1787
Qy 1740 GGGCCACTGCCCCATGCTCAAGCTGTGAGCCAGACAGCGGGGTGATGAAACGCCCA 1799
Db 1788 GGGCCACTGCCCCATGCTCAAGCTGTGAGCCAGACAGCGGGGTGATGAAACGCCCA 1847
Qy 1800 GACGCTGATGAGAGAGACGCGCATTTGACCTGTGCGCACAGCGCGGACATACCGGTGGC 1859
Db 1848 GACGCTGATGAGAGAGACGCGCATTTGACCTGTGCGCACAGCGCGGACATACCGGTGGC 1907
Qy 1860 CCGCATCTCATGACCTGTGCTTCCAGCTTCAACGTGTGACAGCTGTGCGACAGACACC 1919
Db 1908 CCGCATCTCATGACCTGTGCTTCCAGCTTCAACGTGTGACAGCTGTGCGACAGACACC 1967
Qy 1920 CCTGCACTGAGCGCGGAGACGGGGACACAGAGCACTGCGAGGCTGCTCCGACATCGGGG 1979
Db 1968 CCTGCACTGAGCGCGGAGACGGGGACACAGAGCACTGCGAGGCTGCTCCGACATCGGGG 2027
Qy 1980 CGCTGAGAGAGAGCGCTGTGACCTTCAAGCGCTACACCGCTCTGACCTGTGCGCGCAA 2039
Db 2028 CGCTGAGAGAGAGCGCTGTGACCTTCAAGCGCTACACCGCTCTGACCTGTGCGCGCAA 2087
Qy 2040 CGGACACTGTGGCCACTGTCAAGCTGTGTTCGAGAGAAAGCGGATGTGCTGCGCGGG 2099
Db 2088 CGGACACTGTGGCCACTGTCAAGCTGTGTTCGAGAGAAAGCGGATGTGCTGCGCGGG 2147
Qy 2100 ACCCTGAAACAGACGGCGCTGACCTGTGCTGCGGCCACGGGACCTCGAGGTGTGGA 2159
Db 2148 ACCCTGAAACAGACGGCGCTGACCTGTGCTGCGGCCACGGGACCTCGAGGTGTGGA 2207
Qy 2160 GAGATTGTGACGCGCGATGTCAATTGACCTGTTCAGAGACAGGGGCTCAGCGGCTGCA 2219
Db 2208 GAGATTGTGACGCGCGATGTCAATTGACCTGTTCAGAGACAGGGGCTCAGCGGCTGCA 2267
Qy 2220 CTTGGCGCCCAAGGGCGGGACCGACAGACGAGTGAAGACTTGTCAAGGATGTGGGCCA 2279
Db 2268 CTTGGCGCCCAAGGGCGGGACCGACAGACGAGTGAAGACTTGTCAAGGATGTGGGCCA 2327
Qy 2280 CATCAACTGCAAGAGCTCAAGTTTCAAGGGCGGGCATGAGCCCGCGCGCACTCTGCG 2339
Db 2328 CATCAACTGCAAGAGCTCAAGTTTCAAGGGCGGGCATGAGCCCGCGCGCACTCTGCG 2387
Qy 2340 GCGAAGCAAGACTTAC 2355
Db 2388 GCGAAGCAAGACTTAC 2403

RESULT 7
AAD64343
ID AAD64343 standard; DNA; 2355 BP.

Db 421 CACCTGACCTCAAGCCCGGCAATCTCTGTCGATGTCCTCACTACAGATGATTTCT 480
 Qy 481 GATTTGGTCTGGCCAGTGCACCGGCTGTCTCCACTGCACTGACCTTCAAGATGATGGC 540
 Db 481 GATTTGGTCTGGCCAGTGCACCGGCTGTCTCCACTGCACTGACCTTCAAGATGATGGC 540
 Qy 541 CTGTTGGCAATGCTCTACTCTCTCCAGGCGCATCAGGGAATAAGCGGCTCTTC 600
 Db 541 CTGTTGGCAATGCTCTACTCTCTCCAGGCGCATCAGGGAATAAGCGGCTCTTC 600
 Qy 601 GACACCAAGCAGATGATATACAGCTTTGCGATGCTCATCTGGGGGCTGCTCAACAGAAG 660
 Db 601 GACACCAAGCAGATGATATACAGCTTTGCGATGCTCATCTGGGGGCTGCTCAACAGAAG 660
 Qy 661 AAGCGTTTGCAGATGAGAAGAACATCTGCACATCATGTGTAAGGTGTAAGGGCCAC 720
 Db 661 AAGCGTTTGCAGATGAGAAGAACATCTGCACATCATGTGTAAGGTGTAAGGGCCAC 720
 Qy 721 CGCCCTGAGCTGCGCCGCTGTGTCAGAGCCCGGCGGCTGCAAGCCCTGATAGC 780
 Db 721 CGCCCTGAGCTGCGCCGCTGTGTCAGAGCCCGGCGGCTGCAAGCCCTGATAGC 780
 Qy 781 CTGATGAGCGGTGTCGAGGAGGAGATCGAGATTAGGCGCCACTTCCAGAAATTAAT 840
 Db 781 CTGATGAGCGGTGTCGAGGAGGAGATCGAGATTAGGCGCCACTTCCAGAAATTAAT 840
 Qy 841 TCTGAAACCGAGAGCCTGTGTGAAAAAGCTGATGACGAAGTGAAGAACTGCTCATGAT 900
 Db 841 TCTGAAACCGAGAGCCTGTGTGAAAAAGCTGATGACGAAGTGAAGAACTGCTCATGAT 900
 Qy 901 CTGGAACGTGAAAAAGCCCCCGGAGCCCAAGAGCGAGGTGTGCTGCGAAGGTTCAAAGG 960
 Db 901 CTGGAACGTGAAAAAGCCCCCGGAGCCCAAGAGCGAGGTGTGCTGCGAAGGTTCAAAGG 960
 Qy 961 GCGCTGACCCGACCTTGATACGATACAGCTCTCTCCAGCTTCTCTCAAGCTGAC 1020
 Db 961 GCGCTGACCCGACCTTGATACGATACAGCTCTCTCCAGCTTCTCTCAAGCTGAC 1020
 Qy 1021 TCTGAGTTTCCAGAGCTGTGAGGGCCCGAGAGCTCAGCGAGCTCTCTGATGTC 1080
 Db 1021 TCTGAGTTTCCAGAGCTGTGAGGGCCCGAGAGCTCAGCGAGCTCTCTGATGTC 1080
 Qy 1081 AAGCTGACCTGCTCGGCGAGTGGGAAGAGCTCTCGGGGTGTCTCTCGGTGACCTCGGC 1140
 Db 1081 AAGCTGACCTGCTCGGCGAGTGGGAAGAGCTCTCGGGGTGTCTCTCGGTGACCTCGGC 1140
 Qy 1141 TTTCTTCCAGAGGATCACTGTGCTGTCTTGTGAGCGGAACTTTCACACAGCATCTG 1200
 Db 1141 TTTCTTCCAGAGGATCACTGTGCTGTCTTGTGAGCGGAACTTTCACACAGCATCTG 1200
 Qy 1201 GGTACCAAGAGCTGTGAGAGAGAGGCTTGTGATGTCATCTGTGTC-GGAGACACAG 1259
 Db 1201 GGTACCAAGAGCTGTGAGAGAGAGGCTTGTGATGTCATCTGTGTC-GGAGACACAG 1259
 Qy 1260 CAAACTGATGAAGATCTTGCAGCCGCGAGACCTGCGCATCTGGAACAGGGGTCCAG 1319
 Db 1260 CAAACTGATGAAGATCTTGCAGCCGCGAGACCTGCGCATCTGGAACAGGGGTCCAG 1319
 Qy 1320 CCGTGTGACCTGCGGCTGAGAGCGGCGGAGAGAGAGTGCAGCAAGTGTCTGCTCA 1379
 Db 1320 CCGTGTGACCTGCGGCTGAGAGCGGCGGAGAGAGTGCAGCAAGTGTCTGCTCA 1379
 Qy 1380 CAATGCCAACCCCAACTGAGGAACTGTAGGGGCTTCAACCGGTGCAATGAGCGTGA 1439
 Db 1380 CAATGCCAACCCCAACTGAGGAACTGTAGGGGCTTCAACCGGTGCAATGAGCGTGA 1439
 Qy 1440 GAGGAGGGTGTGCGGGGTGTGTGTGAGCTCTGTGTCGCAAGGAAATGATGTAAGCCCA 1499
 Db 1440 GAGGAGGGTGTGCGGGGTGTGTGTGAGCTCTGTGTCGCAAGGAAATGATGTAAGCCCA 1499
 Qy 1500 GATGAGGACAGTGCAGAGCCCTCACTTTGCAAGCCAGAACGGGGAAGATCTAGCAC 1559
 Db 1500 GATGAGGACAGTGCAGAGCCCTCACTTTGCAAGCCAGAACGGGGAAGATCTAGCAC 1559

Qy 1560 ACGGCTGCTGTTGGAGAGAACGCTTGCTCAACGAGGTGAACTTTGAGGGCCGAGCC 1619
 Db 1560 ACGGCTGCTGTTGGAGAGAACGCTTGCTCAACGAGGTGAACTTTGAGGGCCGAGCC 1619
 Qy 1620 CATGCAAGTGTGCTGCGAGCAGGCGAGAGAAATATGTGTCGATCTGTGCTGCGAGG 1679
 Db 1620 CATGCAAGTGTGCTGCGAGCAGGCGAGAGAAATATGTGTCGATCTGTGCTGCGAGG 1679
 Qy 1680 CTGTGACGTGAGCTTGCAGAGGCAAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCA 1739
 Db 1680 CTGTGACGTGAGCTTGCAGAGGCAAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCA 1739
 Qy 1740 GGGGCACTGCGCCATGCTCAAGCTGTGCGCAAGCAGCAGGCGGAGTGAAGTGAAGCCCA 1799
 Db 1740 GGGGCACTGCGCCATGCTCAAGCTGTGCGCAAGCAGCAGGCGGAGTGAAGTGAAGCCCA 1799
 Qy 1800 GACGCTGATGAGAGAGAGCCCAATTGCACTGCGCGCAAGGCGGCACTAACCGGTGCGC 1859
 Db 1800 GACGCTGATGAGAGAGAGCCCAATTGCACTGCGCGCAAGGCGGCACTAACCGGTGCGC 1859
 Qy 1860 CCGCATCTCATGCACTGTGCTGCTGCAAGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCA 1919
 Db 1860 CCGCATCTCATGCACTGTGCTGCTGCAAGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCA 1919
 Qy 1920 CTGTCAGTGTGCGCGGAGACGCGGCGCAACAGAGCACTGCGAGGCTGCTGCTGCTGCTG 1979
 Db 1920 CTGTCAGTGTGCGCGGAGACGCGGCGCAACAGAGCACTGCGAGGCTGCTGCTGCTGCTG 1979
 Qy 1980 CGCTGCAAGAGAGCGCTGTGACCTTCAAGCAGCTGACACCGCTTGTGCACTGTGCTGCGCAA 2039
 Db 1980 CGCTGCAAGAGAGCGCTGTGACCTTCAAGCAGCTGACACCGCTTGTGCACTGTGCTGCGCAA 2039
 Qy 2040 CGGACACTGTGCTCACTGCTCAAGCTGCTTGTGAGAGAGAGCCGATGTGCTGCTGCGG 2099
 Db 2040 CGGACACTGTGCTCACTGCTCAAGCTGCTTGTGAGAGAGAGCCGATGTGCTGCTGCGG 2099
 Qy 2100 ACCCTGAAACAGAGCGGCGCTGCACTGCGTGTGCGGCGCCAGCGGCACTGCGAGTGTG 2159
 Db 2100 ACCCTGAAACAGAGCGGCGCTGCACTGCGTGTGCGGCGCCAGCGGCACTGCGAGTGTG 2159
 Qy 2160 GAGATTGTGACGCGCCGATGTCATTGACCTGTTGCAAGAGAGAGGCTCAAGCGGCTGCA 2219
 Db 2160 GAGATTGTGACGCGCCGATGTCATTGACCTGTTGCAAGAGAGAGGCTCAAGCGGCTGCA 2219
 Qy 2220 CTTGCGCGCCAGGCGCGGCAAGCAAGAGCGTGAAGCTTGTCTCAGGCACTGCGGCTGCA 2279
 Db 2220 CTTGCGCGCCAGGCGCGGCAAGCAAGAGCGTGAAGCTTGTCTCAGGCACTGCGGCTGCA 2279
 Qy 2280 CATCAACTGTGAGAGCTTCAAGGTTCCAGGCGGCGCATGAGCCCGCCGCAACTCTGCG 2339
 Db 2280 CATCAACTGTGAGAGCTTCAAGGTTCCAGGCGGCGCATGAGCCCGCCGCAACTCTGCG 2339
 Qy 2340 GCGAAGCAAGACTAG 2355
 Db 2340 GCGAAGCAAGACTAG 2355

RESULT 9
 AAD64341
 ID AAD64341 standard; DNA; 2355 BP.
 XX AAD64341;
 AC 12-FEB-2004 (first entry)
 DT 12-FEB-2004 (first entry)
 XX 12-FEB-2004 (first entry)
 DE Human protein kinase C-associated kinase (PKC) variant DNA #3.
 XX Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK;
 KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
 OS Homo sapiens.
 XX

US2003199462-A1.
23-OCT-2003.
23-APR-2002; 2002US-00128174.
23-APR-2002; 2002US-00128174.
(NUNEZ/) NUNEZ G.
(INOH/) INOHARA N.
(MUTO/) MUTO A.
Munez G, Inohara N, Muto A;
WPI; 2003-852808/79.
New nucleic acid encoding RICK3, useful in preparing a composition for inhibiting PKK induced NF-KB activation for treating hyperglycemia.
Disclosure: SEQ ID NO 16; Opp; English.
The invention relates to methods and compositions for modulating cellular signalling. In particular the present invention relates to protein kinase C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids encoding such proteins. The invention further relates to the use of PKK and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid molecules of the invention are useful in preparing a composition for inhibiting PKK induced NF-kappaB activation for treating hyperglycemia. The invention is also used in gene therapy. The present sequence is human PKK variant DNA
Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;
Query Match 98.8%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
1 ATGAGGGGCGACGGGGGAGACCCCATGGGCGCTGGCGCATGCGCACTTGAGCGGGG 60
1 ATGAGGGGCGACGGGGGAGACCCCATGGGCGCTGGCGCATGCGCACTTGAGCGGGG 60
61 GAGTTCACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAAGTGGC 120
61 GAGTTCACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAAGTGGC 120
121 CATGTCCATGGAGAGCTGGCTGGCCATCAAGTCTGCCAGCTTCGACGTGACGAC 180
121 CATGTCCATGGAGAGCTGGCTGGCCATCAAGTCTGCCAGCTTCGACGTGACGAC 180
181 AGGAGGCCATGGAGCTTTTGGAGAGCAAGCAAGATGAGATGGCCAAAGTTTCGTAC 240
181 AGGAGGCCATGGAGCTTTTGGAGAGCAAGCAAGATGAGATGGCCAAAGTTTCGTAC 240
241 ATCTGCTGTGTATGATGATCTGCGCGAAGCTGTGGCTGTGTATGATGATGATGAG 300
241 ATCTGCTGTGTATGATGATCTGCGCGAAGCTGTGGCTGTGTATGATGATGATGAG 300
301 ACGGCTCTCTGGAAAAGCTGTGGCTTCGAGACCATTTGCCATGGGATCTCGGTTCCGA 360
301 ACGGCTCTCTGGAAAAGCTGTGGCTTCGAGACCATTTGCCATGGGATCTCGGTTCCGA 360
361 ATTCATCCAGAGAGCGGCGGTGGGATGAACTTCGCACTGGATGGCCCGGCACTCTCG 420
361 ATTCATCCAGAGAGCGGCGGTGGGATGAACTTCGCACTGGATGGCCCGGCACTCTCG 420
421 CACCTGGAAGCTTCAAGCCCGGCAAGATCTGTGTGATGGCCATACCAAGTCAAGATTCT 480
421 CACCTGGAAGCTTCAAGCCCGGCAAGATCTGTGTGATGGCCATACCAAGTCAAGATTCT 480
481 GATTTTGGTCTGGCCAAAGTGAAGCGGCTGTCCACTGGCATGACTTCAAGATGATGATG 540
481 GATTTTGGTCTGGCCAAAGTGAAGCGGCTGTCCACTGGCATGACTTCAAGATGATGATG 540

541 CTGTTTGGCAATACGCTTACTCTCTCCAGAGCGATCAGGAGAAAGACCGGCTCTTC 600
541 CTGTTTGGCAATACGCTTACTCTCTCCAGAGCGATCAGGAGAAAGACCGGCTCTTC 600
601 GACACCAAGCAGATGTATACAGCTTTGCGATGTCATCTGGGGCGTGTCAACAGAG 660
601 GACACCAAGCAGATGTATACAGCTTTGCGATGTCATCTGGGGCGTGTCAACAGAG 660
661 AAGCCGTTTGCATGAGAAAGAAATCTCTGCAATCATGTGTGAAGGTGGAGGGGCGAC 720
661 AAGCCGTTTGCATGAGAAAGAAATCTCTGCAATCATGTGTGAAGGTGGAGGGGCGAC 720
721 CGCCCCGAGCTGCGCCGCTGTGCAAGAGCCGGCCGCGCTGAGCCACTGTATAGC 780
721 CGCCCCGAGCTGCGCCGCTGTGCAAGAGCCGGCCGCGCTGAGCCACTGTATAGC 780
781 CTATGCAAGCGGTGCTGGCAGGGGGATCCGCGAGTTAGCCCACTTCCAAGAAATTACT 840
781 CTATGCAAGCGGTGCTGGCAGGGGGATCCGCGAGTTAGCCCACTTCCAAGAAATTACT 840
841 TCTGAAACCGAGACCTGTGTGAAAAGCTGTATGACGAATGAAAAGAACTGCTCATGAT 900
841 TCTGAAACCGAGACCTGTGTGAAAAGCTGTATGACGAATGAAAAGAACTGCTCATGAT 900
901 CTGGAAGTGAAGAGCCCGCGAGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
901 CTGGAAGTGAAGAGCCCGCGAGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
961 GCTCTGCCCCCACTTTGATTAAGACTACAGCTCTCCAGCTTCTTCAACAGCTGAG 1020
961 GCTCTGCCCCCACTTTGATTAAGACTACAGCTCTCCAGCTTCTTCAACAGCTGAG 1020
1021 TCTGGAATTTCCAGAGCTGTGAGGGGCGCGAGAGTCAAGCGAGCTCTGAGTTC 1080
1021 TCTGGAATTTCCAGAGCTGTGAGGGGCGCGAGAGTCAAGCGAGCTCTGAGTTC 1080
1081 AAGCTGCATCTGTCGGCAGTGGAGAGAGCTCTCGGGGGTGTCTTCTGTGATCTCCGC 1140
1081 AAGCTGCATCTGTCGGCAGTGGAGAGAGCTCTCGGGGGTGTCTTCTGTGATCTCCGC 1140
1141 TTCTCTTCCAGAGATCATGTGTGCTGTCTTTGAGCGGGAACCTTCAACAGCATCTG 1200
1141 TTCTCTTCCAGAGATCATGTGTGCTGTCTTTGAGCGGGAACCTTCAACAGCATCTG 1200
1201 GGTACCAAGAGCTGCAAGAGAAAGAGCTTTGAGATGCCATGATGTC-C-GGGAACAG 1259
1201 GGTACCAAGAGCTGCAAGAGAAAGAGCTTTGAGATGCCATGATGTC-C-GGGAACAG 1259
1260 CAAACTGATGAAGATCTTGCAGCGCGCAGAGCTGCACTGGCACTGCAAGCGGTGCAG 1319
1260 CAAACTGATGAAGATCTTGCAGCGCGCAGAGCTGCACTGGCACTGCAAGCGGTGCAG 1319
1320 CTTGCTCACTGGCGGTGAGAGCGCGGCAAGAGATGCGCAAGTGGCTGCTCTCA 1379
1320 CTTGCTCACTGGCGGTGAGAGCGCGGCAAGAGATGCGCAAGTGGCTGCTCTCA 1379
1380 CTTGCTCACTGGCGGTGAGAGCGCGGCAAGAGATGCGCAAGTGGCTGCTCTCA 1439
1380 CTTGCTCACTGGCGGTGAGAGCGCGGCAAGAGATGCGCAAGTGGCTGCTCTCA 1439
1440 GAGGAGGTGCGGGGTGTCTGTGAGCTCTGTGCGCGGGAAGTCAAGTCAACGCGCAA 1499
1440 GAGGAGGTGCGGGGTGTCTGTGAGCTCTGTGCGCGGGAAGTCAAGTCAACGCGCAA 1499
1500 GGAATGAGAACAGTGAAGAGCAAGCTTCACTTTGCAAGCCCAAGCGGAGTGAATGAC 1559
1500 GGAATGAGAACAGTGAAGAGCAAGCTTCACTTTGCAAGCCCAAGCGGAGTGAATGAC 1559
1560 ACGGCTCTGTGTGAAGAAAGCGCTGTGTCACGAGGTGAACTTTGAGGGCGGAGCGC 1619
1560 ACGGCTCTGTGTGAAGAAAGCGCTGTGTCACGAGGTGAACTTTGAGGGCGGAGCGC 1619
1620 CATGCAAGTGGCTGCGCAAGACGGGCGAGAAATATGTCGATCTCTGTGCGCGCAGG 1679

[illegible]

PR 23-APR-2002; 2002US-00128174.
XX
XX (NUNEZ G,
PA (INOH/) INOHARA N.
PA (MOTO/) MOTO A.
XX
XX
PI Nunez G, Inohara N, Muto A;
XX
XX WPI, 2003-652808/79.
DR
XX
XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
PS
XX
XX Disclosure; SEQ ID NO 19; 0pp; English.

The invention relates to methods and compositions for modulating cellular signalling. In particular the present invention relates to protein kinase C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids encoding such proteins. The invention further relates to the use of PKK and RICK3 proteins in modulating NF-kappaB signaling. Nucleic acid molecules of the invention are useful in preparing a composition for inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia. The invention is also used in gene therapy. The present sequence is human PKK variant DNA

Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;

Query Match	98.8%	Score 2327.2;	DB 10;	Length 2355;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2351; Conservative	0;	Mismatches 3;	Indels 2;	Gaps 2

[illegible]

Dh 601 GACACCAAGCAGATGTATACAGCTTTGCGATCGTCATCGGGGCTGCTCACACAGAG 660
Qy 661 AAGCGTTTGCAGATGAGAGAAACATCTTGCACATATGTGAAAGTGTGAAGGGCCAC 720
Dh 661 AAGCGTTTGCAGATGAGAGAAACATCTTGCACATATGTGAAAGTGTGAAGGGCCAC 720
Qy 721 GGGCCGAGCTGCGCGCGGTGTGCAGAGCCGGCGCGCGCTGCAAGCACCTGATACG 780
Dh 721 GGGCCGAGCTGCGCGCGGTGTGCAGAGCCGGCGCGCGCTGCAAGCACCTGATACG 780
Qy 781 CTCATGCAAGCGGTGTGCAGAGGGAGATCGGAGTTAGGCCCACTTCCAAAGAAATTACT 840
Dh 781 CTCATGCAAGCGGTGTGCAGAGGGAGATCGGAGTTAGGCCCACTTCCAAAGAAATTACT 840
Qy 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTATGACGAAGTGAAGAAAGAACTGTATAT 900
Dh 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTATGACGAAGTGAAGAAAGAACTGTATAT 900
Qy 901 CTGGAAGTGAAGAGCCCGGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Dh 901 CTGGAAGTGAAGAGCCCGGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Qy 961 GCCTCTGCCCCACCTTGATTAACGATACGACTCTTCCAGCTTCTCTCAAGCTGAC 1020
Dh 961 GCCTCTGCCCCACCTTGATTAACGATACGACTCTTCCAGCTTCTCTCAAGCTGAC 1020
Qy 1021 TCTGAAGTTTCCCAAGCTGTGAGGGCCCCGAGAGGCTCAGCCGAGAGTCTCTTGAATCC 1080
Dh 1021 TCTGAAGTTTCCCAAGCTGTGAGGGCCCCGAGAGGCTCAGCCGAGAGTCTCTTGAATCC 1080
Qy 1081 AAGCTGACATGCTCGGAGTGTGAAGAGAGCTCTCGGGGGTGTCTCGGTGAGACTCGGC 1140
Dh 1081 AAGCTGACATGCTCGGAGTGTGAAGAGAGCTCTCGGGGGTGTCTCGGTGAGACTCGGC 1140
Qy 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAACTTTCACACGAGATCTG 1200
Dh 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAACTTTCACACGAGATCTG 1200
Qy 1201 GGTATCCAAAGACGTTCAGAAAGAAAGACTTGTGATGCTATCGTGTCC-GGAGACAG 1259
Dh 1201 GGTATCCAAAGACGTTCAGAAAGAAAGACTTGTGATGCTATCGTGTCC-GGAGACAG 1259
Qy 1260 CAATCTGATGAAGATCTGACGCGCAGAGACGTGACCTTGAGACTGAGACAGCGGTG 1319
Dh 1260 CAATCTGATGAAGATCTGACGCGCAGAGACGTGACCTTGAGACTGAGACAGCGGTG 1319
Qy 1320 CCTGCTGACCTGCGGCTGAGAGCGGCAAGAGAGTGCCTCAAGTGGCTGTCTCAA 1379
Dh 1320 CCTGCTGACCTGCGGCTGAGAGCGGCAAGAGAGTGCCTCAAGTGGCTGTCTCAA 1379
Qy 1380 CAATGCCAACCCCAACCTGAGAACCTGTAGAGGGCTCCACCCGTTGCAATGAGCGGTG 1439
Dh 1380 CAATGCCAACCCCAACCTGAGAACCTGTAGAGGGCTCCACCCGTTGCAATGAGCGGTG 1439
Qy 1440 GAGGAGGTGCGGAGTGTCTGAGAGCTCTGCTGCGACAGAAATCACTGTCAAGCCAA 1499
Dh 1440 GAGGAGGTGCGGAGTGTCTGAGAGCTCTGCTGCGAGAAATCACTGTCAAGCCAA 1499
Qy 1500 GGATGAGGACAGTGAAGAGCCCTTCACTTTGACGCCCAAGCGGAGTGAATGATGACAC 1559
Dh 1500 GGATGAGGACAGTGAAGAGCCCTTCACTTTGACGCCCAAGCGGAGTGAATGATGACAC 1559
Qy 1560 ACGGCTGCTGTTGAGAGAAAGCTCGGTCAACAGAGTGAACCTTTGAGGGCGGACGCC 1619
Dh 1560 ACGGCTGCTGTTGAGAGAAAGCTCGGTCAACAGAGTGAACCTTTGAGGGCGGACGCC 1619
Qy 1620 CATGCAAGTGGCTTGCACAGAGCGGCAAGAAATATCTGAGCACTCTGCTGCGCGAGG 1679
Dh 1620 CATGCAAGTGGCTTGCACAGAGCGGCAAGAAATATCTGAGCACTCTGCTGCGCGAGG 1679
Qy 1680 CGTGAACGTGAAGCTTGAAGAGAGATGCTGCTGCGACCTGAAGTCTGCTGCGCA 1739
Dh 1680 CGTGAACGTGAAGCTTGAAGAGAGATGCTGCTGCGACCTGAAGTCTGCTGCGCA 1739

Qy 1740 GGGCCACCTGCCCATGCTGCAAGCTGTGCGCAAGAGAGCCGGGGGTGAGTGAACGCCCA 1799
Dh 1740 GGGCCACCTGCCCATGCTGCAAGCTGTGCGCAAGAGAGCCGGGGGTGAGTGAACGCCCA 1799
Qy 1800 GACGCTGATGAGAGAGAGCGCCATTTGACCTGAGCGGCAAGCGGGGCACTACCGCGTGGC 1859
Dh 1800 GACGCTGATGAGAGAGAGCGCCATTTGACCTGAGCGGCAAGCGGGGCACTACCGCGTGGC 1859
Qy 1860 CCGCATCTTATGACCTGTGTCTCCAGCTGCAAGTGTGACAGCTGCTGTGCAAGACACC 1919
Dh 1860 CCGCATCTTATGACCTGTGTCTCCAGCTGCAAGTGTGACAGCTGCTGTGCAAGACACC 1919
Qy 1920 CTTGCAAGTGGCGCGGAGCGGGGCAAGAGACATGCAAGGCTGCTCTGCAATCGGGG 1979
Dh 1920 CTTGCAAGTGGCGCGGAGCGGGGCAAGAGACATGCAAGGCTGCTCTGCAATCGGGG 1979
Qy 1980 CGCTGCAAGAGAGCGCTGACCTCAGACGACTCAACCGCTCTGCAAGCTGAGCTGCCCAA 2039
Dh 1980 CGCTGCAAGAGAGCGCTGACCTCAGACGACTCAACCGCTCTGCAAGCTGAGCTGCCCAA 2039
Qy 2040 CGGACACTTGGCCACTGTCAAGCTGTGTGCGAGAGAGAGCCGATGTGCTGCGCGGG 2099
Dh 2040 CGGACACTTGGCCACTGTCAAGCTGTGTGCGAGAGAGAGCCGATGTGCTGCGCGGG 2099
Qy 2100 ACCCTGAAACGAGCGGCGCTGACCTGAGCTGCGGCCCAAGGGGACTCGGAGTGTGGA 2159
Dh 2100 ACCCTGAAACGAGCGGCGCTGACCTGAGCTGCGGCCCAAGGGGACTCGGAGTGTGGA 2159
Qy 2160 GAGTTGTGACGCGCGCATGTCAATTGACCTGTTGACGAGCAGAGGGGCTCAGCGGCTGCA 2219
Dh 2160 GAGTTGTGACGCGCGCATGTCAATTGACCTGTTGACGAGCAGAGGGGCTCAGCGGCTGCA 2219
Qy 2220 CTTGCGCGCCAGAGGCGCGGCAAGAGAGAGAGCTGTCTCAGGCAATGGGGCCCA 2279
Dh 2220 CTTGCGCGCCAGAGGCGCGGCAAGAGAGAGAGCTGTCTCAGGCAATGGGGCCCA 2279
Qy 2280 CATCAACTGTGAAGAGCTCAAGTTCCAGGGGCGGCAATGGGCCGCGCAACTCTCTGCG 2339
Dh 2280 CATCAACTGTGAAGAGCTCAAGTTCCAGGGGCGGCAATGGGCCGCGCAACTCTCTGCG 2339
Qy 2340 GCGAAGCAGAGCTTAG 2355
Dh 2340 GCGAAGCAGAGCTTAG 2355

RESULT 11
AAH15762
ID AAH15762 standard; cDNA; 3876 BP.
XX
AC AAH15762;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14188.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
FN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.

XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

PS Claim 8: SEQ ID NO 14188; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX Sequence 3876 BP; 798 A; 1080 C; 1186 G; 812 T; 0 U; 0 Other;

Query Match 98.8%; Score 2327.2; DB 4; Length 3876;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 ATGGAAGGCGAAGCGCGGACCCCATGAGCCCTGCGCTGCGGACCTTCCACCGCGGCG 60
DB ATGGAAGGCGAAGCGCGGACCCCATGAGCCCTGCGCTGCGGACCTTCCACCGCGGCG 125
QY 61 GAGTTACCGGCTGGGAGAGGCTGGGCGGCTTGGGCGAGGTGTACAAGGTGCGC 120
DB GAGTTACCGGCTGGGAGAGGCTGGGCGGCTTGGGCGAGGTGTACAAGGTGCGC 185
QY 126 GAGTTACCGGCTGGGAGAGGCTGGGCGGCTTGGGCGAGGTGTACAAGGTGCGC 185
DB GAGTTACCGGCTGGGAGAGGCTGGGCGGCTTGGGCGAGGTGTACAAGGTGCGC 245
QY 121 CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGC 180
DB CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGC 245
QY 186 CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGC 245
DB CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGC 245
QY 181 AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGATGAGATGAGCTTCCCTAC 240
DB AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGATGAGATGAGCTTCCCTAC 305
QY 246 AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGATGAGATGAGCTTCCCTAC 305
DB AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGATGAGATGAGCTTCCCTAC 305
QY 241 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGGCTGTGTCATGAGATCATGAG 300
DB ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGGCTGTGTCATGAGATCATGAG 365
QY 306 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGGCTGTGTCATGAGATCATGAG 365
DB ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGGCTGTGTCATGAGATCATGAG 425
QY 301 ACGGGCTCCCTGAGAAAAGCTGTGCTGCGACCATTTGCGATGAGATCTCCGGTTCCGA 360
DB ACGGGCTCCCTGAGAAAAGCTGTGCTGCGACCATTTGCGATGAGATCTCCGGTTCCGA 425
QY 366 ACGGGCTCCCTGAGAAAAGCTGTGCTGCGACCATTTGCGATGAGATCTCCGGTTCCGA 425
DB ACGGGCTCCCTGAGAAAAGCTGTGCTGCGACCATTTGCGATGAGATCTCCGGTTCCGA 425
QY 361 ATCATCCAGAGAGCGGCGGTGGGATGAATTTCTGTCATGATGAGCCCGGATCTCTG 420
DB ATCATCCAGAGAGCGGCGGTGGGATGAATTTCTGTCATGATGAGCCCGGATCTCTG 485
QY 426 ATCATCCAGAGAGCGGCGGTGGGATGAATTTCTGTCATGATGAGCCCGGATCTCTG 485
DB ATCATCCAGAGAGCGGCGGTGGGATGAATTTCTGTCATGATGAGCCCGGATCTCTG 485
QY 421 CACTGGAAGCTCAAGCCCGGAGCATCTGCTGATGAGCCCATACCAAGTCAAGATTTCT 480
DB CACTGGAAGCTCAAGCCCGGAGCATCTGCTGATGAGCCCATACCAAGTCAAGATTTCT 545

QY 481 GATTTGGTCTGAGCAAGTGCAGAGGCTGTGCCACTGCAATGACCTCAGATGATGAGC 540
DB GATTTGGTCTGAGCAAGTGCAGAGGCTGTGCCACTGCAATGACCTCAGATGATGAGC 605
QY 541 CTGTTTGGCAATGCGCTTACCTTCCAGAGGCGCATCAGAGAGAAAGCGGCTCTTC 600
DB CTGTTTGGCAATGCGCTTACCTTCCAGAGGCGCATCAGAGAGAAAGCGGCTCTTC 665
QY 601 GACACCAAGCAGATGATACAGCTTTGGCATCTGATCTGAGGCGGTCTACACAGAG 660
DB GACACCAAGCAGATGATACAGCTTTGGCATCTGATCTGAGGCGGTCTACACAGAG 725
QY 661 AAGCGTTTGGAGATGAGAGAAACATCTGCAATCATGAGTGAAGTGAAGGCGCAC 720
DB AAGCGTTTGGAGATGAGAGAAACATCTGCAATCATGAGTGAAGTGAAGGCGCAC 785
QY 726 AAGCGTTTGGAGATGAGAGAAACATCTGCAATCATGAGTGAAGTGAAGGCGCAC 785
DB AAGCGTTTGGAGATGAGAGAAACATCTGCAATCATGAGTGAAGTGAAGGCGCAC 845
QY 721 CGCCCGAGCTGCGCGCGGTGTGAGAGCCCGGCGCGCTGCAAGCCTGATACG 780
DB CGCCCGAGCTGCGCGCGGTGTGAGAGCCCGGCGCGCTGCAAGCCTGATACG 845
QY 781 CTATGAGCGGTGTGAGAGCGGAGATCGGAGTTAGGCTTCCAGAAATTAATCT 840
DB CTATGAGCGGTGTGAGAGCGGAGATCGGAGTTAGGCTTCCAGAAATTAATCT 905
QY 841 TCTGAAACCGAGAGACCTGTGTAAGAAAGCTGTGATGACGAAAGAAAGTCTCATGAT 900
DB TCTGAAACCGAGAGACCTGTGTAAGAAAGCTGTGATGACGAAAGAAAGTCTCATGAT 965
QY 901 CTGAGCTGAAAGAGCCCGCGAGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
DB CTGAGCTGAAAGAGCCCGCGAGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 1025
QY 961 GCTTGTGCGCCCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB GCTTGTGCGCCCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
QY 1026 GCTTGTGCGCCCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
DB GCTTGTGCGCCCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
QY 1021 TCTGAGATTTTCCAGAGCTGTGAGAGGCGCCAGAGAGCTCAGCGGACCTCTGATGTC 1080
DB TCTGAGATTTTCCAGAGCTGTGAGAGGCGCCAGAGAGCTCAGCGGACCTCTGATGTC 1145
QY 1086 TCTGAGATTTTCCAGAGCTGTGAGAGGCGCCAGAGAGCTCAGCGGACCTCTGATGTC 1145
DB TCTGAGATTTTCCAGAGCTGTGAGAGGCGCCAGAGAGCTCAGCGGACCTCTGATGTC 1205
QY 1081 AAGCTGCAATGTCGCGAGTGTGAGAGAGGCTCTTGGGAGGTGTCTGCTGAGACTCGGCG 1140
DB AAGCTGCAATGTCGCGAGTGTGAGAGAGGCTCTTGGGAGGTGTCTGCTGAGACTCGGCG 1205
QY 1141 TTTCTTTCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTCAACAGCATCTG 1200
DB TTTCTTTCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTCAACAGCATCTG 1265
QY 1206 TTTCTTTCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTCAACAGCATCTG 1265
DB TTTCTTTCAGAGATCACTGTGCTGTCTTTTGAAGCGGAACTTCAACAGCATCTG 1325
QY 1201 GGTATCCAAAGACCTTCCAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1259
DB GGTATCCAAAGACCTTCCAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1324
QY 1266 GGTATCCAAAGACCTTCCAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1324
DB GGTATCCAAAGACCTTCCAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1384
QY 1260 CAATCTGATGAGATCTTGCAGCGCAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1319
DB CAATCTGATGAGATCTTGCAGCGCAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1384
QY 1325 CAATCTGATGAGATCTTGCAGCGCAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1384
DB CAATCTGATGAGATCTTGCAGCGCAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 1444
QY 1330 CTTGCTGCACTGTGCGGTGAGAGCGGCGCAAGAGAGTGTGCGCAAGTGTGCTCTCA 1379
DB CTTGCTGCACTGTGCGGTGAGAGCGGCGCAAGAGAGTGTGCGCAAGTGTGCTCTCA 1444
QY 1385 CTTGCTGCACTGTGCGGTGAGAGCGGCGCAAGAGAGTGTGCGCAAGTGTGCTCTCA 1444
DB CTTGCTGCACTGTGCGGTGAGAGCGGCGCAAGAGAGTGTGCGCAAGTGTGCTCTCA 1504
QY 1380 CAATCCAAAGCTTGCAG 1439
DB CAATCCAAAGCTTGCAG 1504
QY 1445 CAATCCAAAGCTTGCAG 1504
DB CAATCCAAAGCTTGCAG 1564
QY 1440 GAGAGAGGTGCGGAGGTGTGTGAGAGCTCTGTGCGCAAGAGATCAAGTGTCAAGCCCA 1499
DB GAGAGAGGTGCGGAGGTGTGTGAGAGCTCTGTGCGCAAGAGATCAAGTGTCAAGCCCA 1564
QY 1500 GATGAGAGCAAGTGTGAG 1559
DB GATGAGAGCAAGTGTGAG 1624

[illegible]

PT	CDS		1..2355	
FT		/.*tag=	a	
FR		/product=	"Human PKK protein"	
PX	PN	US2003199462-A1.		
PX	PD	23-OCT-2003.		
PX	PE	23-APR-2002; 2002US-00128174.		
PX	PR	23-APR-2002; 2002US-00128174.		
PX	PA	(NUNEZ/) NUNEZ G.		
PX	PA	(INOH/) INOHARA N.		
PX	PI	(MUTO/) MUTO A.		
PX	Nunez G,	Inohara N,	Muto A;	
DR	WPI;	2003-852808/79.		
XX	P-PSDB;	ABMW02412.		
PT	New nucleic acid encoding RICK3,	useful in preparing a composition for inhibiting PKK induced NF-KB activation for treating hyperglycemia.		
XX	Disclosure;	SEQ ID NO 1; Ovp; English.		
CC	The invention relates to methods and compositions for modulating cellular signalling. In particular the present invention relates to protein kinase C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids encoding such proteins. The invention further relates to the use of PKK and RICK3 proteins in modulating NF-kappab signalling. Nucleic acid molecules of the invention are useful in preparing a composition for inhibiting PKK induced NF-kappab activation for treating hyperlycaemia.			
CC	The invention is also used in gene therapy. The present sequence is human PKK DNA			
CC	Sequence 2355 BP; 462 A; 740 C; 762 G; 391 T; 0 U; 0 Other;			
SQ				
Query Match		98.8%; Score 2325.6; DB 10; Length 2355;		
Best Local Similarity		99.7%; Pred. No. 0;		
Matches 2350; Conservative %		0; Mismatches 4; Indels 2; Gaps 2;		
OY	1 ATGAGGGCGCAACGCCGCGGCATCCTGGGCGCTGTGTCGCCACTTTCGAAGCGGCG	60		
Dd	1 ATGAGGGCGCGACGCGCGGACCCTCATGGGCGCTGTGCTGTGCCACTTTGACGCGGCG	60		
OY	61 GAGTTTCAACGGGCTTGAGAAGAGGTGGGGCTTGCGGCGGAGTTCACAAGTGTGGCG	120		
Dd	61 GAGTTTCAACGGGCTTGAGAAGAGGTGGGGCTTGCGGCGGAGTTCACAAGTGTGGCG	120		
OY	121 CATGTCCACTGGAAAGAACCTGTGGCTGGCCATCAAAGTGTCTGGCCACCTGTGACGAC	180		
Dd	121 CATGTCCACTGGAAAGAACCTGTGGCTGGCCATCAAAGTGTCTGGCCACCTGTGACGAC	180		
OY	181 AGGAGCGCATGAGAGCTTTTGAAGAAGCCAAAGATGAGATGGGCCAATTTCGCTAC	240		
Dd	181 AGGAGCGCATGAGAGCTTTTGAAGAAGCCAAAGATGAGATGGGCCAATTTCGCTAC	240		
OY	241 ATTCTGCTGTGTATNGGATCTGCGCGGAACCTGTGGGCGGTGCATGAGTAATGAGAG	300		
Dd	241 ATTCTGCTGTGTATNGGATCTGCGCGGAACCTGTGGGCGGTGCATGAGTAATGAGAG	300		
OY	301 ACGGGCTCCCTGAAAAAGCTGTGGCTTCGGAGCCATTGCCCATTCTCCGGTTCCGA	360		
Dd	301 ACGGGCTCCCTGAAAAAGCTGTGGCTTCGGAGCCATTGCCCATTCTCCGGTTCCGA	360		
OY	361 ATCATTCACGAGAGCGGCGGTGGGCAATACTTCCTGCACTGCAATGAGCCCCGCACTCTG	420		
Dd	361 ATCATTCACGAGAGCGGCGGTGGGCAATACTTCCTGCACTGCAATGAGCCCCGCACTCTG	420		
OY	421 CACTGTGACCTCAAGCCCGGCAACATCTGTGTGATGCCCATCACAGTCAAAATTCT	480		
Dd	421 CACTGTGACCTCAAGCCCGGCAACATCTGTGTGATGCCCATCACAGTCAAAATTCT	480		
OY	421 CACTGTGACCTCAAGCCCGGCAACATCTGTGTGATGCCCATCACAGTCAAAATTCT	480		
Dd	421 CACTGTGACCTCAAGCCCGGCAACATCTGTGTGATGCCCATCACAGTCAAAATTCT	480		

QY 481 GATTTTGGTCTGGCCAAAGTGAACGGGCTGTCCACTGTGCATGACCTTGAAGATGATGGC 540
 DB 481 GATTTTGGTCTGGCCAAAGTGAACGGGCTGTCCACTGTGCATGACCTTGAAGATGATGGC 540
 QY 541 CTGTTTGGCAAGATGGCTTACCTCCCTCAGAGGCGCATCAGGAGAAAGAGCGGCTTTC 600
 DB 541 CTGTTTGGCAAGATGGCTTACCTCCCTCAGAGGCGCATCAGGAGAAAGAGCGGCTTTC 600
 QY 601 GACACCAAGCAGATGTATACAGCTTTCGATCTCATCTGCGGCGTGTCAACAGAG 660
 DB 601 GACACCAAGCAGATGTATACAGCTTTCGATCTCATCTGCGGCGTGTCAACAGAG 660
 QY 661 AAGCGTTTGCAGATGAGAAAGAACTCTGCAATCATATGTGTGAAGGTGTGAAGGCGAC 720
 DB 661 AAGCGTTTGCAGATGAGAAAGAACTCTGCAATCATATGTGTGAAGGTGTGAAGGCGAC 720
 QY 721 CGCCCGAGCTGCGCGCGTGTGAGAGCGCGCGCGCGCTGTGAGCGCACTGATAGC 780
 DB 721 CGCCCGAGCTGCGCGCGTGTGAGAGCGCGCGCGCGCTGTGAGCGCACTGATAGC 780
 QY 781 CTATGACAGCGGTGTGAGAGGAGATCCGAGATTAGGCGCACTTCCAGAAATTACT 840
 DB 781 CTATGACAGCGGTGTGAGAGGAGATCCGAGATTAGGCGCACTTCCAGAAATTACT 840
 QY 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTATGACAAAGTGAAGAACTGTCTATGAT 900
 DB 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTATGACAAAGTGAAGAACTGTCTATGAT 900
 QY 901 CTGAGACGTGAAGAGCGCGCGCGAGCGCGAGAGAGGTGTGCTGCGAGGCTCAAGCGG 960
 DB 901 CTGAGACGTGAAGAGCGCGCGAGCGCGAGAGAGGTGTGCTGCGAGGCTCAAGCGG 960
 QY 961 GCGTGTGCGCCCACTTCGATTAACGACTACAGCTCTCCGAGCTTCTCAAGCTGAGC 1020
 DB 961 GCGTGTGCGCCCACTTCGATTAACGACTACAGCTCTCCGAGCTTCTCAAGCTGAGC 1020
 QY 1021 TCTGAGATTTTCCAGAGCTGTGCGAGGCGCGAGAGCTCAAGCGGAGCTCTGATGTC 1080
 DB 1021 TCTGAGATTTTCCAGAGCTGTGCGAGGCGCGAGAGCTCAAGCGGAGCTCTGATGTC 1080
 QY 1081 AAGCTGCGCATCGTCCGCGAGTGGGAAAGAGGCTCTGCGGAGGTGCTCCGCTGAGC 1140
 DB 1081 AAGCTGCGCATCGTCCGCGAGTGGGAAAGAGGCTCTGCGGAGGTGCTCCGCTGAGC 1140
 QY 1141 TTCTCTTCAGAGATCACTGTGCTGTCTTGAAGCGGAACTTCAACAGCATCTG 1200
 DB 1141 TTCTCTTCAGAGATCACTGTGCTGTCTTGAAGCGGAACTTCAACAGCATCTG 1200
 QY 1201 GGTACCAAGACGTTCAGAGAAAGAGGCTTGTGATGTCATGTGTTC-GGAGACAG 1259
 DB 1201 GGTACCAAGACGTTCAGAGAAAGAGGCTTGTGATGTCATGTGTTC-GGAGACAG 1259
 QY 1260 CAAACTGATGAAGATCTGCAAGCGGAGAGCTGTGAGCTGTGAGACAGCGGTGCGAG 1319
 DB 1260 CAAACTGATGAAGATCTGCAAGCGGAGAGCTGTGAGCTGTGAGACAGCGGTGCGAG 1319
 QY 1320 CTTGCTGCACTGTGCGGTGAGAGCGGCGGAGAGAGGTGCGCAAGTGTCTGTCTCA 1379
 DB 1320 CTTGCTGCACTGTGCGGTGAGAGCGGCGGAGAGAGGTGCGCAAGTGTCTGTCTCA 1379
 QY 1380 CAATGCAACCCCAACTGAGCAACGATGAGGCTTCAACCGGTTGCAATGCGGTGGA 1439
 DB 1380 CAATGCAACCCCAACTGAGCAACGATGAGGCTTCAACCGGTTGCAATGCGGTGGA 1439
 QY 1440 GAGGAGGAGCGGCGGTGTGTGAGCTCTGCTGAGCAAGAGATGATGATGATGATGATG 1499
 DB 1440 GAGGAGGAGCGGCGGTGTGTGAGCTCTGCTGAGCAAGAGATGATGATGATGATGATG 1499
 QY 1500 GATGAGGACAGTGTGACAGCCCTTCACTTTGAGCGCAAGACGGGAGATGATGATGATG 1559
 DB 1500 GATGAGGACAGTGTGACAGCCCTTCACTTTGAGCGCAAGACGGGAGATGATGATGATG 1559

QY 1560 ACGGCTGCTGTGAGAGAAAGCGCTTCGATCAACGAGTGTGAAGCTTGAAGGCGGAGCGC 1619
 DB 1560 ACGGCTGCTGTGAGAGAAAGCGCTTCGATCAACGAGTGTGAAGCTTGAAGGCGGAGCGC 1619
 QY 1620 CATGACGTGAGCTGTGAGAGAGAGAGAAATATGTGCGCATCTGCTGCGCGAGG 1679
 DB 1620 CATGACGTGAGCTGTGAGAGAGAGAGAAATATGTGCGCATCTGCTGCGCGAGG 1679
 QY 1680 CTGTGAGAGCTGTGAGAGGAGAGAGAGTGTGCTGCGCGCATCTGACATGACCTGCTGGA 1739
 DB 1680 CTGTGAGAGCTGTGAGAGGAGAGAGAGTGTGCTGCGCGCATCTGACATGACCTGCTGGA 1739
 QY 1740 GGGCACCTGCGCATCTGTCAAGCTGTGAGCAAGCAGCGGAGTGAAGTGAAGCGCCA 1799
 DB 1740 GGGCACCTGCGCATCTGTCAAGCTGTGAGCAAGCAGCGGAGTGAAGTGAAGCGCCA 1799
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 DB 1800 GACGCTGATGAGAGAGCGCATTTGCACTGTGCGCGCAACAGCGGCGCATACCGCTGAGC 1859
 QY 1860 CCGCATCTCATGACCTGTGTCCGAGCTCAACGTCGTGAGAGCTGTGAGAGAGAGC 1919
 DB 1860 CCGCATCTCATGACCTGTGTCCGAGCTCAACGTCGTGAGAGAGCTGTGAGAGAGAGC 1919
 QY 1920 CTTGCAAGTGTGCGCGGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1979
 DB 1920 CTTGCAAGTGTGCGCGGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1979
 QY 1980 CGCTGAGAGAGAGCGGTGACCTTCAAGCGGCTTCAAGCGGCTTGTGAGAGAGAGAGAG 2039
 DB 1980 CGCTGAGAGAGAGCGGTGACCTTCAAGCGGCTTCAAGCGGCTTGTGAGAGAGAGAGAG 2039
 QY 2040 CGGACACTGTGCGCATCTGTCAAGCTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2099
 DB 2040 CGGACACTGTGCGCATCTGTCAAGCTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2099
 QY 2100 ACCCTGAAACAGAGAGCGGCTGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2159
 DB 2100 ACCCTGAAACAGAGAGCGGCTGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2159
 QY 2160 GAGATGTGTGAGAGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2219
 DB 2160 GAGATGTGTGAGAGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2219
 QY 2220 CTTGCGCGCGCGAGGCGGAG 2279
 DB 2220 CTTGCGCGCGCGAGGCGGAG 2279
 QY 2280 CATCAACCTGTGAGAGAGCTCAAGTTCAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2339
 DB 2280 CATCAACCTGTGAGAGAGCTCAAGTTCAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2339
 QY 2340 GCGAAGCAAGACTAG 2355
 DB 2340 GCGAAGCAAGACTAG 2355

RESULT 13
 AAD64348
 ID AAD64348 standard; DNA; 2355 BP.
 XX
 AC AAD64348;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human protein kinase C-associated kinase (PKK) variant DNA #10.
 XX
 KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
 KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
 OS Homo sapiens.
 XX
 PN US2003199462-A1.

XX 23-OCT-2003.
PD 23-APR-2002; 2002US-00128174.
XX 23-APR-2002; 2002US-00128174.
XX 23-APR-2002; 2002US-00128174.
PR 23-APR-2002; 2002US-00128174.
XX (NINEZ/) NINEZ G.
XX (INOH/) INOHARA N.
PA (MUTO/) MUTO A.
XX Nunez G, Inohara N, Muto A;
XX WPI; 2003-852808/79.
DR
XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
PS Disclosure; SEQ ID NO 23; 0bp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signaling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signaling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
XX
SQ Sequence 2355 BP; 461 A; 740 C; 763 G; 391 T; 0 U; 0 Other;

Query Match 98.7%; Score 2324; DB 10; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;

Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 ATGGAGGCGCAGACGGGAGACCCCATGGGCGCTGTGCGCAGCTTCGACGCGGCG 60
DB 1 ATGGAGGCGCAGACGGGAGACCCCATGGGCGCTGTGCGCAGCTTCGACGCGGCG 60
QY 61 GAGTTCACGGGCTGGGAGAGAGTGGGCTCGGCGCGCTTCGCGGCAAGTGTACAGGTGCGC 120
DB 61 GAGTTCACGGGCTGGGAGAGAGTGGGCTCGGCGCGCTTCGCGGCAAGTGTACAGGTGCGC 120
QY 121 CATGTCCATGGAAGACCTGTGCTGGCCATCAAGTCTGCGGCGGCGGCGGCGGCGGCG 180
DB 121 CATGTCCATGGAAGACCTGTGCTGGCCATCAAGTCTGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 AGGAGCGCATGAGAGCTTTTGGAGAGACCAAGATGAGATGAGATGAGATGAGATGAGATG 240
DB 181 AGGAGCGCATGAGAGCTTTTGGAGAGACCAAGATGAGATGAGATGAGATGAGATGAGATG 240
QY 241 ATCTGCTGTGTATGAGCATCTGCGCGAGACCTGTGCGGCTGTGCTGTGCTGTGCTGTG 300
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGAGACCTGTGCGGCTGTGCTGTGCTGTGCTGTG 300
QY 301 ACGGCTCCCTGGGAGAAAGCTGTGCTTCGAGCGCATTTGGCAATGGAGATCTCCGGTTCCGA 360
DB 301 ACGGCTCCCTGGGAGAAAGCTGTGCTTCGAGCGCATTTGGCAATGGAGATCTCCGGTTCCGA 360
QY 361 ATCATCCAGAGACGGCGGTGGGAGTGAATTTCTTCGCACTGATGAGCCCGGCACTCTTG 420
DB 361 ATCATCCAGAGACGGCGGTGGGAGTGAATTTCTTCGCACTGATGAGCCCGGCACTCTTG 420
QY 421 CACCTGACCTTAAAGCCCGGAGAAACATCTGTGATGAGCCCACTACAGCTCAAGATTTCT 480
DB 421 CACCTGACCTTAAAGCCCGGAGAAACATCTGTGATGAGCCCACTACAGCTCAAGATTTCT 480
QY 481 GATTTTGTGTGGCAGATGAGACGGGCTGTCCCACTGTGATGAGTCAAGATGAGATGAGC 540
DB 481 GATTTTGTGTGGCAGATGAGACGGGCTGTCCCACTGTGATGAGTCAAGATGAGATGAGC 540
QY 541 CTGTTTGGCAATGCGCTACCTCCCTCGAAGCGCATCAAGGAGAGAGAGCGGCTCTTC 600

DB 541 CTGTTTGGCAATGCGCTACCTCCCTCGAAGCGCATCAAGGAGAGAGAGCGGCTCTTC 600
QY 601 GACACCAAGCAGATGTATACAGTTTGCATGTCTATCTGGGCGCTCTCAACAGAG 660
DB 601 GACACCAAGCAGATGTATACAGTTTGCATGTCTATCTGGGCGCTCTCAACAGAG 660
QY 661 AAGCGTTTGCAGATGAGAGAAACATCTGCAATCATGTGTGAAGGTGTGAAGGGCCAC 720
DB 661 AAGCGTTTGCAGATGAGAGAAACATCTGCAATCATGTGTGAAGGTGTGAAGGGCCAC 720
QY 721 CGCCCGAGCTGCGCGCGGTGTGCAAGACCGGCGCGGCGCTGCAAGCACTGATACG 780
DB 721 CGCCCGAGCTGCGCGCGGTGTGCAAGACCGGCGCGGCGCTGCAAGCACTGATACG 780
QY 781 CTCATGACGGGTGTGCGGAGGGGATCCCGGAGTTAGGCCCACTTCCAAAGAAATTACT 840
DB 781 CTCATGACGGGTGTGCGGAGGGGATCCCGGAGTTAGGCCCACTTCCAAAGAAATTACT 840
QY 841 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAACTGCTCATGAT 900
DB 841 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAACTGCTCATGAT 900
QY 901 CTGACCTGTGAAGAAAGCCCGGAGGCCAGAGCGAGGTGTGCTGTGAGGCTCAAGCGG 960
DB 901 CTGACCTGTGAAGAAAGCCCGGAGGCCAGAGCGAGGTGTGCTGTGAGGCTCAAGCGG 960
QY 961 GCTCTGCCCCCACTTTCGATTAACGACTACAGCTTCCGAGCTTCTCTACAGTGTGAC 1020
DB 961 GCTCTGCCCCCACTTTCGATTAACGACTACAGCTTCCGAGCTTCTCTACAGTGTGAC 1020
QY 1021 TCTGGAATTTCCAGAGCTGTGAGGGGCCGAGAGAGCTCAAGCGGAGCTCTCTGAGTTC 1080
DB 1021 TCTGGAATTTCCAGAGCTGTGAGGGGCCGAGAGAGCTCAAGCGGAGCTCTCTGAGTTC 1080
QY 1081 AAGCTGCATCTGTCCGAGTGTGGAAGAGGCTCTCGGAGGTGTCTTCTGATGACTCCGCC 1140
DB 1081 AAGCTGCATCTGTCCGAGTGTGGAAGAGGCTCTCGGAGGTGTCTTCTGATGACTCCGCC 1140
QY 1141 TTTCTTTCAGAGATATCTGTGCTGTCTTCTTGAAGGGGAACTTCAACAGATCTG 1200
DB 1141 TTTCTTTCAGAGATATCTGTGCTGTCTTCTTGAAGGGGAACTTCAACAGATCTG 1200
QY 1201 GGTACCAAGAGCGTCCAGAGAAAGAGCTTGTGATGGCATGTGTCC-GGAGACACAG 1259
DB 1201 GGTACCAAGAGCGTCCAGAGAAAGAGCTTGTGATGGCATGTGTCC-GGAGACACAG 1259
QY 1260 CAAACTGATGAAGATCTGTGACGCGAGAGCTGTGACCTGTGACAGCGGTCAG 1319
DB 1260 CAAACTGATGAAGATCTGTGACGCGAGAGCTGTGACCTGTGACAGCGGTCAG 1319
QY 1320 CTGTGTCACCTGTGCGGTGTGAGAGCGCGGCAAGAGAGTGGCCAGTGTGCTCTCAA 1379
DB 1320 CTGTGTCACCTGTGCGGTGTGAGAGCGCGGCAAGAGAGTGGCCAGTGTGCTCTCAA 1379
QY 1380 CAATGCAACCCCAACTGTAGCAACGTTAGGGGCTCCACCCGTTGCAATGGCCGTGGA 1439
DB 1380 CAATGCAACCCCAACTGTAGCAACGTTAGGGGCTCCACCCGTTGCAATGGCCGTGGA 1439
QY 1440 GAGAGGGGTGCGGGGTGTGTGTGAGCTCTGTGTGACAGGAGATCAAGTCAACGCGCAA 1499
DB 1440 GAGAGGGGTGCGGGGTGTGTGTGAGCTCTGTGTGACAGGAGATCAAGTCAACGCGCAA 1499
QY 1500 GGATGAGAGACATGTGACAGCCCTTCCACTTTGACAGCCCAAGGGGATAGTCTAGCAC 1559
DB 1500 GGATGAGAGACATGTGACAGCCCTTCCACTTTGACAGCCCAAGGGGATAGTCTAGCAC 1559
QY 1560 ACGGCTGTGTGGAAGAAAGCGCTGTGCAAGAGTGTGCACTTTGAGGGCGGAGCGCC 1619
DB 1560 ACGGCTGTGTGGAAGAAAGCGCTGTGCAAGAGTGTGCACTTTGAGGGCGGAGCGCC 1619
QY 1620 CATGCACTGTGCTGTGCAAGAGCGGCGAGAGAAATATGTGCGCATCTGTGCGCGAGG 1679

DB 1620 CATGACGCTGCGCTGCGCAGCAGGAGAGAAATATCGTGGCATCTGCTGCGCCGAGG 1679
 QY 1680 CGTGGACGTGAGCCTGCAAGGAGAGATGCTGCTGCACTGCACTGACCTGCTGCA 1739
 DB 1680 CGTGGACGTGAGCCTGCAAGGAGAGATGCTGCTGCACTGCACTGACCTGCTGCA 1739
 QY 1740 GGGGCCACTGCGCCATGCTCAAGCTGCTGCGCAGCAGCGGGGGTGAATGTGAAGCCCA 1799
 DB 1740 GGGGCCACTGCGCCATGCTCAAGCTGCTGCGCAGCAGCGGGGGTGAATGTGAAGCCCA 1799
 QY 1800 GACGCTGATGAGGAGAGAGCCATTGCACTGCGCCAGCAGCGGGGCACTACCGCTGAC 1859
 DB 1800 GACGCTGATGAGGAGAGAGCCATTGCACTGCGCCAGCAGCGGGGCACTACCGCTGAC 1859
 QY 1860 CCGCATCTCATGACCTGCTGCTGCGCAGCTCAACCTGCTGCGCAGCAGCAGCAGCAGC 1919
 DB 1860 CCGCATCTCATGACCTGCTGCTGCGCAGCTCAACCTGCTGCGCAGCAGCAGCAGCAGC 1919
 QY 1920 CCGCATCTGCGCGCGGAGAGAGCGGGGCACTGCGCAGCAGCTGCTGCGCAGCAGCAGC 1979
 DB 1920 CCGCATCTGCGCGCGGAGAGAGCGGGGCACTGCGCAGCAGCTGCTGCGCAGCAGCAGC 1979
 QY 1980 CCGTGGCAAGAGAGCGCTGCAAGCCTGCAAGCAGCTGCAACCTGCTGCGCAGCAGCAGC 2039
 DB 1980 CCGTGGCAAGAGAGCGCTGCAAGCCTGCAAGCAGCTGCAACCTGCTGCGCAGCAGCAGC 2039
 QY 2040 CCGACACCTGCGCCTGCTGCAAGCCTGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGC 2099
 DB 2040 CCGACACCTGCGCCTGCTGCAAGCCTGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGC 2099
 QY 2100 ACCCTGAAACAGAGCGCGCTGCACTGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGC 2159
 DB 2100 ACCCTGAAACAGAGCGCGCTGCACTGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGC 2159
 QY 2160 GGAATGTGTCAGAGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2219
 DB 2160 GGAATGTGTCAGAGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2219
 QY 2220 CCGTGGCGCGCAGCGCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2279
 DB 2220 CCGTGGCGCGCAGCGCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2279
 QY 2280 CATCAACCTGCAAGAGCTCAAGTTCCAGGCGCGCCATGCGCGCGCGCGCGCGCGCGC 2339
 DB 2280 CATCAACCTGCAAGAGCTCAAGTTCCAGGCGCGCCATGCGCGCGCGCGCGCGCGCGC 2339
 QY 2340 GCGAAGCAAGACCTAG 2355
 DB 2340 GCGAAGCAAGACCTAG 2355

XX (NUNE/) NUNEZ G.
 PA (INOH/) INOHARA N.
 PA (MUTO/) MUTO A.
 XX Nunez G, Inohara N, Muto A;
 DR WPI: 2003-852808/79.
 XX New nucleic acid encoding RICK3, useful in preparing a composition for
 PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
 XX Disclosure; SEQ ID NO 17; Opp: English.
 XX The invention relates to methods and compositions for modulating cellular
 CC signalling. In particular the present invention relates to protein kinase
 CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
 CC encoding such proteins. The invention further relates to the use of PKK
 CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
 CC molecules of the invention are useful in preparing a composition for
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 CC The invention is also used in gene therapy. The present sequence is human
 CC PKK variant DNA
 SQ Sequence 2355 BP; 462 A; 740 C; 763 G; 390 T; 0 U; 0 Other;
 Query Match 98.7%; Score 2324; DB 10; Length 2355;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
 QY 1 ATGAGAGGCGAGCGGAGAGCCCATGAGGAGCCCTGAGCTGCGCAGCAGCAGCAGCAGCAGC 60
 DB 1 ATGAGAGGCGAGCGGAGAGCCCATGAGGAGCCCTGAGCTGCGCAGCAGCAGCAGCAGCAGC 60
 QY 61 GAGTTCAAGGCTGAGGAGAGGAGTGGGCTGCGGCGGCTTGGGCGAGTGTACAGAGTGGC 120
 DB 61 GAGTTCAAGGCTGAGGAGAGGAGTGGGCTGCGGCGGCTTGGGCGAGTGTACAGAGTGGC 120
 QY 121 CATGTCACTGAGAGAGCTGCGCTGCGCATCAAGTGTCTGCCACCTGCAAGTGTGAGCAGC 180
 DB 121 CATGTCACTGAGAGAGCTGCGCTGCGCATCAAGTGTCTGCCACCTGCAAGTGTGAGCAGC 180
 QY 121 CATGTCACTGAGAGAGCTGCGCTGCGCATCAAGTGTCTGCCACCTGCAAGTGTGAGCAGC 180
 DB 121 CATGTCACTGAGAGAGCTGCGCTGCGCATCAAGTGTCTGCCACCTGCAAGTGTGAGCAGC 180
 QY 181 AGGAGAGCGCATGAGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAGTTTCGCTAC 240
 DB 181 AGGAGAGCGCATGAGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAGTTTCGCTAC 240
 QY 181 AGGAGAGCGCATGAGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAGTTTCGCTAC 240
 DB 181 AGGAGAGCGCATGAGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAGTTTCGCTAC 240
 QY 241 ATCTGCTGTGTATGAGCATGCGCGAAGCTTGGCGCTGATCATGAGATGAGAG 300
 DB 241 ATCTGCTGTGTATGAGCATGCGCGAAGCTTGGCGCTGATCATGAGATGAGAG 300
 QY 301 ACGGCTCTCTGAGAAAGCTGCTGCTGCGAGCATTGCGATGAGATCTCCGTTCCGA 360
 DB 301 ACGGCTCTCTGAGAAAGCTGCTGCTGCGAGCATTGCGATGAGATCTCCGTTCCGA 360
 QY 301 ACGGCTCTCTGAGAAAGCTGCTGCTGCGAGCATTGCGATGAGATCTCCGTTCCGA 360
 DB 301 ACGGCTCTCTGAGAAAGCTGCTGCTGCGAGCATTGCGATGAGATCTCCGTTCCGA 360
 QY 361 ATCATTCAGAGAGGCGGCGTGGGATGAACCTTCCGACAGTGCATGAGCCCGCACTCTG 420
 DB 361 ATCATTCAGAGAGGCGGCGTGGGATGAACCTTCCGACAGTGCATGAGCCCGCACTCTG 420
 QY 421 CACCTGACCTCAAGCCCGCAGACATCTGCTGATGAGCCCACTACAGAGTGAATTTCT 480
 DB 421 CACCTGACCTCAAGCCCGCAGACATCTGCTGATGAGCCCACTACAGAGTGAATTTCT 480
 QY 481 GATTTGTGTCGCGCAAGTGCAGAGGCTGTTCCTCACTGCAATGACCTTCAAGATGATGCG 540
 DB 481 GATTTGTGTCGCGCAAGTGCAGAGGCTGTTCCTCACTGCAATGACCTTCAAGATGATGCG 540
 QY 541 CTGTTTGGCAATGAGCTTACCTCCCTCAGAGGCGCATCAGGAGAGAGCGGCTCTTC 600
 DB 541 CTGTTTGGCAATGAGCTTACCTCCCTCAGAGGCGCATCAGGAGAGAGCGGCTCTTC 600
 QY 601 GACACCAAGCAGATGTATACAGCTTTCAGATGCTCATCTGAGGCGTGTCTACACAGAG 660
 DB 601 GACACCAAGCAGATGTATACAGCTTTCAGATGCTCATCTGAGGCGTGTCTACACAGAG 660

QY	661	AAGCGTTTGCAGATGAGAAACAATCTCTGCACATCATGTGTGAAGATGTGTGAAGGCCAC	720
Db	661	AAGCGTTTGCAGATGAGAAACAATCTCTGCACATCATGTGTGAAGATGTGTGAAGGCCAC	720
QY	721	CGCCCGGAGCTCGCGCCCGTGTGCAGAACCCGCGCCGCGCTGCAGCCACTTGATACGC	780
Db	721	CGCCCGGAGCTCGCGCCCGTGTGCAGAACCCGCGCCGCGCTGCAGCCACTTGATACGC	780
QY	781	CTCATGCAAGCGGTGTGGCAAGGGGGATTCGGGAGTTAAGCCCACTTCCAAAGAAATTACT	840
Db	781	CTCATGCAAGCGGTGTGGCAAGGGGGATTCGGGAGTTAAGCCCACTTCCAAAGAAATTACT	840
QY	841	TCTGAAACCGAGGACCTGTGTGTAAGAAAGCCTGATGTGACGAAGTGAAGAAAGAACTGCTCATGAT	900
Db	841	TCTGAAACCGAGGACCTGTGTGTAAGAAAGCCTGATGTGACGAAGTGAAGAAAGAACTGCTCATGAT	900
QY	901	CTGGAACGTGAAAAGCCCCCGGAGGCCAGAGACGAGGTGTGTCTCGAGGCTCAAGCGG	960
Db	901	CTGGAACGTGAAAAGCCCCCGGAGGCCAGAGACGAGGTGTGTCTCGAGGCTCAAGCGG	960
QY	961	GCCTCTGCGCCCACTTGTGATTAACGACTACAGCCCTCTCCGAGCTTCTCAACAGCTGCAC	1020
Db	961	GCCTCTGCGCCCACTTGTGATTAACGACTACAGCCCTCTCCGAGCTTCTCAACAGCTGCAC	1020
QY	1021	TCTGGAAGTTTCCCAAGCTGTGCAGGGGCCCGAGAGACTCAAGCCGACGCTCTCTTGAATCC	1080
Db	1021	TCTGGAAGTTTCCCAAGCTGTGCAGGGGCCCGAGAGACTCAAGCCGACGCTCTCTTGAATCC	1080
QY	1081	AAAGCTGCATAGTCTCCGGCAGTGTGGAAAGAGCTCTTGCGGGGTGTCTCGGTGACCTCGCC	1140
Db	1081	AAAGCTGCATAGTCTCCGGCAGTGTGGAAAGAGCTCTTGCGGGGTGTCTCGGTGACCTCGCC	1140
QY	1141	TTCTCTTCCAGAGGATCACTGTGCTGTCTCTTGTGACGGGAACTTCAACAGACGATCTG	1200
Db	1141	TTCTCTTCCAGAGGATCACTGTGCTGTCTCTTGTGACGGGAACTTCAACAGACGATCTG	1200
QY	1201	GGTACCCACAGAAGCTCCAGAAAGAAAGACTTGTGATGCTCATGCTCCCGGGACACAG	1255
Db	1201	GGTACCCACAGAAGCTCCAGAAAGAAAGACTTGTGATGCTCATGCTCCCGGGACACAG	1255
QY	1260	CAAACTGATGAAGATCCCTGCAGCGCGGCAAGAGTGTGCACTGAGCAAGCGGTGCCAG	1315
Db	1260	CAAACTGATGAAGATCCCTGCAGCGCGGCAAGAGTGTGCACTGAGCAAGCGGTGCCAG	1315
QY	1320	CCTGCTGCACCTTGCAGTGTGAGGCGCGGCAAGAGAGTGTCCGCAAGTGGCTGTCTCA	1375
Db	1320	CCTGCTGCACCTTGCAGTGTGAGGCGCGGCAAGAGAGTGTCCGCAAGTGGCTGTCTCA	1375
QY	1380	CAATGCCCAACCCCAACTCTGAGGAAACCTGTAGGGGCTCCACCCCGTTTGCAATGTGGCTGTGA	1435
Db	1380	CAATGCCCAACCCCAACTCTGAGGAAACCTGTAGGGGCTCCACCCCGTTTGCAATGTGGCTGTGA	1435
QY	1440	GAGGAGGGTGCAGGGGTGTCTGTGAGACTCTCTGCTGCAGCGGAAGATCAAGTGTCAAGCCCA	1495
Db	1440	GAGGAGGGTGCAGGGGTGTCTGTGAGACTCTCTGCTGCAGCGGAAGATCAAGTGTCAAGCCCA	1495
QY	1500	GGATGAGGACCAAGTGTGAGAGAGAGCCCTTCCACTTTTGCAACCCAGAACCGGGGACGAGTCTAAGAC	1555
Db	1500	GGATGAGGACCAAGTGTGAGAGAGAGCCCTTCCACTTTTGCAACCCAGAACCGGGGACGAGTCTAAGAC	1555
QY	1560	ACGGCTGCTGTGAGAGAGAAAGCCTCGGTCAACAGAGGTGGACTTTGAGGGGCGGACCGC	1615
Db	1560	ACGGCTGCTGTGAGAGAGAAAGCCTCGGTCAACAGAGGTGGACTTTGAGGGGCGGACCGC	1615
QY	1620	CATGCAACGTGGCTTGCAGCAAGGCAAGAGAAATTATCGTGCATCTTGTGCGCCAGAG	1675
Db	1620	CATGCAACGTGGCTTGCAGCAAGGCAAGAGAAATTATCGTGCATCTTGTGCGCCAGAG	1675
QY	1680	CGTGAACGTGAGCTTGCAGAGGGGAAAGATGCTGTGTGCTGCACCTGACCTAAGCTGTGCTGGCA	1735
Db	1680	CGTGAACGTGAGCTTGCAGAGGGGAAAGATGCTGTGTGCTGCACCTGACCTAAGCTGTGCTGGCA	1735

QY	1740	GGGCCA	CGTGGCCCA	TGCTGCA	AGCTGCTGG	CCCA	ACAGC	AGCCGGGGGTG	AGTGGAA	CGCCCA	1739	
Db	1740	GGGGCACC	CTGGCCCA	TGCTGCA	AGCTGCTGG	CCCA	ACAGC	AGCCGGGGGTG	AGTGGAA	CGCCCA	1739	
QY	1800	GACCGTGG	ATGGAGG	AGCCAT	TCGAC	CTTGAG	CCGCA	CAGGCGCGG	CACTAC	CCGCGTGGC	1859	
Db	1800	GACCGTGG	ATGGAGG	AGCCAT	TCGAC	CTTGAG	CCGCA	CAGGCGCGG	CACTAC	CCGCGTGGC	1859	
QY	1860	CCGCACTCT	CATTCGA	CCCTGTC	CCGAC	CGTTC	CAAC	CGTCTG	CAGCCTG	CTGGCAGAC	1919	
Db	1860	CCGCACTCT	CATTCGA	CCCTGTC	CCGAC	CGTTC	CAAC	CGTCTG	CAGCCTG	CTGGCAGAC	1919	
QY	1920	CCTGCG	ACGTGGCC	CCGCGAG	ACGCGG	CCACA	CGAC	CACTGCG	AGCTCT	CTTCGAT	1979	
Db	1920	CCTGCG	ACGTGGCC	CCGCGAG	ACGCGG	CCACA	CGAC	CACTGCG	AGCTCT	CTTCGAT	1979	
QY	1980	CGCTGG	CAGGAGG	CCGTGAC	CTTGACA	CGGCTA	CAC	CGGCTTG	CACTGAG	CCGCGCA	2039	
Db	1980	CGCTGG	CAGGAGG	CCGTGAC	CTTGACA	CGGCTA	CAC	CGGCTTG	CACTGAG	CCGCGCA	2039	
QY	2040	CGGAC	CACTGGC	CACTGT	CAAGCTG	CTTGT	GAGAG	AGAAAGG	CCGATGT	CTGGCCCGG	2099	
Db	2040	CGGAC	CACTGGC	CACTGT	CAAGCTG	CTTGT	GAGAG	AGAAAGG	CCGATGT	CTGGCCCGG	2099	
QY	2100	ACCCCTGA	ACCA	CAGAC	CGCGCTG	CA	CTTG	GGCTCCG	CCCA	CGGGCA	CTTCGAG	2155
Db	2100	ACCCCTGA	ACCA	CAGAC	CGCGCTG	CA	CTTG	GGCTCCG	CCCA	CGGGCA	CTTCGAG	2155
QY	2160	GGAAGTGG	TCAG	CCGCCA	TGTCAT	TGAC	CTGT	TGACA	CGAG	CAGGGGG	CTCAG	2219
Db	2160	GGAAGTGG	TCAG	CCGCCA	TGTCAT	TGAC	CTGT	TGACA	CGAG	CAGGGGG	CTCAG	2219
QY	2220	CCTGG	CCGCCA	CGGCG	CCGCA	CGCA	CGGT	TGAGA	CTTG	CTC	CAGG	2279
Db	2220	CCTGG	CCGCCA	CGGCG	CCGCA	CGCA	CGGT	TGAGA	CTTG	CTC	CAGG	2279
QY	2280	CATCA	CACTG	CAG	AGCTCA	AGTTCC	AGGG	CGGCC	ATGG	CCCCCG	CCCA	2339
Db	2280	CATCA	CACTG	CAG	AGCTCA	AGTTCC	AGGG	CGGCC	ATGG	CCCCCG	CCCA	2339
QY	2340	GCGA	AGCA	AGCA	CTAG	2355						
Db	2340	GCGA	AGCA	AGCA	CTAG	2355						
RESULT 15												
AAd64345												
ID AAd64345 standard; DNA; 2355 BP.												
AC AAd64345;												
DT 12-FEB-2004 (first entry)												
DE Human protein kinase C-associated kinase (PKC) variant DNA #7.												
KW Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK; RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.												
OS Homo sapiens.												
PN US2003199462-A1.												
PD 23-OCT-2003.												
PF 23-APR-2002; 2002US-00128174.												
PR 23-APR-2002; 2002US-00128174.												
PA (NINEZ/) NINEZ G.												
PA (INOHA/) INOHARA N.												
PA (MUTO/) MUTO A.												
PI Nunez G, Inohara N, Muto A;												

XX WPI; 2003-852808/79.

XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.

XX Disclosure; SEQ ID NO 20; 0bp; English.

XX The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
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CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA

XX Sequence 2355 BP; 462 A; 740 C; 761 G; 392 T; 0 U; 0 Other;

XX Query Match 98.7%; Score 2324; DB 10; Length 2355;

XX Best Local Similarity 99.7%; Pred. No. 0;

XX Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 ATGAGGGCGACGCGGGACCCATGGGCGCTGGGCTGCTCCGACCTTTCAGCGCGGC 60
DB 1 ATGAGGGCGACGCGGGACCCATGGGCGCTGGGCTGCTCCGACCTTTCAGCGCGGC 60
QY 61 GAGTTTCAGGGGCTGGGAGAGGTTGGGCTCGGGGCGCTTCGAGCAGTGTACAGGTTGGC 120
DB 61 GAGTTTCAGGGGCTGGGAGAGGTTGGGCTCGGGGCGCTTCGAGCAGTGTACAGGTTGGC 120
QY 121 CATGTCCACTGAGAACCTGTGGCTGCATCAAGTCTCGGCCCATGCTGACGTCGACGAC 180
DB 121 CATGTCCACTGAGAACCTGTGGCTGCATCAAGTCTCGGCCCATGCTGACGTCGACGAC 180
QY 181 AGGAGCGCATGAGACTTTTGGAGAGCCAGAGAGATGAGATGAGCCAAAGTTTGCTAC 240
DB 181 AGGAGCGCATGAGACTTTTGGAGAGCCAGAGAGATGAGATGAGCCAAAGTTTGCTAC 240
QY 241 ATCCGCGCTGTGTAGGACATCGCGCGAACCTGTGGGCTGTGATGAGATGATGAGAG 300
DB 241 ATCCGCGCTGTGTAGGACATCGCGCGAACCTGTGGGCTGTGATGAGATGATGAGAG 300
QY 241 ATCCGCGCTGTGTAGGACATCGCGCGAACCTGTGGGCTGTGATGAGATGATGAGAG 300
DB 241 ATCCGCGCTGTGTAGGACATCGCGCGAACCTGTGGGCTGTGATGAGATGATGAGAG 300
QY 301 ACGGCGCTCCCTGGAAAAGCTGTGGCTTCGAGCCATTGCGATTCCTGGTTCCGA 360
DB 301 ACGGCGCTCCCTGGAAAAGCTGTGGCTTCGAGCCATTGCGATTCCTGGTTCCGA 360
QY 361 ATCATCCAGAGACGCGGCTGGCATGAACTTCTGCACTGATGCGCCGCACTCTG 420
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RESULT 2
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 LOCUS AR406003 3860 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 1 from patent US 6630335.
ACCESSION AR406003
VERSION AR406003.1 GI:40155103
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3860)
AUTHORS Kapeller-Libermann, R.
TITLE 14711 protein kinase, a novel human protein kinase and uses thereof
JOURNAL Patent: US 6630335-A 1 07-OCT-2003;
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LOCUS HSA278016 3879 bp mRNA linear PRI 19-NOV-2000
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VERSION AJ278016.1 GI:9886710
KEYWORDS dlk gene; protein kinase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 Bhur C., Rohwer A., Stempka L., Rincke G., Marks F. and Geschwendt M.
Dlk, a novel protein kinase that interacts with protein kinase
Cdelta. Cloning, characterization, and gene analysis
J. Biol. Chem. 275 (46), 36350-36357 (2000)

JOURNAL
MEDLINE 20549657
PUBMED 10948194
REFERENCE 2 (bases 1 to 3879)
AUTHORS Geschwendt M.
TITLE Direct Submision
JOURNAL Submitted (18-May-2000) Geschwendt M., Biochemistry of
Tissue-specific Regulation, German Cancer Research Center, Im
Neuenheimer Feld 280, D-69151 Heidelberg, GERMANY

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ORIGIN
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Qy 61 GAGTTCAAGGCGCTGGAGAAAGTGAGGCTCGGAGCGGCTTCGAGAGGTGTCAAAGTGGC 120
Db 109 GAGTTCAAGGCGCTGGAGAAAGTGAGGCTCGGAGCGGCTTCGAGAGGTGTCAAAGTGGC 168
Qy 121 CATGTCACTGAGAAAGCTGAGTGGCCATCAAGTCTGCGCCAGCTTCAGCTGACGAC 180
Db 169 CATGTCACTGAGAAAGCTGAGTGGCCATCAAGTCTGCGCCAGCTTCAGCTGACGAC 228
Qy 181 AGGAGAGCGCATGAGGCTTTTGAAGAAAGCCAAAGATGAGATGGCAAGTTTCGCTAC 240
Db 229 AGGAGAGCGCATGAGGCTTTTGAAGAAAGCCAAAGATGAGATGGCAAGTTTCGCTAC 288
Qy 241 ATCTGACCTGTGTGATGAGCATCTGCGGAACTGTGCGGCTGTGATGATGATGAG 300
Db 289 ATCTGACCTGTGTGATGAGCATCTGCGGAACTGTGCGGCTGTGATGATGATGAG 348
Qy 301 ACGGAGCTCCCTGAGAAAGCTGCTGAGGCTTCGAGGCTTCGATGAGATCTCCGTTCCGA 360
Db 349 ACGGAGCTCCCTGAGAAAGCTGCTGAGGCTTCGAGGCTTCGATGAGATCTCCGTTCCGA 408
Qy 361 ATCATCCACAGACGCGGCTGTGAGATGAATCTCTGACATGACATGAGGCGGCACTCTG 420
Db 409 ATCATCCACAGACGCGGCTGTGAGATGAATCTCTGACATGACATGAGGCGGCACTCTG 468
Qy 421 CACCTGACCTCAAGCCCGGAAATCATCTGTGATGCCCATCACTCAAGTCAAGATTTCT 480
Db 469 CACCTGACCTCAAGCCCGGAAATCATCTGTGATGCCCATCACTCAAGTCAAGATTTCT 528
Qy 481 GATTTGTGCTGAGCAAGTGAAGAGGCTGTCCCATGCTGATGACCTCAAGTCAAGATTTCT 540
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Qy 541 CTGTTTGGCAAAATCGCTCACTCTCCCAAGAGGCAATCAAGGAGAAAGAGCGGCTCTTC 600
Db 589 CTGTTTGGCAAAATCGCTCACTCTCCCAAGAGGCAATCAAGGAGAAAGAGCGGCTCTTC 648
Qy 601 GACACCAAGCAGATGATACAGCTTGTGATGATCTGATGAGGCGGTGCTCACAAGAG 660
Db 649 GACACCAAGCAGATGATACAGCTTGTGATGATCTGATGAGGCGGTGCTCACAAGAG 708
Qy 661 AAGCGTTTGAGATGAGAAAGACATCTCTGACATCATGTGAAGTGTGAGAGGCGCAC 720

Db	709	AAGCGTTTGCAGATGAGAAAGAACTCTGCACTCATGTGGAAAGTGTGAAGCGCAC	766
Qy	721	CGCCCGGAGCTGCGCCCGGTGTGCAGAGCCGCGCGCTGACGCACTGATACGC	780
Db	769	CGCCCGGAGCTGCGCCCGGTGTGCAGAGCCGCGCGCGCTGACGCACTGATACGC	828
Qy	781	CTCATGCAAGCGGTGTGTGCAGAGGGGATCCCGGAGTTAGGCCCACTTCCAGAAATTACT	840
Db	829	CTCATGCAAGCGGTGTGTGCAGAGGGGATCCCGGAGTTAGGCCCACTTCCAGAAATTACT	888
Qy	841	TCTGAAACCGAGAGCTGTGTGAAAGGCTGATGCAGAGTGAAGAAAGAACTGTCATGAT	900
Db	889	TCTGAAACCGAGAGCTGTGTGAAAGGCTGATGCAGAGTGAAGAAAGAACTGTCATGAT	948
Qy	901	CTGAGACGTGAAAGGCCCCCGGAGGCCGAGAGCGAGTGTGCTGCGAGGCTCAAGCGG	960
Db	949	CTGAGACGTGAAAGGCCCCCGGAGGCCGAGAGCGAGTGTGCTGCGAGGCTCAAGCGG	1008
Qy	961	GCTCTGCCCCCACTTGTGATTAAGACTACAGCTCTCCAGGCTTCTCTCAAGCTGAC	1020
Db	1009	GCTCTGCCCCCACTTGTGATTAAGACTACAGCTCTCCAGGCTTCTCTCAAGCTGAC	1068
Qy	1021	TCTGGAATTTCCAGGCGTGTGAGGGGCCCGAGAGGCTCAACCGAGCTCTCTGAAGTCC	1080
Db	1069	TCTGGAATTTCCAGGCGTGTGAGGGGCCCGAGAGGCTCAACCGAGCTCTCTGAAGTCC	1128
Qy	1081	AAGCTGCATCGTCCGGGAGTGGGAAAGAGCTCTCGGGGTGTCTCGGTGAACTCGCC	1140
Db	1129	AAGCTGCATCGTCCGGGAGTGGGAAAGAGCTCTCGGGGTGTCTCGGTGAACTCGCC	1188
Qy	1141	TTCTCTTCCAGAGATCACTGTGCTGTTCCTTTGAGCGGAACTTCAACAGGAGATCTG	1200
Db	1189	TTCTCTTCCAGAGATCACTGTGCTGTTCCTTTGAGCGGAACTTCAACAGGAGATCTG	1248
Qy	1201	GGTACCAAGAGCGTGCAGAGAAAGAAAGCTGTGATGCAATCGGTGCC-GGAGACACAG	1259
Db	1249	GGTACCAAGAGCGTGCAGAGAAAGAAAGCTGTGATGCAATCGGTGCCGGGAGACACAG	1307
Qy	1260	CAAACTGATGAAGATCTTGACGCGCAGAGACTGAGACTGAGCAAGCGGTCCAG	1319
Db	1308	CAAACTGATGAAGATCTTGACGCGCAGAGACTGAGACTGAGCAAGCGGTCCAG	1367
Qy	1320	CCTGCTGCACTTGCGGGTGTGAGAGCGCGGCGAAGAGATGTCCCAAGTGGCTGTCTAA	1379
Db	1368	CCTGCTGCACTTGCGGGTGTGAGAGCGCGGCGAAGAGATGTCCCAAGTGGCTGTCTAA	1427
Qy	1380	CATATGCCAACCCCAACTGAGAGAACCTTGAAGGGCTCAACCCGTTCGACATGGCGGTGGA	1439
Db	1428	CATATGCCAACCCCAACTGAGAGAACCTTGAAGGGCTCAACCCGTTCGACATGGCGGTGGA	1487
Qy	1440	GAGAGAGGGTGCAGGGGTGTGTGGAAGCTCTGTGTGCACGGAAGATCAAGTGTCAAGCCAA	1499
Db	1488	GAGAGAGGGTGCAGGGGTGTGTGGAAGCTCTGTGTGCACGGAAGATCAAGTGTCAAGCCAA	1547
Qy	1500	GGATGAGAGCAAGTGCAGAGCCCTTCACTTTGACGCCGAAGCGGGATGAGTCTTAGCAC	1558
Db	1548	GGATGAGAGCAAGTGCAGAGCCCTTCACTTTGACGCCGAAGCGGGATGAGTCTTAGCAC	1607
Qy	1560	ACGGCTGCTGTGTGAGAGAAAGAGCTTCGGTCAACAGAGTGCACCTTTGAGGGCCGGAGCC	1619
Db	1608	ACGGCTGCTGTGTGAGAGAAAGAGCTTCGGTCAACAGAGTGCACCTTTGAGGGCCGGAGCC	1667
Qy	1620	CATGCAAGTGGCGCTGCAGACAGGGCAGAGAAATACGTGCATCTGTGCAGCGCGAGG	1679
Db	1668	CATGCAAGTGGCGCTGCAGACAGGGCAGAGAAATACGTGCATCTGTGCAGCGCGAGG	1722
Qy	1680	CGTGAACGTGAGCTTGCAAGGCGCAAGATGCTTGCTGCACCTACCTACCTGCTGGCA	1739
Db	1728	CGTGAACGTGAGCTTGCAAGGCGCAAGATGCTTGCTGCACCTACCTACCTGCTGGCA	1787
Qy	1740	GGGCGCACGTGCCCATGTGCAAGCTGTGCACAGCAGCGGGGGGTGAAGTGAAGCCCA	1799
Db	1788	GGGCGCACGTGCCCATGTGCAAGCTGTGCACAGCAGCGGGGGGTGAAGTGAAGCCCA	1847

OY		1800	GACGCTGGATGGAGAGCAGCCATTGGACA	CCTTGTGCCGCACAGCGGGGAGCATACCGCGTGAGC	1859
Dd		1848	GACGCTGGATGGAGAGCAGCCATTGGACA	CCTTGTGCCGCACAGCGGGGAGCATACCGCGTGAGC	1907
OY		1860	CCGGAATCCTAATGCACTCTGTCTCCGACT	CAACAGTCGTGAGCGCTGTGGCACAGACCC	1919
Dd		1908	CCGGAATCCTAATGCACTCTGTCTCCGACT	CAACAGTCGTGAGCGCTGTGGCACAGACCC	1967
OY		1920	CCTTCGACGTGGCCGCGGAGACGCGGGCA	CACGAGCACTGCCAGGCTGCTCTTGATCGGG	1979
Dd		1968	CCTTCGACGTGGCCGCGGAGACGCGGGCA	CACGAGCACTGCCAGGCTGCTCTTGATCGGG	2027
OY		1980	CGCTGGCAAGAAGGCGCTGTAACTTCAGAC	GGGCTTCAACCGCTGTGACCTTGGCTGGCCAA	2039
Dd		2028	CGCTGGCAAGAAGGCGCTGTAACTTCAGAC	GGGCTTCAACCGCTGTGACCTTGGCTGGCCAA	2087
OY		2040	CGGACACCTGGCCACTGTCAAAGCTGTGTC	TGTCGAGAGAAAGCCGATGTGTGCGCCGGG	2099
Dd		2088	CGGACACCTGGCCACTGTCAAAGCTGTGTC	TGTCGAGAGAAAGCCGATGTGTGCGCGGG	2147
OY		2100	ACCCTTAACCAAGACGCGCGCTGCACTTG	TGTCGAGAGAAAGCCGATGTGTGCGCGGG	2159
Dd		2148	ACCCTTAACCAAGACGCGCGCTGCACTTG	TGTCGAGAGAAAGCCGATGTGTGCGCGGG	2207
OY		2160	GGAGTTGGTCAAGGCGCGATGTCAATTTGA	CTGTTCGAGAGAGGGGCTCAGCGGCTGCA	2219
Dd		2208	GGAGTTGGTCAAGGCGCGCGATGTCAATTT	GAACGAGAGAGGGGCTCAGCGGCTGCA	2267
OY		2220	CCTGGCGCGCCAGGAGCGCGCA	CGGACAGACGGTAGAGACTTCTGTCAGGCA	2279
Dd		2268	CCTGGCGCGCCAGGAGCGCGCA	CGGACAGACGGTAGAGACTTCTGTCAGGCA	2327
OY		2280	CATCAACCTTGAGAGGCTCAAGTTCCAGAG	GGCGGCGGCAACACACTGCTGGG	2339
Dd		2328	CATCAACCTTGAGAGGCTCAAGTTCCAGAG	GGCGGCGGCAACACACTGCTGGG	2387
OY		2340	GCGAAGCAAGACTTAG	2355	
Dd		2388	GCGAAGCAAGACTTAG	2403	
RESULT 4					
BD157754			3876 bp	DNA linear	PAT 17-JAN-2003
LOCUS					
DEFINITION			BD157754		
ACCESSION			BD157754		
VERSION			BD157754.1		GI:27863512
KEYWORDS			JP 2002191363-A/12597.		
SOURCE			Homo sapiens (human)		
ORGANISM			Homo sapiens		
REFERENCE			Bukacinski, Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE			I (baaes 1 to 3876)		
JOURNAL			Ota,T., Isegawa,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.		
COMMENT			Primer for synthesizing full-length cDNA and use thereof		
			Patent: JP 2002191363-A 12597 09-JUL-2002;		
			HELIX RESEARCH INSTITUTE		
			OS Homo sapiens (human)		
			PN JP 2002191363-A/12597		
			PD 09-JUL-2002		
			PF 28-JUL-2000 JP 2000280990		
			PI TOSHIO OTA, TAKAO ISOGLI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,		
			PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,		
			PI KEIICHI NAGAI, TETSUJI OTSUKI		
			PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC		
			10,		
			PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC		
			Primer for synthesizing full-length cDNA and use thereof FH Key		
			Location/Qualifiers		

FEATURES		FT	CDS	(66)..(2417).
SOURCE		Location/Qualifiers		1..3876
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				/mol_type="genomic DNA"
				/db_xref="taxon:9606"
ORIGIN				
Query Match		98.8%;	Score 2327.2;	DB 6; Length 3876;
Best Local Similarity		99.8%;	Pred. No. 0;	
Matches 2351;		Conservative 0;	Mismatches 3;	Indels 2; Gaps 2;
Qy	1	ATGAGGCGCAGACGGGCGGAGCCCATGAGGCGCTGCGCTGTCGCGACCTTGACGCGGCGC	60	
Db	66	ATGAGGCGCAGACGGGCGGAGCCCATGAGGCGCTGCGCTGTCGCGACCTTGACGCGGCGC	125	
Qy	61	GAGTTCAAGGCTGGGAGAGAGTGGGCTTCGGGCGGCTTCGGGCGAGTGTACAGAGTGGC	120	
Db	126	GAGTTCAAGGCTGGGAGAGAGTGGGCTTCGGGCGGCTTCGGGCGAGTGTACAGAGTGGC	185	
Qy	121	CATGTCCATGGAAGACCTGCGCTGGCCATCAAGTCTGGCCCAAGCTTGCACGTGACGAC	180	
Db	186	CATGTCCATGGAAGACCTGCGCTGGCCATCAAGTCTGGCCCAAGCTTGCACGTGACGAC	245	
Qy	181	AGGAGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGAGCCCAAGTTTGCTAC	240	
Db	246	AGGAGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGAGCCCAAGTTTGCTAC	305	
Qy	241	ATCTGCTGTGTATGAGCATCTGCCGACACCTGTGGCTGTGTATGAGATACATGAG	300	
Db	306	ATCTGCTGTGTATGAGCATCTGCCGACACCTGTGGCTGTGTATGAGATACATGAG	365	
Qy	301	ACGGGCTCCCTGGAGAAAGCTGTGGCTTCGAGCCATTGGCCATGGAGATCTCGGTTCGA	360	
Db	366	ACGGGCTCCCTGGAGAAAGCTGTGGCTTCGAGCCATTGGCCATGGAGATCTCGGTTCGA	425	
Qy	361	ATCATCCAGAGACGGCGGTGGCATGAACCTTCTGCACCTGCATGAGGCCCGCCACTCTCG	420	
Db	426	ATCATCCAGAGACGGCGGTGGCATGAACCTTCTGCACCTGCATGAGGCCCGCCACTCTCG	485	
Qy	421	CACCTGACCTCAAGCCCGGAGAACATCTGTGTGATGCGCCACTACAGCTCAAGATTTCT	480	
Db	486	CACCTGACCTCAAGCCCGGAGAACATCTGTGTGATGCGCCACTACAGCTCAAGATTTCT	545	
Qy	481	GATTTTGGTCTGGCCAAATGTCAGACGGGCTGTCCCATGGCATGACCTGACATGATGAGC	540	
Db	546	GATTTTGGTCTGGCCAAATGTCAGACGGGCTGTCCCATGGCATGACCTGACATGATGAGC	605	
Qy	541	CTGTTTGGCACAATGCTTACCTCCCTCCAGAGCGCATCAGGAGAGAAAGCGGCTCTTC	600	
Db	606	CTGTTTGGCACAATGCTTACCTCCCTCCAGAGCGCATCAGGAGAGAAAGCGGCTCTTC	665	
Qy	601	GACACCAAGCAGATGTATACAGCTTTTGCATGTGATCTGGGCGTGTCTCACACAGAG	660	
Db	666	GACACCAAGCAGATGTATACAGCTTTTGCATGTGATCTGGGCGTGTCTCACACAGAG	725	
Qy	661	AAGCGTTTGGCAGATGAGAGAAACATCTGTGCACATCAGTGTGAAAGTGTGAAGGCGAC	720	
Db	726	AAGCGTTTGGCAGATGAGAGAAACATCTGTGCACATCAGTGTGAAAGTGTGAAGGCGAC	785	
Qy	721	CGCCCGAGCTGCGCCGCTGTGACAGACCGCGCGCGCTGACGCACTGTATACGC	780	
Db	786	CGCCCGAGCTGCGCCGCTGTGACAGACCGCGCGCGCTGACGCACTGTATACGC	845	
Qy	781	CTCATGCAAGCGGTGTGCAAGGCGGATCCGCAAGTTAGGCCCACTTCCAAAGAAATTAAT	840	
Db	846	CTCATGCAAGCGGTGTGCAAGGCGGATCCGCAAGTTAGGCCCACTTCCAAAGAAATTAAT	905	
Qy	841	TCTGAACCGGAGACCTGTGTGAAAAGCTGTATGACAGAGTGAAGAAATGCTCATAT	900	
Db	906	TCTGAACCGGAGACCTGTGTGAAAAGCTGTATGACAGAGTGAAGAAATGCTCATAT	965	
Qy	901	CTGACGTGAAAAGCCCCCGGAGGCCAGAGCAGAGTGTGTGCTGACAGGCTCAAGCGG	960	

Db	966	CTGACGTGAAAAGCCCCCGGAGGCCAGAGCGAGGTGTGCTGTGAGAGCTCAAGCGG	1025	
Qy	961	GCTCTGCCCCCACCTTTCGATTAACGACTTCTCCGAGCTTCTCTACAGCTGAGC	1020	
Db	1026	GCTCTGCCCCCACCTTTCGATTAACGACTTCTCCGAGCTTCTCTACAGCTGAGC	1085	
Qy	1021	TCTGAGATTTCCAGGCTGTGAGGCGCCGAGAGAGCTCAGCCGACGCTCTCTGAGTTC	1080	
Db	1086	TCTGAGATTTCCAGGCTGTGAGGCGCCGAGAGAGCTCAGCCGACGCTCTCTGAGTTC	1145	
Qy	1081	AACTGCGCATGTTCGGCAGTGGAGAGAGGCTCTCGGAGGTGTCTTCGATGACCTCGGC	1140	
Db	1146	AACTGCGCATGTTCGGCAGTGGAGAGAGGCTCTCGGAGGTGTCTTCGATGACCTCGGC	1205	
Qy	1141	TTCTCTTCCAGAGATACATGTGTGCTCTTCTTGAAGGAGAACCTTAAACAGAGATCTG	1200	
Db	1206	TTCTCTTCCAGAGATACATGTGTGCTCTTCTTGAAGGAGAACCTTAAACAGAGATCTG	1265	
Qy	1201	GGTACCAAGAGCGTCCAGAGAGAAAGCTTGTGATGGCATGTGTCC--GGGACACAG	1259	
Db	1266	GGTACCAAGAGCGTCCAGAGAGAAAGCTTGTGATGGCATGTGTCC--GGGAGACACAG	1324	
Qy	1260	CAAACTGATGAAGATCCTTGCAGCGCAGACGTGACCTTGACCTGACAGCGGTGCGAG	1319	
Db	1325	CAAACTGATGAAGATCCTTGCAGCGCAGACGTGACCTTGACCTGACAGCGGTGCGAG	1384	
Qy	1320	CTGTCTGCACCTGCGGCTGAGAGGCTCGGCGCAAGAGAGTGTGCCCAATGTGCTGCTCA	1379	
Db	1385	CTGTCTGCACCTGCGGCTGAGAGGCTCGGCGCAAGAGAGTGTGCCCAATGTGCTGCTCA	1444	
Qy	1380	CAATGCGAACCCCAACCTGAGCAACGCTAGAGGCTCCACCCCGTGGACATGACCGTGG	1439	
Db	1445	CAATGCGAACCCCAACCTGAGCAACGCTAGAGGCTCCACCCCGTGGACATGACCGTGG	1504	
Qy	1440	GAGAGGGGTGCGGGGTGTCTGTGAGCTCTGTGCGACCGAGAGATCAGTGTCAAACGCAA	1499	
Db	1505	GAGAGGGGTGCGGGGTGTCTGTGAGCTCTGTGCGACCGAGAGATCAGTGTCAAACGCAA	1564	
Qy	1500	GGATGAGAGACCATGTGACACGACCTTCCACTTTGACAGCCCAAGAGGGAGTAAAGTCTACAC	1559	
Db	1565	GGATGAGAGACCATGTGACACGACCTTCCACTTTGACAGCCCAAGAGGGAGTAAAGTCTACAC	1624	
Qy	1560	ACGGCTGCTGTGGAGAAAGAACGCTGTGATCAACGAGGTGATCTTTGAGGGCGGACGCC	1619	
Db	1625	ACGGCTGCTGTGGAGAAAGAACGCTGTGATCAACGAGGTGATCTTTGAGGGCGGACGCC	1684	
Qy	1620	CATGCAAGTGGCTGCCAGACCGGCGAGAGAAATATGTGCGCATCTGTGCGCCGAGG	1679	
Db	1685	CATGCAAGTGGCTGCCAGACCGGCGAGAGAAATATGTGCGCATCTGTGCGCCGAGG	1744	
Qy	1680	CTGTGAGAGTGAAGCTTGCAGAGGCAAGATGTCTGTGCTGCACCTGACCTGCTGGCA	1739	
Db	1745	CTGTGAGAGTGAAGCTTGCAGAGGCAAGATGTCTGTGCTGCACCTGACCTGCTGGCA	1804	
Qy	1740	GGGCGACCTGCCCATGTCTAAGAGCTGTGCGCAAGCAGCGGAGGTGAGTGTGAACGCCCA	1799	
Db	1805	GGGCGACCTGCCCATGTCTAAGAGCTGTGCGCAAGCAGCGGAGGTGAGTGTGAACGCCCA	1864	
Qy	1800	GACGCTGATGAGAGAGCGCATTTGACCTGTGCGCGCACAGCGCGGACCTAACCGCTGTGC	1859	
Db	1865	GACGCTGATGAGAGAGCGCATTTGACCTGTGCGCGCACAGCGCGGACCTAACCGCTGTGC	1924	
Qy	1860	CCGATCTCTATGACCTGTGTCTCCAGCTGCAAGCTGTGCAAGCTGTGCGACAGACACC	1919	
Db	1925	CCGATCTCTATGACCTGTGTCTCCAGCTGCAAGCTGTGCAAGCTGTGCGACAGACACC	1984	
Qy	1920	CTGTGAGTGGCGCGGAGAGCGGCGCACAGAGCATGCGAGGCTGTCTCTGACATCGGGG	1979	
Db	1985	CTGTGAGTGGCGCGGAGAGCGGCGCACAGAGCATGCGAGGCTGTCTCTGACATCGGGG	2044	
Qy	1980	CGCTGCGAAGGAGGCTGTGACCTTCAACGCGCTACACCGCTCTGACCTGTGCTGCGCGCAA	2039	

Db	2045	CGCTGGCAGAGAGGCGCTGACCTCAGAGGGCTACACGCGCTTGACACTGGCTGGCCGGGAA	2104
Qy	2040	CGGACACCTGGGCCCACTGTCAAGCTGCTTGTGCGAGGAGAGAGGCCCAATGTGCTGGCCCGGG	2099
Db	2105	CGGACACCTGGGCCCACTGTCAAGCTGCTTGTGCGAGGAGAGAGGCCCAATGTGCTGGCCCGGG	2164
Qy	2100	AACCCCTGAAACGAGCGGCTGCGACCTGCGCGGCCCAACGGGGCACTCGAGAGTGGTGGGA	2159
Db	2165	AACCCCTGAAACGAGCGGCTGCGACCTGCGCGGCCCAACGGGGCACTCGAGAGTGGTGGGA	2224
Qy	2160	GGAAGTGGTCAAGCGCCGATGTCAATGACCTGTTCGACGAGGAGGGGCTCAAGCGGCTGCA	2219
Db	2225	GGAAGTGGTCAAGCGCCGATGTCAATGACCTGTTCGACGAGGAGGGGCTCAAGCGGCTGCA	2284
Qy	2220	CCTGGCGGCCCAAGGGCGCGGCAAGCAGACGCGTGGAGACTTGTCTCAGGCACTGGGGCCCA	2279
Db	2285	CCTGGCGGCCCAAGGGCGCGGCAAGCAGACGCGTGGAGACTTGTCTCAGGCACTGGGGCCCA	2344
Qy	2280	CATCAACCTGCAAGACCTCAAGTTCACAGGGCGGCCCATGGCCCGCGCAACTGCTGGCG	2339
Db	2345	CATCAACCTGCAAGACCTCAAGTTCACAGGGCGGCCCATGGCCCGCGCAACTGCTGGCG	2404
Qy	2340	GCGAGCAAGACCTAG 2355	
Db	2405	GCGAGCAAGACCTAG 2420	
RESULT 5			
LOCUS	AX879283	3876 bp	DNA
DEFINITION	Sequence 14188 from Patent EP1074617.	linear	PAT 17-DEC-2003
ACCESSION	AX879283		
VERSION	AX879283.1	GI:40034019	
KEYWORDS			
SOURCE			
ORGANISM	<p>Homio sapiens (human)</p> <p>Homio sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.</p>		
REFERENCE	1		
AUTHORS	Ota,T., Iseoga,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishi,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.		
TITLE	Primers for synthesizing full-length cDNA and their use		
JOURNAL	Patent: EP 1074617-A 14188 07-FEB-2001;		
FEATURES	Research Association for Biotechnology (JP)		
source	location/Qualifiers		
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	/note="unnamed protein product"		
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ORIGIN			
Query Match	98.8%	Score 2337.2	DB 6; Length 3876;
Best Local Similarity	99.8%	Pred. No. 0;	
Matches 2351; Conservative	0;	Mismatches 3;	Indels 2; Gaps 2

QY	1	ATGAGAGGCGACGCGGGAGACCCCAATGGACCTGGCGCTGCTGCGCACCTTTCAGCGCGAGC	60
Db	66	ATGAGAGGCGACGCGGGAGACCCCAATGGAGCCCTGGCGCTGCTGCGCACCTTTCAGCGCGAGC	125
QY	61	GAGTTCAACGGGCTGGAGAAAGTGGAGCTCGAGCGGCTTTCGAGCGAGTTACAGAGTGGCGC	120
Db	126	GAGTTCAACGGGCTGGAGAAAGTGGAGCTCGAGCGGCTTTCGAGCGAGTTACAGAGTGGCGC	185
QY	121	CATGTCCATCTGGAGAGACCTGGCTGGCCATCAATAGTGGCTGGCCAGGCTGCAAGTGGAGAC	180
Db	186	CATGTCCATCTGGAGAGACCTGGCTGGCCATCAATAGTGGCTGGCCAGGCTGCAAGTGGAGAC	245
QY	181	AGGAGGCGCATGAGAGCTTTTGGAGAAAGCCAGAGAGATGAGATGGCCAAATTTCGTAC	240
Db	246	AGGAGGCGCATGAGAGCTTTTGGAGAAAGCCAGAGAGATGAGATGGCCAAATTTCGTAC	305
QY	241	ATCTGCTCTGTGTATGCGATTTGCGCGGGAACCTGTGGCGCTGTGTCAATGAGTAAATGGAG	300
Db	306	ATCTGCTCTGTGTATGCGATTTGCGCGGGAACCTGTGGCGCTGTGTCAATGAGTAAATGGAG	365
QY	301	ACGGAGCTCCCTGGAGAAAGCTGCTGGCTTTCGAGGCAATTGGCCATGGAGATCTCCGTTCCGA	360
Db	366	ACGGAGCTCCCTGGAGAAAGCTGCTGGCTTTCGAGGCAATTGGCCATGGAGATCTCCGTTCCGA	425
QY	361	ATCATTCACAGAGCGGCGGTGGAGTGAACCTTCTTGCACTGCGATGGCGCCCGCCACTCTG	420
Db	426	ATCATTCACAGAGCGGCGGTGGAGTGAACCTTCTTGCACTGCGATGGCGCCCGCCACTCTG	485
QY	421	CACCTGGAACCTCAAGACCCCGGAGAACATCTGTGTGGATGCGCATACATGCAAGTGAATTTCT	480
Db	486	CACCTGGAACCTCAAGACCCCGGAGAACATCTGTGTGGATGCGCATACATGCAAGTGAATTTCT	545
QY	481	GATTTTGGTCTGGGCGAAAGTGAGCAGGGCTGTGCCACTGCAATGACCTCAGCATGAGATGGC	540
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VERSION
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Homo sapiens (human)
SOURCE
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Organism
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Wakamatsu,A., Hayashi,M., Sato,H., Nagai,K., Kimura,K., Makita,H.,
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Iehli,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
Nagahari,K., Murakami,K., Yasuda,T., Inayangi,T., Wagatsuna,M.,
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Nagase,T., Nomura,N., Kikuchi,H., Masuo,Y., Yamaishita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isegai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
JOURNAL
PUBMED
14702039
REFERENCE
AUTHORS
2
Isegai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuna,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Iehida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Matanabe,S., Kimura,K., Murakami,K.,
Iehli,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuo,Y., Nimomiya,K. and Inayangi,T.
NEO human cDNA sequencing project
Unpublished
3 (bases 1 to 3876)

AUTHORS Isegai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isegai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genome@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan, cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'- & 3'- and one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
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Location/Qualifiers

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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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 1 (sites)
 AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
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 JOURNAL Published Only in Database (2001)
 REFERENCE
 2 (bases 1 to 3882)
 AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
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 JOURNAL Submitted (25-AUG-2000) Nobuyoshi Shimizu, Keio University, School
 of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo
 160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,
 Tel:81-3-3351-2370, Fax:81-3-3351-2370)
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ORIGIN

Query Match 98.8%; Score 2327.2; DB 9; Length 3882;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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DEFINITION IMAGE:5760485), partial cds.
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VERSION BC035755.1 GI:23242902
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 3867)
Strausberg, R.L., Collins, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Wagner, F.S., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Dichtenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebli, T.B., Toshimiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Cay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heltón, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 3867)
Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@bglr1.nih.gov
Ahter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, P., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Manduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McQuowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, J., H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Place: 79 Row: 0 Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10190675.
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ORIGIN
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AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.			
TITLE	Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof			
JOURNAL	Patent: WO 02068579-A; 17738 06-SRP-2002;			
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RESULT 10
AX16548
LOCUS AX16548 2499 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 39 from Patent WO0138503.
ACCESSION AX16548

VERSION AX166548.1 GI:14546893
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., Planagan, P., and Clary, D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNML Patent: WO 0138503-A 39 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
source 1..2499
Location/Qualifiers
/organism="Homo sapiens"
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ORIGIN
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Best Local Similarity 94.0%; Pred. No. 0;
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DB 61 GAGTTCACGGGCTGGGAGAGAGTGGGCTGGGCGGCTTGCGGACAGTGTACAGGTTGCGC 120
QY 121 CATGTCCATGTGAAGACCTGGCTGGCCATCAAGTGTGCTGCCACGCTTGACGTCAGAC 180
DB 121 CATGTCCATGTGAAGACCTGGCTGGCCATCAAGTGTGCTGCCACGCTTGACGTCAGAC 180
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DB 241 ATCTGCTGTGTATGGCATCTGCGCGAACCTGTGCGGCTGGTGTATGTAGATGATGAG 300
QY 301 ACGGGCTCCCTGGAAAAGCTGTGCTGGAGCCATTGCAATGGGATCTCGGTTCCGC 360
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DB 1800 CGTGGCATCTGCTGCGCGAGGAGGCTGGAAGCTGTGAGGAGGAGGAGGAGGAGGAGGAG 1859

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Db	2040	CTGCAAGCTGTGCGCAACAGACACCCTTCAAGTGGCCGCGAGAGAGGGGGCAACAGAGCAC	2099
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LOCUS	AF302127		
DEFINITION	Mus musculus PKC-regulated kinase PKR mRNA, complete cds.		
ACCESSION	AF302127		
VERSION	AF302127.3 GI:18087895		
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 3559)		
AUTHORS	Chen, L., Haider, K., Ponda, M., Cariappa, A., Rowitch, D. and Pillai, S.		
TITLE	Protein kinase C-associated kinase (PKC), a novel membrane-associated, ankyrin repeat-containing protein kinase		
JOURNAL	J. Biol. Chem. 276 (24), 21737-21744 (2001)		
MEDLINE	21293027		
PUBMED	11278382		
REFERENCE	2 (bases 1 to 3559)		
AUTHORS	Chen, L., Haider, K., Cariappa, A. and Pillai, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-SEP-2000) Cancer Center, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA		
REFERENCE	3 (bases 1 to 3559)		
AUTHORS	Chen, L., Haider, K., Cariappa, A. and Pillai, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-JAN-2002) Cancer Center, Massachusetts General		

REMARK	Hospital, 149 13th Street; Charleston, MA 02129-2060, USA
REFERENCE	Sequence update by submitter
AUTHORS	4 (bases 1 to 3559)
TITLE	Chen, J., Haider, K., Cariappa, A. and Pillai, S.
JOURNAL	Direct Submission
REMARK	Submitted (08-JAN-2002) Cancer Center, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
COMMENT	Nucleotide sequence update by submitter
FEATURES	On Jan 8, 2002 this sequence version replaced gi:18086161.
SOURCE	Location/Qualifiers
CDS	<p>1..3559</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="BALB/c"</p> <p>/db_xref="taxon:10090"</p> <p>50..2410</p> <p>/note="protein kinase C-beta-regulated kinase"</p> <p>/codon_start=1</p> <p>/product="PKC-regulated kinase PKX"</p> <p>/protein_id="AA030871.2"</p> <p>/db_xref="gi:18086162"</p> <p>/translation="MSEGRGRMAALGLRTPDAGEFAGMEKSGRGVGVYKHWM KTMVLAKSPSLHVDDERMELLESKQNMAMAFRYLLPYGICQEPVGA.VMEYETG SLEKLASEPLPMDLPRRIVHETAVGNNFLCMSPPLLIDLPKANILLDAHVKIS DFGIACNGSMSHSDLSMDGLFGTIAVIPERIREKSRLPDTHDKVSFAIVIGWLT OKKPFADKKMIHLIMKYVGHRELPEPICRPBPRAASLIGLMORCMADPOVRPTF OETSITFEDI.CEKDPERKDLAGHPCKSLSESSEAPRESSLRASAPPNDSCSL SELLSDSDSGISQTLEBERELSRSSSCCTPSSSCGRLSGVSSVASPSSGLISL FERASTGDGDPDIQKKUDVATISDTIRLKMLDPPDYDVLYDSASLIHLAYVA GOEBCRWMLLNANPNLNRKSGSTPLMAVERKGAIVELILARKTSVAKEDOWTG ALHPAQNQDLNEANSFTRLLEKNASVNEVDPEGRIPMVHAQCHGENIVRTLIRGVDVG LOGDAWLPLHYAMOGHLPILVKLAQOPGSVAOQLDERTPLHLAQGHYVARII LIDCSVPNICSLOAQTEPHVAETGHTSTARLIHLHGKAELTSGTYALHIAON GHATVYLILEBKRDWMPARPINOTAHLIAAAGHSVVEIVASDILDSDEGSA LHLAAGHSOTVETTLKRGAHNLQSLKTQGSGSSAATILRSKT"</p>
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Best Local Similarity	84.6%; Pred. No.2.6e-262;
Matches 1999; Conservative	0; Mismatched 355; Indels 8; Gaps 3;
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Dn	<p>241 ATCCGCGCTGTGTATGAGCATCGCGCGGCAACCTGTGGGCTGGTCAATGAGTACATGAGGAG 300</p> <p>290 ATTCACTGTGTATGAGCATATGCGCAGAACTGTGGCTGGTCAATGAGTACATGAGGAG 349</p>
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Db	650	GACACCAAACTGATGTATACAGCTTCGCCATTTGTGATCTGGGGTGTGCTTACACAAAG	709
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Db	830	CTCATGCAACGGTGTGGCAGACCCACAGGGTGGCGGCCCACTTTCAGAAATTAATCC	889
Oy	841	TCTGAACACCGAGAGCTGTGTGTAAGAAAGCTGATGACGAAGTGAAGAAACATGCTCATGAT	900
Db	890	TCTGAACACGAAGACTTGTGTGTAAGAGCTGATGAGAGGTGAAGACTGTGCTCATAGAG	949
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Db	950	CGAGCGAGAAAGACTCTCTAGAGTCCAGAGTGAAGGCCAGGCCCGAATCCTCAAGCCTTC	1009
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Db	1130	GATCCAAAGCTTCCATCGTCCAGAGTGGCAGAGAGGCTCTCGGGGGTGTCTCTCAAGTAC	1189
Oy	1135	TCCGCTTCTCTTCCAGAGATCACTGTGCTGTCTTTGAACGAGAACTTCAACAGC	1194
Db	1190	TCAAGCTTTCCTCCAGAGAGATCGTGTCACTGTCTTTTGAACGAGAACTTCAACAGGC	1249
Oy	1195	GATCTGGGTACCAAAAGCTGTCAAGAGAGAGAGCTTGTGATGTCATCTGTCT--CGGA	1253
Db	1250	GACTTGGGCCCCAC--AGAATCTCAAAAGAGAGTGAAGTGCATTCATATCAACGGGA	1308
Oy	1254	CACCAAGCAAACTGATGAAGATCTGTGAGCGCGAGGACGTAAGCTGTGACCTGACAGAGG	1313
Db	1309	CACCAAGCAAGCTGATGAAGATCTTCAAGCCCAAGATGTGAATTTGTTCTTGAACAGAG	1368
Oy	1314	TGCCAGCTGTGCACTTGGCGGTGAGAGCGCGGCAAGAGAGTGGCGCAAGTGGCTCT	1373
Db	1369	TGCCAGCTGTGCACTTGGCGGTGAGAGCGCGGCAAGAGAGTGTGTCAAGTGGCTCT	1428
Oy	1374	GCTCAACAATGCGAACCCCACTTGAAGCACTGTAGGGGCTTCAACCCGTTTGCATATGGC	1433
Db	1429	GCTTAAACAATGCGAACCCCACTTGAACCAACGAAAGGGCTTCTTCAACACTGCATATGGC	1488
Oy	1434	CGTGAAGAGAGGGGTGGGGGTGTGTGAAGCTCTCGGCTGGCAGCGAAGATCAAGTGTAA	1493
Db	1489	TGTGAAGCGAAGAGAGCTGGAATGTGAGAGCTTCTAGCCCGAAGACCAAGTGTCAA	1548
Oy	1494	CGCAGAAGATGAGACCAATGAGCAAGCCCTTCAACTTTTGAAGCCCAAGACGGGGATGATC	1553
Db	1549	TGCCAAGAGATGAAAGACCAATGAGCTGGCCCTTGAAGCCCAAGATGGGGATGAGAGC	1608
Oy	1554	TAGCAACAGGCTGTGTGGAAGAGAACGCTTCGGTCAACGAGGTGTGACTTTGAGGGCCG	1613

Db		1609	CAGCACAAGGCTGTGGTGAAGAAGATGCTTGTCACAAAGAGTGAACATTGAGGGCCG	1668
OY		1614	GAGGCCATACGATGGCCCTGCCAGCACCGGCGAGGAATATGGTGGCATTCCTGCCTGC	1673
Db		1669	AACACCATTCAATGTAACCTGCCAGCATGGAACAGAGAAACAATGTGTGGACCTGCTCCG	1728
OY		1674	CCGAGGCGTGAACGTGAGCCCTGCAAGGGCAAGAAATGCTGTGCTGCACACTGACATAAGCTGC	1733
Db		1729	CCGTGGTGTGGATGTGGGCTTCGACAGGAAAAGAAATGCTGTGGTTGTCTTGACATATGCTGC	1788
OY		1734	CTGGCAGAGGCACACTGCGCATTCGTCAAGCTGCTGGCCAGACGACGCGGGGGTGAATGTGAA	1793
Db		1789	CTGGCAGAGGCACACTTCCATTGTAAAGCTGTAAGCCAAACAGCTGTGGGTGAATGTGAA	1848
OY		1794	CGCCCAACGCTGGAATGGAGAGAACGCCATTGCACTGTGGCCGACAGGGCGGGGCACTACCG	1853
Db		1849	TGCCCAACAACATAACGAGAGAGAACCCCTGCACTGTGGCTGACAGAGGGGGCAATTACCG	1908
OY		1854	CGTGGCCCGCATCTCAACACCTGTGCTCCGACGTCAACGTCGTGACGCTGTGGACACA	1913
Db		1909	TGTGGCTTCGATTTCTCAATGAACCTGTGCTGTGAATGTAACTGCAAGCCTAAGGGACACA	1968
OY		1914	GACACCCCTTGACGCTGGCCGCGGAGACGAGGCGCACAGACACTGCAAGGCTGTCTTGCA	1973
Db		1969	GACACCTCTGTGATTTGCTGAGAGACATGGAACAATAATATCTCCAGGCTAATCTTGCA	2028
OY		1974	TGCGGGCGCTGGCAGAGAGCCGTGACCTCAAGACGCTACACCGCTCTGCACTGTGGCTGC	2033
Db		2029	TCTGTGTGTGGCAAGAGGCTTTGACCTCAAGAGGCTATATCTGCTTGCACTGTGGACGC	2088
OY		2034	CCGCAAGGGACACCTGGCGCATCTGTCAAGCTGTGTGAGAGAGAAAGCCGATGTGCTGGC	2093
Db		2089	CCAAGATGACACTGTGGCTACTGTCAAGCTGCTCATAGAGAGAAAGCTGATGTGATGTGC	2148
OY		2094	CCGGGGAACCCCTGTAACCAAGACGAGCGCTGCACTTGGCTGCGCCGACGAGCATCTGGAGGT	2153
Db		2149	TGCGGGGTCCCCTGAATCAGACAGACACTGGCACTGGCTGTGSCCGTGGACACTCAGAGGT	2208
OY		2154	GGTGAGAGAGTTGGTCAGCCGCCATGTTCATTTGACTCTGTTGCAAGACAGAGGGGCTCAAGGC	2213
Db		2209	GGTAGAAGAGCTGTGCTGAGTGTGAACCTCAATTGAACCTGTCTGATATGACAGGGCTCAAGGC	2266
OY		2214	GCTGCACCTTGGCCGCCACAGGGCCGGGCAACGACACGSGTGAAGCTGCTCAGGCAATGG	2273
Db		2269	ACTGCACCTGTGCTCTCAAGGCAAGCAATTCAACACTGTGGAACACTGCTCAAAATATGG	2322
OY		2274	GGCCCAACTCAACTGTCAGAGGCTCAAGATTTCAGAGGCGAGCCATGAGCCCCCGCACACT	2333
Db		2339	AGCACACATCAACTTGCAGAGTCTCAAGTTCCAAAGAGAGGCCAAGAGCTGTGTGCCACGTT	2388
OY		2334	CTTGCAGGAGAAAGAAAGCTTNG	2355
Db		2389	GCTCCGACGACGAGAAACCTAG	2410
RESULT 12				
BC057871		3558 bp	mRNA	linear
LOCUS				ROD 20-JUL-2004
DEFINITION	Mus musculus receptor-interacting serine-threonine kinase 4, mRNA			
ACCESSION	BC057871			(cDNA clone MGC:67753 IMABR:5294197), complete cde.
VERSION	BC057871.1			GI:37046719
KEYWORDS	MGC.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE				
AUTHORS	Straubberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhate,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,			

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Db 1210 GACTGTGGGCCCCAC-AGACATCCAGAGAAAGAGTGTGAGTGCATGTATTCAGGGGA 1268
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Db 1269 CACCGAGAGCTGTGATGAGATCTGTACAGCTCCAGAGTGTGAGCTGTGTCTGAGACAG 1328
Qy 1314 TCCAGAGCTGTGACCTGTGCGGTGAGGCGCGGCAAGAGAGTGCAGAGTGTGCT 1373
Db 1329 TCCAGAGCTGTGACCTGTGCGGTGAGGCGCGGCAAGAGAGTGTGTCAAGTGTGCT 1388
Qy 1374 GCTCAAGATGCCAACCCCACTTGAAGCAAGCTGTAGGGGCTCAAGCCGTTGCAATGAG 1433
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Qy 1494 CGCAGAGATGAGAGCAAGTGTGACAGCTTCACTTTCAGCCAGAGCGGGATGAGTC 1553
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Qy 1614 GAGCCCATGACAGTGTGCGCGAGAGCGGGAGAGAAATGTGTGTGAGCTGTGCTGCG 1673
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Qy 1674 CCGAGAGCTGTGACAGTGTGCGCGAGAGAGAGTGTGCTGTGCTGCGACTGTGACTGTG 1733
Db 1689 CCGTGTGTGTGAGTGTGCGCGAGAGAGAGAGTGTGCTGTGCTGCGACTGTGACTGTG 1748
Qy 1734 CTGCGAGAGCGACCTGTGCTGTCAAGCTGTGCGCGAGAGAGCGGGGTGTGTGAG 1793
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Qy 1794 CGCGCAGAGCGT 1853
Db 1809 TGCCTCAGAGCTGT 1868

Qy 1854 CTTGCGCGAGCTGTGATGACCTGTGTGCTGAGAGTGTCAAGTGTGTGAGCGCTGTGACA 1913
Db 1869 TGTGCTGTGACCTTCTCATTTAGACCTGTGTCTGTGATGTAACTGTGTGAGCGTCAAGGACA 1928
Qy 1914 GACACCCCTGTGACGTGTGCGCGAGAGAGCGGGGACACAGAGCTGTGCGAGGCTGTGCA 1973
Db 1929 GACACCTGTGACTGT 1988
Qy 1974 TCGGGGCGTGTGAGAGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAG 2033
Db 1989 TCGTGTGTGTGTGAGAGAGGCTTGTGACTGTGAGAGGCTGTATCTGTCTTGTGAGAGG 2048
Qy 2034 CCGAGAGAGACACCTGTGACCTGTGACAGCTGTGTGAGAGAGAGCGGCTGTGAGAG 2093
Db 2049 CAGAGATGAGACCTGT 2108
Qy 2094 CCGGGAGACCCCTGTGACAGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAG 2153
Db 2109 TCGGGGTCTCTGTATGATGAGACAGCACTGTGAGCTGTGAGAGCACTGTGAGAG 2168
Qy 2154 GGTGAGAGAGTGTGTGAGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2213
Db 2169 GTTGAAGAGCTGT 2228
Qy 2214 GCTGTGACCTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2273
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Qy 2274 GCGCCATCATCACTGTGAGAGCTGTGAGAGTGTGAGAGCGGCGGCGGCGGCGGCGG 2333
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Qy 2334 CTTGCGCGGAGAGAGAGAGCTGTG 2355
Db 2349 GCTCCGAGCGAGAGAGAGAGCTGTG 2370

RESULT 13
BD251844 2370 bp DNA linear PART 17-JUL-2003
LOCUS BD251844
DEFINITION Death associated kinase containing ankyrin repeats (DAKAR).
ACCESSION BD251844.1 GI:33061614
VERSION 1
KEYWORDS JP 2002526038-A/1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2370)
AUTHORS Bird,T.A. and Virca,D.G.
TITLE Death associated kinase containing ankyrin repeats (DAKAR)
JOURNAL Patent: JP 2002526038-A 1 20-AUG-2002;
IMMUNEX CORP
COMMENT OS Mus musculus (mouse)
PN JP 2002526038-A/1
PD 20-AUG-2002
PF 04-AUG-1998 JP 2000563800
PR 04-AUG-1998 US 60/095269, 11-SEP-1998 US 60/099973 PR
09-FEB-1999 US 60/119353
PI TIMOTHY A BIRD, DUKE G VIRCA
PC C12N15/09,A61K45/00,A61P29/00,A61P37/02,A61P43/00,A61P43/00,
PC C07K16/40,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12Q1/48,G06F17/
PC 30//
PC G01N27/447,G01N27/447,C12N15/00,C12N5/00,G01N27/26,G01N27/26
CC Death associated kinase containing ankyrin repeats (DAKAR) FH
Key Location/Qualifiers
FT source 1..2370
FT location/Qualifiers
1..2370
/organism="Mus musculus (mouse)".

ORIGIN

/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 74.1%; Score 1745.4; DB 6; Length 2370;

Best Local Similarity 84.6%; Pred. No. 7.2e-262;

Matches 1997; Conservative 0; Mismatches 356; Indels 8; Gaps 3;

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DB 11 TGAAGGCGAGGCGCGGCGCGTGGGCTCTGGGGCTGCTGCGCACTTCACGCGGGCG 70
QY 62 AGTTACCGGCTGGGAGAGAGGAGGCTCGGGCGGCTTCGGGCAAGGTGTAACAAGTGCSC 121
DB 71 AATTGCGAGGCTGGAGAGAGGAGGCTCGGGCGGCTTCGGGCAAGGTGTAACAAGTGCSC 130
QY 122 ATGTCCACTGGAGAGACTGTGGCTGGCCATCAAGTGTCTGCCAGGCTTCGACGTCGACGA 181
DB 131 ATGTGCACTGGAGAGAGTGGCTCGGATCAAGTGTCTGCCAGGCTTCGACGTCGACGA 190
QY 182 GGAAGCGCATGGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGGCCCAAGTTTGGCTACA 241
DB 191 GGAAGCGATGAGCTCTGGAGAGAGCTTAAGAGATGAGATGGCCCAAGTTTGGCTACA 250
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DB 251 TTCTACCTGTGTACGCGCATATGCCAGAGAACTGTGCGGCTGGTCAATGAGTACATGAGAGA 310
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QY 362 TCATCCAGAGAGAGCGGCGGTGGGAGTGAATCTTCGTCATGTCATGAGCCCGGCACTCCG 421
DB 371 TCGTCACAGAGACACCGCGTGGGATGAATCTTCGTCATGTCATGAGCCCGGCACTCCG 430
QY 422 ACCTGACCTCAAGCGCGGAAATCTCTGTCGATGAGCCCACTACCACTCAAGATTTCTG 481
DB 431 ACCTGACCTCAAGCGCGGAAATCTCTGTCGATGAGCCCACTACCACTCAAGATTTCTG 490
QY 482 ATTTTGTCTGGCAAGTGCAGCGGCTGTCCACTCGCATGACCTCAAGCATGATGAGCC 541
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QY 542 TGTTTGGGCAATTCGCTCACTCCCTCCAGAGCGGATCAAGGAGAGCGGCTCTG 601
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QY 1435 GTGAGAGAGAGGAGTGGCGGAGTGTGTGAGAGCTCTGTGTCAGAGAAATCAAGTGTCAAC 1494
DB 1450 GTGAGAGGAGAGAGAGTGTGAGAGTGTGTGAGAGTGTGTGAGAGTGTGTGAGAGTGT 1509
QY 1495 GCCAAGATGAGAGCAAGTGAACAGCTTCCATTTGACGCCCAAGACGAGGATGAGCT 1554
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QY 1555 AGCAACAGGCTGTGTGAGAGAGAGAGCTTGAAGGAGCTTGAAGGAGCGG 1614
DB 1570 AGCAACAGGCTGTGTGAGAGAGAGAGTCTTGTGATGAGAGGAGCTTGAAGGAGCGG 1629
QY 1615 AGCGCCATGACAGTGTGCTGTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 1674
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DB 1690 CGTGTGTGATGTGTGAG 1749
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Db 2350 CTCCAGCGCAGCAAGCACTTACG 2370

RESULT 14
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LOCUS AR258256 Sequence 1 from patent US 6489130.
DEFINITION AR258256
ACCESSION AR258256
VERSION AR258256.1 GI:27308494
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 2370)
AUTHORS Bird,T.A. and Virca,G.D.
TITLE Death associated kinase containing ankyrin repeats (DAKAR)
JOURNAL Patent: US 6489130-A 1 03-DEC-2002;
FEATURES
source 1..2370
Location/Qualifiers
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ORIGIN
Query Match 74.1%; Score 1745.4; DB 6; Length 2370;
Best Local Similarity 84.6%; Pred. No. 7.2e-262;
Matches 1997; Conservative 0; Mismatches 356; Indels 8; Gaps 3;
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Db 431 ACCTAGACCTGAAACCGAGCAATCTGCTGATGTCGCACTACAGATTTCTG 490
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Db 731 GCCCGAGCTGCGCGCTGTGCAAGAGCGCGCGCGCGCTGTGCAAGCCACTGATAGGC 790
Qy 782 TCAATGACGGTGTGCGAGAGGAGATCCGCAAGTTAGGCCCACTTCCAAAGAAATTAAT 841
Db 791 TCAATGACGGTGTGCGAGAGGAGATCCGCAAGTTAGGCCCACTTCCAAAGAAATTAAT 850
Qy 842 CTGAACCGAGAGACTGTGTGTAAGAAAGCTGATGACGAATGAGAAAGAACTGCTCATGATC 901
Db 851 CTGAACCGAGAGACTGTGTGTAAGAAAGCTGATGAGAGAGTGAAGAACTGCTCATGATGAGC 910
Qy 902 TGAAGTGAAGAAAGCCCGGAGAGCCGAGAGCGAGTGTGCTG-----GAGGCTCA 955
Db 911 CAGGCGAAGAAAGCTCTTGAAGTTCGAAGTGAAGGCGGAGGCTCTCAAGCTCTCA 970
Qy 956 AGCGGCGCTTGGCGCCCACTTTCATTAACGATCAAGCTCTCGAGCTTCTGCAAGC 1015
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Qy 1016 TGGACTGTGAGATTTCCAGAGCTGTGCAAGGAGCCCGAGAGACTCAAGCTCTCTG 1075
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Qy 1076 AGTCCAGCTGCATGTCGCGCAGTGGAAAGAGCTCTCGGGGCTGTCTGCTGAGACT 1135
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DEFINITION	Compositions isolated from skin cells and methods for their use.		
ACCESSION	BD209707		
VERSION	BD209707.1	GI:33019477	
KEYWORDS	JP 2002512798-A/179.		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

REFERENCE	1 (bases 1 to 3516)
AUTHORS	Strachan, J., Sleeman, M., Watson, J.D., Ornust, R., Kumble, A. and Muijsen, J.G.
TITLE	Compositions isolated from skin cells and methods for their use
JOURNAL	Patent: JP 2002512798-A 179 08-MAY-2002; Patent: JP 2002512798-A 179 08-MAY-2002; GENESIS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT	OS Mus sp. (mouse) PN JP 2002512798-A/179 PF 08-MAY-2002 PR 29-APR-1999 JP 2000546009 PR 29-APR-1998 US 09/069726, 09-NOV-1998 US 09/188930 PI LOENA STRACHAN, MATTHEW SLEEMAN, JAMES DOUGLAS WATSON, RENE PI ORNUST, PI ANAND KUMBLE, JAMES GREG MUIRSON PC 12N15/09, A61K38/00, A61P9/00, A61P17/00, A61P29/00, A61P31/18, PC A61P35/00,
FEATURES	PC COTK16/47, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12N15/00, PC A61K37/02, C12N5/00 CC Compositions isolated from skin cells and methods for their use. CC use. FH Key Location/Qualifiers FT source 1..3516 FT Location/Qualifiers FT 1..3516 FT /organism="Mus sp. (mouse)". FT /molecule="genomic DNA" FT /db_xref="taxon:10095"
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 02:53:04 ; Search time 4549.9 Seconds
(without alignments)
69.774 Million cell updates/sec

Title: US-10-658-904-2

Perfect score: 4078
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARIES

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7	3976	97.5	784	16	US-10-648-593-153
8	3628	89.0	786	14	US-10-164-080-2
9	3628	89.0	786	14	US-10-299-327-2
10	3628	89.0	786	14	US-10-128-174-13
11	3624	88.9	787	10	US-09-866-050A-334

12	3620	88.8	786	14	US-10-128-174-31	Sequence 31, Appl
13	3619	88.7	786	14	US-10-128-174-32	Sequence 32, Appl
14	3619	88.7	786	14	US-10-128-174-33	Sequence 33, Appl
15	2691	66.0	590	10	US-09-866-050A-409	Sequence 409, App
16	2269	55.6	536	10	US-09-866-050A-185	Sequence 185, App
17	1967	48.2	439	14	US-10-128-174-28	Sequence 28, Appl
18	1804	44.2	335	16	US-10-664-421-140	Sequence 140, App
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20	1661	40.7	347	14	US-10-128-174-30	Sequence 30, Appl
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23	1211.5	29.7	765	14	US-10-128-174-43	Sequence 43, Appl
24	1208.5	29.6	765	14	US-10-128-174-3	Sequence 3, Appl
25	1208.5	29.6	765	14	US-10-128-174-37	Sequence 44, Appl
26	1207.5	29.6	765	14	US-10-128-174-34	Sequence 37, Appl
27	1207.5	29.6	765	14	US-10-128-174-39	Sequence 39, Appl
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34	1198.5	29.4	765	14	US-10-128-174-41	Sequence 41, Appl
35	1196.5	29.3	352	14	US-10-146-473-59	Sequence 59, Appl
36	838	20.5	720	15	US-10-433-794-20	Sequence 20, Appl
37	663	16.3	132	15	US-10-276-774-1509	Sequence 1509, Ap
38	541.5	13.3	540	9	US-09-748-537-1	Sequence 1, Appl
39	541.5	13.3	540	9	US-09-728-721-2	Sequence 2, Appl
40	541.5	13.3	540	9	US-09-771-161A-184	Sequence 184, App
41	541.5	13.3	540	9	US-09-862-027-28	Sequence 28, Appl
42	541.5	13.3	540	10	US-09-981-397A-14	Sequence 14, Appl
43	541.5	13.3	540	13	US-10-133-780-1	Sequence 1, Appl
44	541.5	13.3	540	13	US-10-105-931-2	Sequence 2, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/10658904
; Publication No. US20040048305A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 14171 Protein Kinase, A No. US20040048305A1 Human
; FILE REFERENCE: MP100-010P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/658,904
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 09/781,882
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/182,096
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 784
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-658-904-2

Query Match 100.0%; Score 4078; DB 15; Length 784;
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Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPEREPSTDLGTTTRPEEACGCHRVADTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPEREPSTDLGTTTRPEEACGCHRVADTS 420
Qy 421 KLMLKLOPOVDLALDSGASLHLAVEAGOEBCAKWLLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMLKLOPOVDLALDSGASLHLAVEAGOEBCAKWLLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGVVELLARKISVNAKDEDDWTALHPAQNDESSSTRILLEKNASVNEVDPEGRTP 540
Db 481 RRVGVVELLARKISVNAKDEDDWTALHPAQNDESSSTRILLEKNASVNEVDPEGRTP 540
Qy 541 MHVACOHGOENIVRILLRGVDSLOQKDAMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
Db 541 MHVACOHGOENIVRILLRGVDSLOQKDAMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
Qy 601 TLDEGTPLHLAAQRGHYVARILLIDCSDVNCSLLAQTPLHVALETGHTSTARLLHARG 660
Db 601 TLDEGTPLHLAAQRGHYVARILLIDCSDVNCSLLAQTPLHVALETGHTSTARLLHARG 660
Qy 661 AGKEAVTSDDGTALHAAANGHLAVTKLVEKADVLARGPLNOPLHAAAHGSEVE 720
Db 661 AGKEAVTSDDGTALHAAANGHLAVTKLVEKADVLARGPLNOPLHAAAHGSEVE 720
Qy 721 ELVSAVDLIDFDEOGLSALHLAAQRHAQVETTLRHGAHINLOSLKEQSGHGPAATLLR 780
Db 721 ELVSAVDLIDFDEOGLSALHLAAQRHAQVETTLRHGAHINLOSLKEQSGHGPAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784

RESULT 2
US-10-354-358-38
; Sequence 38, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10397, 1584, 9535, 14124, 4463,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MP102-020P1RMONMIM

; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-38

Query Match 97.6%; Score 3980; DB 14; Length 784;
Best Local Similarity 98.2%; Pred. No. 2.7e-273;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MEGDGTPTMALALARTPDAGEFTGMEKVGSGFGQYKVRHVHKTWLAIKCSPSLHYDD 60
Db 1 MEGDGTPTMALALARTPDAGEFTGMEKVGSGFGQYKVRHVHKTWLAIKCSPSLHYDD 60
Qy 61 RERMELEBEAKMEMAKFRYYILPVYGIORBPVGLVMEYMETGSEKLLASPLPMDLFR 120
Db 61 RERMELEBEAKMEMAKFRYYILPVYGIORBPVGLVMEYMETGSEKLLASPLPMDLFR 120
Qy 121 IIHETAVGMNPLHCAAPPLHLDLKPNILLDAAHYVKISDFGLACKNGLSHSHDLSMDG 180
Db 121 IIHETAVGMNPLHCAAPPLHLDLKPNILLDAAHYVKISDFGLACKNGLSHSHDLSMDG 180
Qy 181 LFGTIAYLPPEIRIREKSLFDTKHDVYSPFAIYWGVLTOKKPFADEKNILHIMVKVYKGH 240
Db 181 LFGTIAYLPPEIRIREKSLFDTKHDVYSPFAIYWGVLTOKKPFADEKNILHIMVKVYKGH 240
Qy 241 RPELPVPCRARPRACSHLIRLMORCMQGDPRVRPTFOBITSETBDLCEKPDDEVKETAHD 300
Db 241 RPELPVPCRARPRACSHLIRLMORCMQGDPRVRPTFOBITSETBDLCEKPDDEVKETAHD 300
Qy 301 LDVSPPEPSEVYPARLKRAAPTFDNDYSLSELSQLDSGVSAQVAGPELSSRSSES 360
Db 301 LDVSPPEPSEVYPARLKRAAPTFDNDYSLSELSQLDSGVSAQVAGPELSSRSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPEREPSTDLGTTTRPEEACGCHRVADTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPEREPSTDLGTTTRPEEACGCHRVADTS 420
Qy 421 KLMLKLOPOVDLALDSGASLHLAVEAGOEBCAKWLLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMLKLOPOVDLALDSGASLHLAVEAGOEBCAKWLLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGVVELLARKISVNAKDEDDWTALHPAQNDESSSTRILLEKNASVNEVDPEGRTP 540
Db 481 RRVGVVELLARKISVNAKDEDDWTALHPAQNDESSSTRILLEKNASVNEVDPEGRTP 540
Qy 541 MHVACOHGOENIVRILLRGVDSLOQKDAMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
Db 541 MHVACOHGOENIVRILLRGVDSLOQKDAMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600

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Db      541 MNAVCOHQENIVRIILRGVDVSLQKDAWLPHTYAMQGHLPVYKLAQPGVSVNAQ 600
Qy      601 TLDRGTPHLAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Db      601 TLDRGTPHLAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Qy      661 AKGKAVTSQGYTALHAAARNGHATYKLVVEEKADYLAARGPLNQTALHAAAHGSEVVE 720
Db      661 AKGKAVTSQGYTALHAAARNGHATYKLVVEEKADYLAARGPLNQTALHAAAHGSEVVE 720
Qy      721 ELVSADVIDLFDQGLSALHAAQGRHAQTVETLLRHGAHINLOSLEKFGGHPAATLLR 780
Db      721 ELVSADVIDLFDQGLSALHAAQGRHAQTVETLLRHGAHINLOSLEKFGGHPAATLLR 780
Qy      781 RSKT 784
Db      781 RSKT 784

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RESULT 3
US-10-128-174-12
; Sequence 12, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Method and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; PENDING FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-174-12

```

```

Query Match      97.6%; Score 3980; DB 14; Length 784;
Best Local Similarity 98.2%; Pred. No. 2.7e-273;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy      1 MEGDGTGFWALALRTFDAGFTGMEKVGSGGFGQYKVRVHMKWTWLAIKCSPLHYDD 60
Db      1 MEGDGTGFWALALRTFDAGFTGMEKVGSGGFGQYKVRVHMKWTWLAIKCSPLHYDD 60
Qy      61 RERMELEBAKMKEMAKFRYILPVYGICREPVGLVMEVMEGSLKELASBPPLPMDLRF 120
Db      61 RERMELEBAKMKEMAKFRYILPVYGICREPVGLVMEVMEGSLKELASBPPLPMDLRF 120
Qy      121 IIHETAVGNMFLHCAWAPPLHLDLKPANILLDAHYVKISDFGLAKCNGLSHSHDLSDMG 180
Db      121 IIHETAVGNMFLHCAWAPPLHLDLKPANILLDAHYVKISDFGLAKCNGLSHSHDLSDMG 180
Qy      181 LFGTTAYLPPERIRKESRLFTDKHDVYSFAIVMGVLTQKKPAPADKNIILHIMVKVVG 240
Db      181 LFGTTAYLPPERIRKESRLFTDKHDVYSFAIVMGVLTQKKPAPADKNIILHIMVKVVG 240
Qy      241 RPELPVPCARAPRACSHILRLMORCMQGDPRVPRPTQETSETEDCEKPDDEVKETAHD 300
Db      241 RPELPVPCARAPRACSHILRLMORCMQGDPRVPRPTQETSETEDCEKPDDEVKETAHD 300
Qy      301 LDVKSPPRSEVVPARLKRASAPTFDNDYSLSELLSQLDSGVSAQVNEGPEELSRSSSS 360
Db      301 LDVKSPPRSEVVPARLKRASAPTFDNDYSLSELLSQLDSGVSAQVNEGPEELSRSSSS 360
Qy      361 KLPSSSSGKRLSGVSSVDNASFSGSLSLSFEREPESTDLGTRRREBEACGHRARD 420
Db      361 KLPSSSSGKRLSGVSSVDNASFSGSLSLSFEREPESTDLGTRRREBEACGHRARD 420
Qy      421 KLMKTIQPODVDAALDSGASILHIAVEAGQECACAKMLLNANPNLSNRGSGTPLMAVE 480
Db      421 KLMKTIQPODVDAALDSGASILHIAVEAGQECACAKMLLNANPNLSNRGSGTPLMAVE 480

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Qy      481 RRVGCVVELLARKISYNANDEDDWTALHRAQNGDESSSTRLLLEKNASVNEVDFEGRT 540
Db      481 RRVGCVVELLARKISYNANDEDDWTALHRAQNGDESSSTRLLLEKNASVNEVDFEGRT 540
Qy      541 MNAVCOHQENIVRIILRGVDVSLQKDAWLPHTYAMQGHLPVYKLAQPGVSVNAQ 600
Db      541 MNAVCOHQENIVRIILRGVDVSLQKDAWLPHTYAMQGHLPVYKLAQPGVSVNAQ 600
Qy      601 TLDRGTPHLAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Db      601 TLDRGTPHLAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Qy      661 AKGKAVTSQGYTALHAAARNGHATYKLVVEEKADYLAARGPLNQTALHAAAHGSEVVE 720
Db      661 AKGKAVTSQGYTALHAAARNGHATYKLVVEEKADYLAARGPLNQTALHAAAHGSEVVE 720
Qy      721 ELVSADVIDLFDQGLSALHAAQGRHAQTVETLLRHGAHINLOSLEKFGGHPAATLLR 780
Db      721 ELVSADVIDLFDQGLSALHAAQGRHAQTVETLLRHGAHINLOSLEKFGGHPAATLLR 780
Qy      781 RSKT 784
Db      781 RSKT 784

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RESULT 4
US-10-164-080-7
; Sequence 7, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: Bird, Timothy, A.
; APPLICANT: Holland, Pamela, M.
; APPLICANT: Peschon, Jacques, J.
; APPLICANT: Virca, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND ME
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; PENDING FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-080-7

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Query Match      97.5%; Score 3977; DB 14; Length 784;
Best Local Similarity 98.1%; Pred. No. 4.4e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy      1 MEGDGTGFWALALRTFDAGFTGMEKVGSGGFGQYKVRVHMKWTWLAIKCSPLHYDD 60
Db      1 MEGDGTGFWALALRTFDAGFTGMEKVGSGGFGQYKVRVHMKWTWLAIKCSPLHYDD 60
Qy      61 RERMELEBAKMKEMAKFRYILPVYGICREPVGLVMEVMEGSLKELASBPPLPMDLRF 120
Db      61 RERMELEBAKMKEMAKFRYILPVYGICREPVGLVMEVMEGSLKELASBPPLPMDLRF 120
Qy      121 IIHETAVGNMFLHCAWAPPLHLDLKPANILLDAHYVKISDFGLAKCNGLSHSHDLSDMG 180
Db      121 IIHETAVGNMFLHCAWAPPLHLDLKPANILLDAHYVKISDFGLAKCNGLSHSHDLSDMG 180
Qy      181 LFGTTAYLPPERIRKESRLFTDKHDVYSFAIVMGVLTQKKPAPADKNIILHIMVKVVG 240
Db      181 LFGTTAYLPPERIRKESRLFTDKHDVYSFAIVMGVLTQKKPAPADKNIILHIMVKVVG 240
Qy      241 RPELPVPCARAPRACSHILRLMORCMQGDPRVPRPTQETSETEDCEKPDDEVKETAHD 300

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Db 241 RPELPVCRARPRACSHLIRLMQRCWQCDPRVRPTFOGTTSETBDLCEKPDDEVKETAHD 300
Qy 301 LDVKSPPRPSRBPVPAULKRAASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Db 301 LDVKSPPRPSRBPVPAULKRAASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPRBPSTSDLGTTTRPBEACGCHRVRTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPRBPSTSDLGTTTRPBEACGCHRVRTS 420
Qy 421 KLMLKLOPOVDYLDLDSGASLHLAVEAGQECAMLLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMLKLOPOVDYLDLDSGASLHLAVEAGQECAMLLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESSTRLLEKNASVNEVDFEGRT 540
Db 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESSTRLLEKNASVNEVDFEGRT 540
Qy 541 MHVACQHQENIVRILRQGVDSLQGDAMLPLHYAMQGLPIVKLAKOPGVVNAQ 600
Db 541 MHVACQHQENIVRILRQGVDSLQGDAMLPLHYAMQGLPIVKLAKOPGVVNAQ 600
Qy 601 TLDSRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Db 601 TLDSRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Qy 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEKADVLARGPLNQTAHLAAAHGSEVVE 720
Db 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEKADVLARGPLNQTAHLAAAHGSEVVE 720
Qy 721 ELVSADVIDLFDQGLSALHLAQRHAQVETTLRHGAHINLSLKFQGGHGAATLLR 780
Db 721 ELVSADVIDLFDQGLSALHLAQRHAQVETTLRHGAHINLSLKFQGGHGAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784

RESULT 5
US-10-258-951-70
; Sequence 70, Application US/10258951
; Publication No. US20040033504A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabinick, Karen
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-258-951-70
Query Match 97.5%; Score 3977; DB 15; Length 784;
Beet Local Similarity 96.1%; Pred. No. 4,4e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MEGDGTTPMALALTRTFDAGEFTGMEKVGSGFGQVYKVRHVWKTALAKCSPLHVD 60
Db 1 MEGDGTTPMALALTRTFDAGEFTGMEKVGSGFGQVYKVRHVWKTALAKCSPLHVD 60
Qy 61 RERMELLEBAKQEMAKFRYILPYGICREBPVGLVMEYMGTSLEKLLASEPLPWDRFR 120
Db 61 RERMELLEBAKQEMAKFRYILPYGICREBPVGLVMEYMGTSLEKLLASEPLPWDRFR 120
Qy 121 ITHETAQGNPILHOMAPPLHLDLKPNITLLDAHYHKISDFGLACKNGLSHSHDLSMDG 180
Db 121 ITHETAQGNPILHOMAPPLHLDLKPNITLLDAHYHKISDFGLACKNGLSHSHDLSMDG 180
Qy 181 LFGTIAVLPERIREKSLPDTKADVSAFAIVIWGLTOKKPPADEKNTLIHWKVYKGH 240
Db 181 LFGTIAVLPERIREKSLPDTKADVSAFAIVIWGLTOKKPPADEKNTLIHWKVYKGH 240
Qy 241 RPELPVCRARPRACSHLIRLMQRCWQCDPRVRPTFOGTTSETBDLCEKPDDEVKETAHD 300
Db 241 RPELPVCRARPRACSHLIRLMQRCWQCDPRVRPTFOGTTSETBDLCEKPDDEVKETAHD 300
Qy 301 LDVKSPPRPSRBPVPAULKRAASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Db 301 LDVKSPPRPSRBPVPAULKRAASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPRBPSTSDLGTTTRPBEACGCHRVRTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPRBPSTSDLGTTTRPBEACGCHRVRTS 420
Qy 421 KLMLKLOPOVDYLDLDSGASLHLAVEAGQECAMLLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMLKLOPOVDYLDLDSGASLHLAVEAGQECAMLLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESSTRLLEKNASVNEVDFEGRT 540
Db 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESSTRLLEKNASVNEVDFEGRT 540
Qy 541 MHVACQHQENIVRILRQGVDSLQGDAMLPLHYAMQGLPIVKLAKOPGVVNAQ 600
Db 541 MHVACQHQENIVRILRQGVDSLQGDAMLPLHYAMQGLPIVKLAKOPGVVNAQ 600
Qy 601 TLDSRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Db 601 TLDSRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Qy 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEKADVLARGPLNQTAHLAAAHGSEVVE 720
Db 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEKADVLARGPLNQTAHLAAAHGSEVVE 720
Qy 721 ELVSADVIDLFDQGLSALHLAQRHAQVETTLRHGAHINLSLKFQGGHGAATLLR 780
Db 721 ELVSADVIDLFDQGLSALHLAQRHAQVETTLRHGAHINLSLKFQGGHGAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784

RESULT 6
US-10-923-035-56
; Sequence 56, Application US/10923035
; Publication No. US20050130189A1
; GENERAL INFORMATION:
; APPLICANT: Pasricha, Pankaj
; APPLICANT: Shenoy, Mohan
; APPLICANT: Winston, John
; TITLE OF INVENTION: Compositions and Methods for Treating and Diagnosing
; Iritable Bowel Syndrome
```

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; FILE REFERENCE: 9511-136-27
; CURRENT APPLICATION NUMBER: US/10/923,035
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/496,716
; PRIOR FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-035-56

Query Match          97.5%; Score 3977; DB 18; Length 784;
Best Local Similarity 98.1%; Pred. No. 4,4e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEGDGTFWALALLRTFDAGEFTGMEKVGSGFGQVYKVRHVMKWTMLAIKCSPLHYDD 60
DB 1 MEGDGTFWALALLRTFDAGEFTGMEKVGSGFGQVYKVRHVMKWTMLAIKCSPLHYDD 60
QY 61 RRMELLEBAKMKEMAKRYIILPYVGI CREPVGLVMEYMETGSLKLLASBPLPMDLFR 120
DB 61 RRMELLEBAKMKEMAKRYIILPYVGI CREPVGLVMEYMETGSLKLLASBPLPMDLFR 120
QY 121 IIHETAVGNMFLHCAAPPLHLDLKRPANILLDAHNVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 IIHETAVGNMFLHCAAPPLHLDLKRPANILLDAHNVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAIYLPERRIREKSLFPTKHDVYSFAIVIGVLTQKKPFADEKNTLIIMVYVVG 240
DB 181 LFGTIAIYLPERRIREKSLFPTKHDVYSFAIVIGVLTQKKPFADEKNTLIIMVYVVG 240
QY 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSETEDLCEKPDDEVKETAHD 300
DB 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSETEDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPRPSRSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSAVGEPELSRSSSES 360
DB 301 LDVKSPPRPSRSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSAVGEPELSRSSSES 360
QY 361 KLPSSSGSKRLSGVSSVDASFSRSLSLFPERBSTDLGTTDVQKKLVDAIVSGDTS 420
DB 361 KLPSSSGSKRLSGVSSVDASFSRSLSLFPERBSTDLGTTDVQKKLVDAIVSGDTS 420
QY 421 KLMKTILOPDVDLALDSGASLLHLAVEAGOEBCAKMLLNANPNLSNRGSTPLHMAVE 480
DB 421 KLMKTILOPDVDLALDSGASLLHLAVEAGOEBCAKMLLNANPNLSNRGSTPLHMAVE 480
QY 481 RRVGVEILLARKISVNAKDEDOWTALHFAAQNDESSSTRLLLEKNASVNEVDPEGTRP 540
DB 481 RRVGVEILLARKISVNAKDEDOWTALHFAAQNDESSSTRLLLEKNASVNEVDPEGTRP 540
QY 541 MHVACOHGQBNIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
DB 541 MHVACOHGQBNIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
QY 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNCSLLAQTPLVAAETGHTSTARLLHRG 660
DB 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNCSLLAQTPLVAAETGHTSTARLLHRG 660
QY 661 AGKEAVTSOGYTLAHLAARNGHLATVKLLVEBKADVLAGPLNQTLALHAAHGSEVVE 720
DB 661 AGKEAVTSOGYTLAHLAARNGHLATVKLLVEBKADVLAGPLNQTLALHAAHGSEVVE 720
QY 721 ELVSAVYIDLFDGQGLSALHLAAQGHAGQVETLHGHGHNINQSLKFGGCHPATTLR 780
DB 721 ELVSAVYIDLFDGQGLSALHLAAQGHAGQVETLHGHGHNINQSLKFGGCHPATTLR 780
QY 781 RSKT 784
DB 781 RSKT 784

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RESULT 7
US-10-648-593-153
; Sequence 153; Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-153

Query Match          97.5%; Score 3976; DB 16; Length 784;
Best Local Similarity 98.1%; Pred. No. 5.2e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEGDGTFWALALLRTFDAGEFTGMEKVGSGFGQVYKVRHVMKWTMLAIKCSPLHYDD 60
DB 1 MEGDGTFWALALLRTFDAGEFTGMEKVGSGFGQVYKVRHVMKWTMLAIKCSPLHYDD 60
QY 61 RRMELLEBAKMKEMAKRYIILPYVGI CREPVGLVMEYMETGSLKLLASBPLPMDLFR 120
DB 61 RRMELLEBAKMKEMAKRYIILPYVGI CREPVGLVMEYMETGSLKLLASBPLPMDLFR 120
QY 121 IIHETAVGNMFLHCAAPPLHLDLKRPANILLDAHNVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 IIHETAVGNMFLHCAAPPLHLDLKRPANILLDAHNVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAIYLPERRIREKSLFPTKHDVYSFAIVIGVLTQKKPFADEKNTLIIMVYVVG 240
DB 181 LFGTIAIYLPERRIREKSLFPTKHDVYSFAIVIGVLTQKKPFADEKNTLIIMVYVVG 240
QY 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSETEDLCEKPDDEVKETAHD 300
DB 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSETEDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPRPSRSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSAVGEPELSRSSSES 360
DB 301 LDVKSPPRPSRSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSAVGEPELSRSSSES 360
QY 361 KLPSSSGSKRLSGVSSVDASFSRSLSLFPERBSTDLGTTDVQKKLVDAIVSGDTS 420
DB 361 KLPSSSGSKRLSGVSSVDASFSRSLSLFPERBSTDLGTTDVQKKLVDAIVSGDTS 420
QY 421 KLMKTILOPDVDLALDSGASLLHLAVEAGOEBCAKMLLNANPNLSNRGSTPLHMAVE 480
DB 421 KLMKTILOPDVDLALDSGASLLHLAVEAGOEBCAKMLLNANPNLSNRGSTPLHMAVE 480
QY 481 RRVGVEILLARKISVNAKDEDOWTALHFAAQNDESSSTRLLLEKNASVNEVDPEGTRP 540
DB 481 RRVGVEILLARKISVNAKDEDOWTALHFAAQNDESSSTRLLLEKNASVNEVDPEGTRP 540
QY 541 MHVACOHGQBNIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
DB 541 MHVACOHGQBNIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
QY 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNCSLLAQTPLVAAETGHTSTARLLHRG 660
DB 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNCSLLAQTPLVAAETGHTSTARLLHRG 660
QY 661 AGKEAVTSOGYTLAHLAARNGHLATVKLLVEBKADVLAGPLNQTLALHAAHGSEVVE 720
DB 661 AGKEAVTSOGYTLAHLAARNGHLATVKLLVEBKADVLAGPLNQTLALHAAHGSEVVE 720

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DB 661 AGKAVTSDGYTALHAAANGHLATVKLLVEBKADVLRGRLNQTALHAAAGHSEVVE 720
 QY 721 ELVSVADVIDLDEQGLSALHAAQGRHAQTYETLLRHGAHINLQSLKQGGHGPATILR 780
 DB 721 ELVSVADVIDLDEQGLSALHAAQGRHAQTYETLLRHGAHINLQSLKQGGHGPATILR 780
 QY 781 RSKT 784
 DB 781 RSKT 784

RESULT 8 US-10-164-080-2

; Sequence 2, Application US/10164080
 ; Publication No. US20030087411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BIRD, Timothy, A.
 ; APPLICANT: HOLLAND, Pamela, M.
 ; APPLICANT: PESCHON, Jacques, J.
 ; APPLICANT: VIRCA, George, D.
 ; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND ME
 ; TITLE OF INVENTION: USE
 ; FILE REFERENCE: 3280-B
 ; CURRENT APPLICATION NUMBER: US/10/164,080
 ; PRIOR FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: 60/295,959
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: 60/334,362
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 786
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-10-164-080-2

Query Match 89.0%; Score 3628; DB 14; Length 786;
 Best Local Similarity 88.9%; Pred. No. 2.5e-248;

Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

QY 1 MEGDGTWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVWKTWLAIKCPSLHAYDD 60
 DB 1 MEGDGRGHWALGLRTFDAGEFAGMEKVGSGGFGQVYKVRHVWKTWLAIKCPSLHAYDD 60
 QY 61 RRRMELBEAKKEMAKFRYYILPVYGIQREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
 DB 61 RRRMELBEAKKEMAKFRYYILPVYGIQREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
 QY 121 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHVHKISDFGLAKCNGLSHSDLSMDG 180
 DB 121 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHVHKISDFGLAKCNGLSHSDLSMDG 180
 QY 181 LFGTIALVLPERRIREKSRLLFTDKHDVYSPAIVWGVLTQKKPFADEKNILLHIMKVYKG 240
 DB 181 LFGTIALVLPERRIREKSRLLFTDKHDVYSPAIVWGVLTQKKPFADEKNILLHIMKVYKG 240
 QY 241 RPELPVPCRAAPRAASHLIRLMQRCMGDPVRPFTFOETSTEDLCEKPDDEVKETAHD 300
 DB 241 RPELPVPCRAAPRAASHLIRLMQRCMGDPVRPFTFOETSTEDLCEKPDDEVKETAHD 300
 QY 301 LDVKSPPPEPSEVVP--ARLKRAAPTFDNDYSLSELSQLDSGVQAVGPEELSRSS 358
 DB 301 LDVKSPPPEPSEVVP--ARLKRAAPTFDNDYSLSELSQLDSGVQAVGPEELSRSS 358
 QY 361 ECKLSSSSSGKRLSGVSVDSAFSSRGSLSLFEREASTGDLGPTDIOQKKLVDAIISGD 420
 DB 361 ECKLSSSSSGKRLSGVSVDSAFSSRGSLSLFEREASTGDLGPTDIOQKKLVDAIISGD 420
 QY 419 TSUKMLKILQPOVDVLDLDSGASLHLAVAGQEBACAKWLLNANPNLSNRGSTPLMA 478
 DB 419 TSUKMLKILQPOVDVLDLDSGASLHLAVAGQEBACAKWLLNANPNLSNRGSTPLMA 478
 QY 421 TSRLMKILQPOVDVLDLDSASLHLAVAGQEBACAKWLLNANPNLSNRGSTPLMA 480
 DB 421 TSRLMKILQPOVDVLDLDSASLHLAVAGQEBACAKWLLNANPNLSNRGSTPLMA 480

QY 479 VERRRGVEILLARKISVANAKDEQWTALHFAAONDESSSTLLLEKNASVNEVDEGR 538
 DB 481 VERKGRIVELLARKISVANAKDEQWTALHFAAONDESSSTLLLEKNASVNEVDEGR 540
 QY 539 TPMHVAQCHQENIVRILLRGVDVSLQGDAMLPHYAAMQGLPIVKKLAQPGVSVN 598
 DB 541 TPMHVAQCHQENIVRILLRGVDVSLQGDAMLPHYAAMQGLPIVKKLAQPGVSVN 600
 QY 599 AQTLDGRTPLHAAORGHYVARILLIDGSDVNCSLAQTPLHVAETGHTSTARLLH 658
 DB 601 AQTLDGRTPLHAAORGHYVARILLIDGSDVNCSLAQTPLHVAETGHTSTARLLH 660
 QY 659 RGAKKAVTSDGYTALHAAANGHLATVKLLVEBKADVLRGRLNQTALHAAAGHSEV 718
 DB 661 RGAKKAVTSDGYTALHAAANGHLATVKLLVEBKADVLRGRLNQTALHAAAGHSEV 720
 QY 719 VEELVADVIDLDEQGLSALHAAQGRHAQTYETLLRHGAHINLQSLKQGGHGPATIL 778
 DB 721 VEELVADVIDLDEQGLSALHAAQGRHAQTYETLLRHGAHINLQSLKQGGHGPATIL 780
 QY 779 LRRSKT 784
 DB 781 LRRSKT 786

RESULT 9 US-10-299-327-2

; Sequence 2, Application US/10299327
 ; Publication No. US20030104482A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corp.
 ; APPLICANT: Bird, Timothy
 ; APPLICANT: Virca, G.D.
 ; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
 ; TITLE OF INVENTION: (DAKAR)
 ; FILE REFERENCE: 2889-US
 ; CURRENT APPLICATION NUMBER: US/10/299,327
 ; PRIOR FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: US/09/509,802
 ; PRIOR FILING DATE: 2000-06-02
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 786
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-10-299-327-2

Query Match 89.0%; Score 3628; DB 14; Length 786;
 Best Local Similarity 88.9%; Pred. No. 2.5e-248;

Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

QY 1 MEGDGTWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVWKTWLAIKCPSLHAYDD 60
 DB 1 MEGDGRGHWALGLRTFDAGEFAGMEKVGSGGFGQVYKVRHVWKTWLAIKCPSLHAYDD 60
 QY 61 RRRMELBEAKKEMAKFRYYILPVYGIQREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
 DB 61 RRRMELBEAKKEMAKFRYYILPVYGIQREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
 QY 121 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHVHKISDFGLAKCNGLSHSDLSMDG 180
 DB 121 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHVHKISDFGLAKCNGLSHSDLSMDG 180
 QY 181 LFGTIALVLPERRIREKSRLLFTDKHDVYSPAIVWGVLTQKKPFADEKNILLHIMKVYKG 240
 DB 181 LFGTIALVLPERRIREKSRLLFTDKHDVYSPAIVWGVLTQKKPFADEKNILLHIMKVYKG 240
 QY 241 RPELPVPCRAAPRAASHLIRLMQRCMGDPVRPFTFOETSTEDLCEKPDDEVKETAHD 300
 DB 241 RPELPVPCRAAPRAASHLIRLMQRCMGDPVRPFTFOETSTEDLCEKPDDEVKETAHD 300
 QY 301 LDVKSPPPEPSEVVP--ARLKRAAPTFDNDYSLSELSQLDSGVQAVGPEELSRSS 358
 DB 301 LDVKSPPPEPSEVVP--ARLKRAAPTFDNDYSLSELSQLDSGVQAVGPEELSRSS 358


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Db 301 PGRSSLSKSBARPESSRLKRAAPFDNDGSLSELLSGLDSGTSQTLGPEBELSRSS 360
Qy 359 ESKLPSSGSGKRLSGVSVDSAFSSRGSLSLSPEREPTSDLGTRRPEBEACGCHVRD 418
Db 361 ECKLPSSSGKRLSGVSVDSAFSSRGSLSLSPEREASTGDLGPTDIQKKLVDAIISGD 420
Qy 419 TSKLMKTIQPOVDVLADSGASLHLAVAGOEBCAKULLNNANPNLSNRGSTPLHMA 478
Db 421 TSKLMKTIQPOVDVLADSGASLHLAVAGOEBCAKULLNNANPNLSNRGSTPLHMA 480
Qy 419 VERRRGVVELLARKISVNAKEDQWTLHFAAQNDEBSTRLLKKNASVNEVDEGR 538
Db 481 VERRRGVVELLARKISVNAKEDQWTLHFAAQNDEBSTRLLKKNASVNEVDEGR 540
Qy 539 TPMHVACQHGQENIVRILRRGVDSLOQKDALPLHYAAMOGHLPIVKLAKOPGVSVN 598
Db 541 TPMHVACQHGQENIVRILRRGVDSLOQKDALPLHYAAMOGHLPIVKLAKOPGVSVN 600
Qy 599 AQTLDGRTPLHLAORGHYRVARILIDCSVNVCSLLAQTPLHYAATGHTSTARLLH 658
Db 601 AQTLDGRTPLHLAORGHYRVARILIDCSVNVCSLLAQTPLHYAATGHTSTARLLH 660
Qy 659 RGAGKEAVTSDGYTALHLAARNGHLATVKLVEBKADVLARGPLNOTALHLAAHGSSEV 718
Db 661 RGAGKEAVTSDGYTALHLAARNGHLATVKLVEBKADVLARGPLNOTALHLAAHGSSEV 720
Qy 719 VEBLSADVIDLDFEGGSLALHLAAQGRHAQTVELTLRHGAHINLSLKFQGGHGPATL 778
Db 721 VEBLSADVIDLDFEGGSLALHLAAQGRHSQVETELTKHGAHINLSLKFQGGHGPATL 780
Qy 779 LRRSKT 784
Db 781 LRRSKT 786

RESULT 10
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohito
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-13

Query Match 89.0%; Score 3628; DB 14; Length 786;
Best Local Similarity 88.9%; Pred. No. 2.5e-248;
Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

Qy 1 MEGDGTTPMALALTPTPDAGEFTGWEKVGSGGQGVYKVRHVHWKTWLAIKCPSLHVD 60
Db 1 MEGBGGRNALGLRTFDAGEFAGWKGSGGQGVYKVRHVHWKTWLAIKCPSLHVD 60
Qy 61 RERMELEBEAKKEMAKFRYLIPVYGCIREPVGLVNEVWETSLEKTLASEPLPMDLRR 120
Db 61 RERMELEBEAKKEMAKFRYLIPVYGCIREPVGLVNEVWETSLEKTLASEPLPMDLRR 120
Qy 121 ITHETAVGNFTHCAAPPLHLHDLKPAHILDAHVYKISDRFLACNGLSHSHDLSMG 180
Db 121 ITHETAVGNFTHCAAPPLHLHDLKPAHILDAHVYKISDRFLACNGLSHSHDLSMG 180
Qy 181 LRFETIYLPERRRERSRLPDTKGDYVFAIVMGVLTQKKPADKNTLIHIVKVVKGH 240

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Db 181 LFTIAYLPEERIREKSRLEFDTKGDYVFAIVMGVLTQKKPADKNTLIHIVKVVKGH 240
Qy 241 RPELPICRARPPACSHLIRLMORCQDPRVPTFOETSETEDLCRFPDEKVTAYHD 300
Db 241 RPELPICRARPPACSHLIRLMORCQDPRVPTFOETSETEDLCRFPDEKVTAYHD 300
Qy 301 LDVSGPPEPSEVVP--ARLKRAAPFDNDGSLSELLSGLDSGVSQVAVGPEBELSRSS 358
Db 301 PGRSSLSKSBARPESSRLKRAAPFDNDGSLSELLSGLDSGTSQTLGPEBELSRSS 360
Qy 359 ESKLPSSGSGKRLSGVSVDSAFSSRGSLSLSPEREPTSDLGTRRPEBEACGCHVRD 418
Db 361 ECKLPSSSGKRLSGVSVDSAFSSRGSLSLSPEREASTGDLGPTDIQKKLVDAIISGD 420
Qy 419 TSKLMKTIQPOVDVLADSGASLHLAVAGOEBCAKULLNNANPNLSNRGSTPLHMA 478
Db 421 TSKLMKTIQPOVDVLADSGASLHLAVAGOEBCAKULLNNANPNLSNRGSTPLHMA 480
Qy 419 VERRRGVVELLARKISVNAKEDQWTLHFAAQNDEBSTRLLKKNASVNEVDEGR 538
Db 481 VERRRGVVELLARKISVNAKEDQWTLHFAAQNDEBSTRLLKKNASVNEVDEGR 540
Qy 539 TPMHVACQHGQENIVRILRRGVDSLOQKDALPLHYAAMOGHLPIVKLAKOPGVSVN 598
Db 541 TPMHVACQHGQENIVRILRRGVDSLOQKDALPLHYAAMOGHLPIVKLAKOPGVSVN 600
Qy 599 AQTLDGRTPLHLAORGHYRVARILIDCSVNVCSLLAQTPLHYAATGHTSTARLLH 658
Db 601 AQTLDGRTPLHLAORGHYRVARILIDCSVNVCSLLAQTPLHYAATGHTSTARLLH 660
Qy 659 RGAGKEAVTSDGYTALHLAARNGHLATVKLVEBKADVLARGPLNOTALHLAAHGSSEV 718
Db 661 RGAGKEAVTSDGYTALHLAARNGHLATVKLVEBKADVLARGPLNOTALHLAAHGSSEV 720
Qy 719 VEBLSADVIDLDFEGGSLALHLAAQGRHAQTVELTLRHGAHINLSLKFQGGHGPATL 778
Db 721 VEBLSADVIDLDFEGGSLALHLAAQGRHSQVETELTKHGAHINLSLKFQGGHGPATL 780
Qy 779 LRRSKT 784
Db 781 LRRSKT 786

RESULT 11
US-09-866-050A-334
; Sequence 334, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, James D.
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Muriison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-334

Query Match 88.9%; Score 3624; DB 10; Length 787;
Best Local Similarity 88.8%; Pred. No. 4.7e-248;
Matches 698; Conservative 35; Mismatches 51; Indels 2; Gaps 1;

Qy 1 MEGDGTTPMALALTPTPDAGEFTGWEKVGSGGQGVYKVRHVHWKTWLAIKCPSLHVD 60

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Db 2 VEGEGRGMALGLRTFDAGEBAGMEKVGSGFGQVYKVRHVHMKWTALIKCSPSLHVD 61
QY 61 RERMELEBAKMEKAFRYILPYVGICREPVGLVMEYMTGSLKLLASEPLPMDLFR 120
Db 62 RERMELEBAKMEKAFRYILPYVGICREPVGLVMEYMTGSLKLLASEPLPMDLFR 121
QY 121 I I HETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKNGSHSHDLSMDG 180
Db 122 I V HETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKNGSHSHDLSMDG 181
QY 181 LFGTIAVLPERRIREKSRLLFTDKHDVYSPAIVWGLTQKKPFADEKNILHIMKVYKG 240
Db 182 LFGTIAVLPERRIREKSRLLFTDKHDVYSPAIVWGLTQKKPFADEKNILHIMKVYKG 241
QY 241 RPELPVCRAPRACSHLIRLMQRCWQGDPRVPTFQETITSETEDLCERKDEEYKETAHD 300
Db 242 RPELPVCRAPRACSHLIRLMQRCWQGDPRVPTFQETITSETEDLCERKDEEYKETAHD 301
QY 301 LDVKSPPRSEVVP--ARLKRAAPTFDNDYSLSELLSOLDGSGVQAQVGEPELSRSS 358
Db 302 PGEKSSLESSEARPESSRLKRAAPFPDNDCSLSSELLSOLDGSGVQAQVGEPELSRSS 361
QY 359 ESKLPSSSGSKRLSGVSVSDSAFSSRGSLSLSEPERPSTDLGTRRBEBAACGCHVRD 418
Db 362 ECKLPSSSGSKRLSGVSVSDSAFSSRGSLSLSEPERPSTDLGTRRBEBAACGCHVRD 421
QY 419 TSKLMKTILOPOVDVLADSGASLHLAVEAGQEECAKWLNNANPNLSNRGSTPLMA 478
Db 422 TSKLMKTILOPOVDVLADSGASLHLAVEAGQEECAKWLNNANPNLSNRGSTPLMA 481
QY 479 VERRVGVVELLARKISVNAKDEDMTALHPAONDESTRLLLEKNAVNEVDPEGR 538
Db 482 VERRVGVVELLARKISVNAKDEDMTALHPAONDESTRLLLEKNAVNEVDPEGR 541
QY 539 TPEHVAOQOGENIVRILIRRGVDVSLQCKDAMLPLHYAAMOGHLPIVYKLLAQPGSVN 598
Db 542 TPEHVAOQOGENIVRILIRRGVDVSLQCKDAMLPLHYAAMOGHLPIVYKLLAQPGSVN 601
QY 599 AQTLDGRTPLHLAORGHYVARILIDLCSDVNVCSLLAQTPLHYAETGHTSTARLLH 658
Db 602 AQTLDGRTPLHLAORGHYVARILIDLCSDVNVCSLLAQTPLHYAETGHTSTARLLH 661
QY 659 RGAGKAVTSDGYTALHLAARNGHLATVYKLLVEEKADVLARGPLNQTALHLAAHGHSEV 718
Db 662 RGAGKAVTSDGYTALHLAARNGHLATVYKLLVEEKADVLARGPLNQTALHLAAHGHSEV 721
QY 719 VEEIVSADVIDLFDQGLSALHLAAGRHQAQVETILLRHGAHINLSLKFQGGSGPAATL 778
Db 722 VEEIVSADVIDLFDQGLSALHLAAGRHQAQVETILLRHGAHINLSLKFQGGSGPAATL 781
QY 779 LRRSKT 784
Db 782 LRRSKT 787

RESULT 12
US-10-128-174-31
; Sequence 31, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match 88.8%; Score 3620; DB 14; Length 786;
Best Local Similarity 88.8%; Pred. No. 9,1e-248;
Matches 698; Conservative 34; Mismatches 52; Indels 2; Gaps 1;
QY 1 MEGDGTTPMALALRTFDAGEFTGWEKVGSGFGQVYKVRHVHMKWTALIKCSPSLHVD 60
Db 1 MEGDGTTPMALALRTFDAGEFTGWEKVGSGFGQVYKVRHVHMKWTALIKCSPSLHVD 60
QY 61 RERMELEBAKMEKAFRYILPYVGICREPVGLVMEYMTGSLKLLASEPLPMDLFR 120
Db 61 RERMELEBAKMEKAFRYILPYVGICREPVGLVMEYMTGSLKLLASEPLPMDLFR 120
QY 121 I I HETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKNGSHSHDLSMDG 180
Db 121 I V HETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKNGSHSHDLSMDG 180
QY 181 LFGTIAVLPERRIREKSRLLFTDKHDVYSPAIVWGLTQKKPFADEKNILHIMKVYKG 240
Db 182 LFGTIAVLPERRIREKSRLLFTDKHDVYSPAIVWGLTQKKPFADEKNILHIMKVYKG 240
QY 241 RPELPVCRAPRACSHLIRLMQRCWQGDPRVPTFQETITSETEDLCERKDEEYKETAHD 300
Db 241 RPELPVCRAPRACSHLIRLMQRCWQGDPRVPTFQETITSETEDLCERKDEEYKETAHD 300
QY 241 RPELPVCRAPRACSHLIRLMQRCWQGDPRVPTFQETITSETEDLCERKDEEYKETAHD 300
Db 241 RPELPVCRAPRACSHLIRLMQRCWQGDPRVPTFQETITSETEDLCERKDEEYKETAHD 300
QY 301 LDVKSPPRSEVVP--ARLKRAAPTFDNDYSLSELLSOLDGSGVQAQVGEPELSRSS 358
Db 301 PGEKSSLESSEARPESSRLKRAAPFPDNDCSLSSELLSOLDGSGVQAQVGEPELSRSS 360
QY 359 ESKLPSSSGSKRLSGVSVSDSAFSSRGSLSLSEPERPSTDLGTRRBEBAACGCHVRD 418
Db 361 ECKLPSSSGSKRLSGVSVSDSAFSSRGSLSLSEPERPSTDLGTRRBEBAACGCHVRD 420
QY 419 TSKLMKTILOPOVDVLADSGASLHLAVEAGQEECAKWLNNANPNLSNRGSTPLMA 478
Db 421 TSKLMKTILOPOVDVLADSGASLHLAVEAGQEECAKWLNNANPNLSNRGSTPLMA 480
QY 479 VERRVGVVELLARKISVNAKDEDMTALHPAONDESTRLLLEKNAVNEVDPEGR 538
Db 481 VERRVGVVELLARKISVNAKDEDMTALHPAONDESTRLLLEKNAVNEVDPEGR 540
QY 539 TPEHVAOQOGENIVRILIRRGVDVSLQCKDAMLPLHYAAMOGHLPIVYKLLAQPGSVN 598
Db 541 TPEHVAOQOGENIVRILIRRGVDVSLQCKDAMLPLHYAAMOGHLPIVYKLLAQPGSVN 600
QY 599 AQTLDGRTPLHLAORGHYVARILIDLCSDVNVCSLLAQTPLHYAETGHTSTARLLH 658
Db 601 AQTLDGRTPLHLAORGHYVARILIDLCSDVNVCSLLAQTPLHYAETGHTSTARLLH 660
QY 659 RGAGKAVTSDGYTALHLAARNGHLATVYKLLVEEKADVLARGPLNQTALHLAAHGHSEV 718
Db 661 RGAGKAVTSDGYTALHLAARNGHLATVYKLLVEEKADVLARGPLNQTALHLAAHGHSEV 720
QY 719 VEEIVSADVIDLFDQGLSALHLAAGRHQAQVETILLRHGAHINLSLKFQGGSGPAATL 778
Db 721 VEEIVSADVIDLFDQGLSALHLAAGRHQAQVETILLRHGAHINLSLKFQGGSGPAATL 780
QY 779 LRRSKT 784
Db 781 LRRSKT 786

RESULT 13
US-10-128-174-32
; Sequence 32, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 32
LENGTH: 786
TYPE: prt
ORGANISM: Mus musculus
US-10-128-174-32

Query Match 88.7%; Score 3619; DB 14; Length 786;
Best Local Similarity 88.5%; Pred. No. 1.1e-247;
Matches 696; Conservative 37; Mismatches 51; Indels 2; Gaps 1;

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DB 61 RRMELLEBAKMEAKERYILPYVGICREPVGLVMEYMETGSEKLLASPELPMDLRF 120
QY 121 ITHETAVGNMFLHCAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSDLSMDG 180
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DB 121 ITHETAVGNMFLHCAPPLHLDLKPANILLDAHNVKISDFGLAKCNGMAHAHDLAMDG 180
QY 181 LFGTAYLPERIRKESLPDTKHVYSFAIVGVLTQKKPDADEKNILHIMKVYVGH 240
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QY 539 TPNHVAQCHQENIYRILLRGVNVSLOGKDAWLPHTYAAOGHLPYVLLAKOPGVSVN 598
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DB 779 LRRSKT 786
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RESULT 14
US-10-128-174-33
; Sequence 33, Application US/10128174
; Publication No. US20030199462A1

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 33
LENGTH: 786
TYPE: prt
ORGANISM: Mus musculus
US-10-128-174-33

Query Match 88.7%; Score 3616; DB 14; Length 786;
Best Local Similarity 88.5%; Pred. No. 1.7e-247;
Matches 696; Conservative 34; Mismatches 54; Indels 2; Gaps 1;

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DB 1 MEGDGTPTALALRTFDGGEFTGMEKVGSGGFGQYKVRHVHMKWTMLAICSPSLHYDD 60
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QY 121 ITHETAVGNMFLHCAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSDLSMDG 180
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QY 419 TSKLMKILOPOVDVLVDSSASLHLAVEAGQECVKMLLNANPNLTNRKGSTPLHMA 478
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QY 539 TPNHVAQCHQENIYRILLRGVNVSLOGKDAWLPHTYAAOGHLPYVLLAKOPGVSVN 598
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DB 601 AQTLDRTPLHLAARGHYVARILIDCSDVNCSLAQPTPLHVAAGTSTARLLH 660
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DB 659 RGAGKEAVTSDGYTALHLAARNGHLATVKLLVEEKADVLARGLPNTALHLAAAGHSEV 718
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DB 719 VEEIVSADVIDLFDQGLSALHLAAGRHAQVETLLRHGAINLQSLKFGGSGAPATL 778
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Db 781 LRRSKT 786

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RESULT 15

US-09-866-050A-409

; Sequence 409, Application US/09866050A

Publication No. US20030040471A1

; GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: MURISON, James G.

APPLICANT: Kumble, Krishanand D

1. TITLE OF INVENTION: Compositions Isolated From Skin Cells

; TITLE OF INVENTION: and Methods for Their Use

FILE REFERENCE: 11000.1011c4U

CURRENT APPLICATION NUMBER: US/09/866,050A

CURRENT FILING DATE: 2001-05-24

; NUMBER OF SEQ ID NOS: 725

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; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 409

LENGTH: 590

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;      TYPE: PRT
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ORGANISM: Mouse

US-09-866-050A-409

Query Match 66.0%; Score 2691; DB 10; Length 590;

Best Local Similarity 87.3%; Pred. No. 4.6e-182;

Matches	514;	Conservative	27;	Mismatches	46;	Indels	2;	Gaps	1;
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Db 122 IYHETA VGNFPHCHMSPPHLHDLKPA NILLDAHNYKISDFGLACNGLSHSHDLSMDC 181
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Db 182 LFGTAIYLPBERIIRKESRLPDTGHDDVSAIYVWGLTQKKPRADBNKILHIMWKYVKG 241
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 02:33:25 ; Search time 942.919 Seconds
(without alignments)
62.068 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4078	100.0	784	US-09-781-882-2	Sequence 2, Appl 1
2	3980	97.6	787	US-09-949-016-11076	Sequence 11076, A
3	3976	97.5	784	US-09-949-016-6974	Sequence 6974, Ap
4	3628	89.0	786	US-09-509-802-2	Sequence 2, Appl 1
5	3624	88.9	787	US-09-188-930-334	Sequence 334, App
6	3624	88.9	787	US-09-312-283C-334	Sequence 334, App
7	2691	66.0	590	US-09-312-283C-409	Sequence 409, App
8	2269	55.6	536	US-09-188-930-185	Sequence 185, App
9	2269	55.6	536	US-09-312-283C-185	Sequence 185, App
10	545	13.4	530	US-09-069-023-3	Sequence 3, Appl 1
11	541.5	13.3	531	US-09-069-023-1	Sequence 1, Appl 1
12	541.5	13.3	540	US-09-019-942-1	Sequence 2, Appl 1
13	541.5	13.3	540	US-09-099-041A-2	Sequence 27, Appl 1
14	541.5	13.3	540	US-09-069-023-27	Sequence 2, Appl 1
15	541.5	13.3	540	US-09-245-281-2	Sequence 2, Appl 1
16	541.5	13.3	540	US-09-470-271-1	Sequence 2, Appl 1
17	541.5	13.3	540	US-09-207-359B-2	Sequence 2, Appl 1
18	541.5	13.3	540	US-09-340-620A-2	Sequence 28, Appl 1
19	541.5	13.3	540	US-09-345-473B-28	Sequence 2, Appl 1
20	541.5	13.3	540	US-09-865-364-2	Sequence 1, Appl 1
21	541.5	13.3	540	US-09-748-537-1	Sequence 4, Appl 1
22	532.5	13.1	300	US-09-099-041A-4	Sequence 4, Appl 1
23	532.5	13.1	300	US-09-245-281-4	Sequence 4, Appl 1
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26	532.5	13.1	300	US-09-865-364-4	Sequence 4, Appl 1
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30	500	12.3	1856	4	US-09-949-016-6964	Sequence 6964, Ap
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33	500	12.3	1883	4	US-09-949-016-9010	Sequence 9010, Ap
34	500	12.3	1883	4	US-09-949-016-9011	Sequence 9011, Ap
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41	498	12.2	1745	2	US-09-031-485-33	Sequence 33, Appl 1
42	498	12.2	1745	2	US-08-847-429A-33	Sequence 33, Appl 1
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ALIGNMENTS

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Sequence 2, Application US/09781882									
Patent No. 6630335									
GENERAL INFORMATION:									
APPLICANT: Kapeller-Libermann, Rosana									
TITLE OF INVENTION: 14171 Protein Kinase, a No. 6630335el Human									
FILE REFERENCE: 035800-209014(5800-6									
CURRENT FILING DATE: 2001-02-12									
PRIOR APPLICATION NUMBER: U.S. 60/182,096									
PRIOR FILING DATE: 2000-02-11									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 2									
LENGTH: 784									
TYPE: PRT									
ORGANISM: H. sapiens									
US-09-781-882-2									
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Best Local Similarity 100.0%; Score 4078; DB 4; Length 784;									
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	241	REPPLPVCRARPRACSHLIRLMQRCWQDPVRRPTFOBITSETEDLCRPPDEVKETAND	300						
DB	241	REPPLPVCRARPRACSHLIRLMQRCWQDPVRRPTFOBITSETEDLCRPPDEVKETAND	300						
QY	301	LDVKSPPPRSVVYVARKASAPTFNDYGLSELGLDGVGSAVAGPELSSSSSS	360						
DB	301	LDVKSPPPRSVVYVARKASAPTFNDYGLSELGLDGVGSAVAGPELSSSSSS	360						
QY	361	KLPSSGSKRLSGVSSVSAFSSRGLSLSPFERPSTDLGTTTRAPBEERACGHRVDRTS	420						

```
Db 361 KLPSSGSGKRLSGVSDSAFSSRGSLSLSPEREPSIDGTTTRRPEEACGCHRVDT 420
Qy 421 KLMKILQPOVDLALDGSALHLHVAEGEBCAKMILLNNANPNLSNRGSTPLHNAVE 480
Db 421 KLMKILQPOVDLALDGSALHLHVAEGEBCAKMILLNNANPNLSNRGSTPLHNAVE 480
Qy 481 RRVGVVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 540
Db 481 RRVGVVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 540
Qy 541 MHVACQHGQENIVRIILRGDVSLQGDAMLPLHYAAMQGHLPYKLLAKOPGVVNAQ 600
Db 541 MHVACQHGQENIVRIILRGDVSLQGDAMLPLHYAAMQGHLPYKLLAKOPGVVNAQ 600
Qy 601 TLDRTPPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 660
Db 601 TLDRTPPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 660
Qy 661 AGKAVTSDGYTALHLAARNGHLATVKLVEEKADVARGPLNOTALHLAAHGSVEVE 720
Db 661 AGKAVTSDGYTALHLAARNGHLATVKLVEEKADVARGPLNOTALHLAAHGSVEVE 720
Qy 721 ELVSADVIDLFDDEGSLALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATILR 780
Db 721 ELVSADVIDLFDDEGSLALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATILR 780
Qy 781 RSKT 784
Db 781 RSKT 784
```

```
RESULT 2
US-09-949-016-11076
; Sequence 11076, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11076
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11076
```

```
Query Match 97.6%; Score 3980; DB 4; Length 787;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy 1 MEGDGGTPTWALALATPAGGFTGMBKVGSGGFGVYVRVHNMKTWLAIKSPSLHYDD 60
Db 4 MEGDGGTPTWALALATPAGGFTGMBKVGSGGFGVYVRVHNMKTWLAIKSPSLHYDD 63
Qy 61 RERMLLEBAKMEKAKFRYILPVYIGCEPVGLVMEVETSLSEKLLASEPLPMDLFR 120
Db 64 RERMLLEBAKMEKAKFRYILPVYIGCEPVGLVMEVETSLSEKLLASEPLPMDLFR 123
Qy 121 IIEHTAVGNMPLHCAAPPLHLIDLPANILDLAHYVKSIDPGLAKCNGLSHSHLSDMG 180
Db 124 IIEHTAVGNMPLHCAAPPLHLIDLPANILDLAHYVKSIDPGLAKCNGLSHSHLSDMG 183
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Qy 181 LFGTIATLPEERIREKSRLEFDTRGDVYSFAIVIMGVLTQKKPPEAKNLIHIMVKVKG 240
Db 184 LFGTIATLPEERIREKSRLEFDTRGDVYSFAIVIMGVLTQKKPPEAKNLIHIMVKVKG 243
Qy 241 RPELIPVCARPRACSHLILMORCWQGDPRVPTFOEITSEIBDLCEKDDVEKETAHD 300
Db 244 RPELIPVCARPRACSHLILMORCWQGDPRVPTFOEITSEIBDLCEKDDVEKETAHD 303
Qy 301 LDVKSPEPSEVVPAPALKRAASAPTFNDVSLSELLSOLDSGVSQAVGPEELSRSSSES 360
Db 304 LDVKSPEPSEVVPAPALKRAASAPTFNDVSLSELLSOLDSGVSQAVGPEELSRSSSES 363
Qy 361 KLPSSGSGKRLSGVSDSAFSSRGSLSLSPEREPSIDGTTTRRPEEACGCHRVDT 420
Db 364 KLPSSGSGKRLSGVSDSAFSSRGSLSLSPEREPSIDGTTTRRPEEACGCHRVDT 423
Qy 421 KLMKILQPOVDLALDGSALHLHVAEGEBCAKMILLNNANPNLSNRGSTPLHNAVE 480
Db 424 KLMKILQPOVDLALDGSALHLHVAEGEBCAKMILLNNANPNLSNRGSTPLHNAVE 483
Qy 481 RRVGVVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 540
Db 484 RRVGVVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 543
Qy 541 MHVACQHGQENIVRIILRGDVSLQGDAMLPLHYAAMQGHLPYKLLAKOPGVVNAQ 600
Db 544 MHVACQHGQENIVRIILRGDVSLQGDAMLPLHYAAMQGHLPYKLLAKOPGVVNAQ 603
Qy 601 TLDRTPPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 660
Db 604 TLDRTPPLHLAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 663
Qy 661 AGKAVTSDGYTALHLAARNGHLATVKLVEEKADVARGPLNOTALHLAAHGSVEVE 720
Db 664 AGKAVTSDGYTALHLAARNGHLATVKLVEEKADVARGPLNOTALHLAAHGSVEVE 723
Qy 721 ELVSADVIDLFDDEGSLALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATILR 780
Db 724 ELVSADVIDLFDDEGSLALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATILR 783
Qy 781 RSKT 784
Db 784 RSKT 787
```

```
RESULT 3
US-09-949-016-6974
; Sequence 6974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6974
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6974
```

```
Query Match 97.5%; Score 3976; DB 4; Length 784;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

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QY 1 MEGDGTWALALARTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTMLAIKCSPLHYDD 60
DB 1 MEGDGTWALALARTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTMLAIKCSPLHYDD 60
QY 61 RERMELEBAKMEAKFRYYLLPVYGIQREBPVGLVMEWMEGSLSEKLLASPELPMDLRFR 120
DB 61 RERMELEBAKMEAKFRYYLLPVYGIQREBPVGLVMEWMEGSLSEKLLASPELPMDLRFR 120
QY 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHAYKISDPGLAKCNGLSHSHDLSDMG 180
DB 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHAYKISDPGLAKCNGLSHSHDLSDMG 180
QY 181 LFGTIAYLPPERIREKSRLLFTKHDVYSFAIVGWGLTQKKPFADEKNIILHMKVYKGH 240
DB 181 LFGTIAYLPPERIREKSRLLFTKHDVYSFAIVGWGLTQKKPFADEKNIILHMKVYKGH 240
QY 241 RPELPPVCARAPRAASHLIRLMORCMQGDPRVRPTFOEITSETBDLCEKPDDEVKETAHD 300
DB 241 RPELPPVCARAPRAASHLIRLMORCMQGDPRVRPTFOEITSETBDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPPEPRSEVVPARLKRAAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
DB 301 LDVKSPPPEPRSEVVPARLKRAAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
QY 361 KLPSSSGSKRLSGVSSVDSAFSSRGSLSLSPFEREPSTDLGTTTRPPEERACGCHRVDTG 420
DB 361 KLPSSSGSKRLSGVSSVDSAFSSRGSLSLSPFEREPSTDLGTTTRPPEERACGCHRVDTG 420
QY 421 KLMKTILOPDDVLDLDSGASLLHLAVEAQOECACWLLNNANPNLSNRGSTPLHMAVE 480
DB 421 KLMKTILOPDDVLDLDSGASLLHLAVEAQOECACWLLNNANPNLSNRGSTPLHMAVE 480
QY 481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGRTP 540
DB 481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGRTP 540
QY 541 MEVACQHOGENIVRILRRGVDSLOGKDAMLPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
DB 541 MEVACQHOGENIVRILRRGVDSLOGKDAMLPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
QY 601 TLDDGRTPPLHAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
DB 601 TLDDGRTPPLHAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
QY 661 ACKEATSDGYTALHAAANGHLATVKLLVEEKADVLARGPLNQTLHLHAAAGHSEVYE 720
DB 661 ACKEATSDGYTALHAAANGHLATVKLLVEEKADVLARGPLNQTLHLHAAAGHSEVYE 720
QY 721 ELVSADVIDLFDQGLSALHLAAQGRHAQTVEITLLRHGAHINLOSLKFOGCHGPAATLLR 780
DB 721 ELVSADVIDLFDQGLSALHLAAQGRHAQTVEITLLRHGAHINLOSLKFOGCHGPAATLLR 780
QY 781 RSKKT 784
DB 781 RSKKT 784

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RESULT 4
 US-09-509-802-2
 ; Sequence 2, Application US/09509802
 ; Patent No. 6489130
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corp.
 ; APPLICANT: Bird, Timothy
 ; APPLICANT: VITCA, G.D.
 ; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKTRIN REPEATS (DATA)
 ; FILE REFERENCE: 2889-US
 ; CURRENT APPLICATION NUMBER: US/09/509,802
 ; CURRENT FILING DATE: 2000-06-02
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent version 3.0
 ; SEQ ID NO 2

```

; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-509-802-2
Query Match      89.0%; Score 3628; DB 4; Length 786;
Best Local Similarity 88.9%; Pred. No. 2,88-314;
Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

QY 1 MEGDGTWALALARTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTMLAIKCSPLHYDD 60
DB 1 MEGDGTWALALARTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTMLAIKCSPLHYDD 60
QY 61 RERMELEBAKMEAKFRYYLLPVYGIQREBPVGLVMEWMEGSLSEKLLASPELPMDLRFR 120
DB 61 RERMELEBAKMEAKFRYYLLPVYGIQREBPVGLVMEWMEGSLSEKLLASPELPMDLRFR 120
QY 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHAYKISDPGLAKCNGLSHSHDLSDMG 180
DB 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHAYKISDPGLAKCNGLSHSHDLSDMG 180
QY 181 LFGTIAYLPPERIREKSRLLFTKHDVYSFAIVGWGLTQKKPFADEKNIILHMKVYKGH 240
DB 181 LFGTIAYLPPERIREKSRLLFTKHDVYSFAIVGWGLTQKKPFADEKNIILHMKVYKGH 240
QY 241 RPELPPVCARAPRAASHLIRLMORCMQGDPRVRPTFOEITSETBDLCEKPDDEVKETAHD 300
DB 241 RPELPPVCARAPRAASHLIRLMORCMQGDPRVRPTFOEITSETBDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPPEPRSEVVPARLKRAAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
DB 301 LDVKSPPPEPRSEVVPARLKRAAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
QY 361 ESKLPSSSGSKRLSGVSSVDSAFSSRGSLSLSPFEREPSTDLGTTTRPPEERACGCHRVDTG 420
DB 361 ESKLPSSSGSKRLSGVSSVDSAFSSRGSLSLSPFEREPSTDLGTTTRPPEERACGCHRVDTG 420
QY 421 TSUKMKTILOPDDVLDLDSGASLLHLAVEAQOECACWLLNNANPNLSNRGSTPLHMAVE 480
DB 421 TSUKMKTILOPDDVLDLDSGASLLHLAVEAQOECACWLLNNANPNLSNRGSTPLHMAVE 480
QY 481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGRTP 540
DB 481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGRTP 540
QY 541 MEVACQHOGENIVRILRRGVDSLOGKDAMLPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
DB 541 MEVACQHOGENIVRILRRGVDSLOGKDAMLPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
QY 601 TLDDGRTPPLHAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
DB 601 TLDDGRTPPLHAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
QY 661 ACKEATSDGYTALHAAANGHLATVKLLVEEKADVLARGPLNQTLHLHAAAGHSEVYE 720
DB 661 ACKEATSDGYTALHAAANGHLATVKLLVEEKADVLARGPLNQTLHLHAAAGHSEVYE 720
QY 721 ELVSADVIDLFDQGLSALHLAAQGRHAQTVEITLLRHGAHINLOSLKFOGCHGPAATLLR 780
DB 721 ELVSADVIDLFDQGLSALHLAAQGRHAQTVEITLLRHGAHINLOSLKFOGCHGPAATLLR 780
QY 781 RSKKT 784
DB 781 RSKKT 784

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RESULT 5
 US-09-188-930-334
 ; Sequence 334, Application US/09188930A
 ; Patent No. 6150502
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna


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DB 602 AQTLLGRTPLHAAQGRHVARILIDCSOVNICSLOAQOTPLHAAETGHTSTRLILH 661
QY 659 RGAGKAVTSDGYTALHLAARNGHLATVLLVEEKADVLARGPLNOTALHLAAHGHSEV 718
DB 662 RAGAGKAVTSDGYTALHLAARNGHLATVLLVEEKADVLARGPLNOTALHLAAHGHSEV 721
QY 719 VELVVSADVIDLFDQGSALHLAAQGRHVAQVETLLRHGANINOSLKFQGGHGPATL 778
DB 722 VELVVSADVIDLFDQGSALHLAAQGRHVAQVETLLRHGANINOSLKFQGGHGPATL 781
QY 779 LRSKPT 784
DB 782 LRSKPT 787

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RESULT 7

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US-09-312-283C-409
/ Sequence 409, Application US/09312283C
/ Patent No. 6573095
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Muirson, James G.
/ APPLICANT: Kumble, Krishanand D.
/ TITLE OF INVENTION: Compositions Isolated from Skin Cells
/ TITLE OF INVENTION: and Methods for Their Use
/ FILE REFERENCE: 11000.1011c2
/ CURRENT APPLICATION NUMBER: US/09/312,283C
/ NUMBER OF FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 425
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 409
/ LENGTH: 590
/ TYPE: PRT
/ ORGANISM: Mouse
/ US-09-312-283C-409

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Query Match 66.0%; Score 2691; DB 4; Length 590;
Best Local Similarity 87.3%; Pred. No. 6e-231;
Matches 514; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 1 MEGDGGTPTWALALRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 60
DB 2 VEGEGRGHMAIGLRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 61
QY 61 RERMEILLBAKKMEAKKRYILLPVYGCIBPVGVLVMEYMETGSLKELASBPLPMDLRR 120
DB 62 RERMEILLBAKKMEAKKRYILLPVYGCIBPVGVLVMEYMETGSLKELASBPLPMDLRR 121
QY 121 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSHDLSMD 180
DB 122 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSHDLSMD 181
QY 181 LFGTIAVLPERRIREKSRFLPTDKHDVYSPFAIVMGVLTOKKPPADEKNILHIMKVVYK 240
DB 182 LFGTIAVLPERRIREKSRFLPTDKHDVYSPFAIVMGVLTOKKPPADEKNILHIMKVVYK 241
QY 241 RPELPVPCRRAPRACSHLIRLMORCMQGDPRVPTFOITSETEDLCEKPDDEVYKTAH 300
DB 242 RPELPVPCRRAPRACSHLIRLMORCMQGDPRVPTFOITSETEDLCEKPDDEVYKTAH 301
QY 301 LDVKSPPBPRSEVVP--ARLKRASAPTFDNDYSLSELSQLDSGVSAVGPBELSRSS 358
DB 302 PGKSSLSLESKEAPRPSRKLKASAPPFNDSCSLSELSQLDSGICITLEGPELSRSS 361
QY 359 BSRLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTDLGTTTRPEBEACGCHRV 418
DB 362 BSRLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTDLGTTTRPEBEACGCHRV 421
QY 419 TSKLMTKLQPDVDLALDSASLHLAABAGQEECAKMLLNANPNLNSRSGSTPLHMA 478

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DB 422 TSKLMTKLQPDVDLALDSASLHLAABAGQEECAKMLLNANPNLNSRSGSTPLHMA 481
QY 479 VERKRGVVELLARKISVANAKDEDOWTALHFAAONDESTRLLKKNASVNVDFEGR 538
DB 482 VERKRGVVELLARKISVANAKDEDOWTALHFAAONDESTRLLKKNASVNVDFEGR 541
QY 539 TPRMVAOCHQENIVRILRRGVDSLOGKADWTLPLHYAAMQCHLPIYK 587
DB 542 TPRMVAOCHQENIVRILRRGVDSLOGKADWTLPLHYAAMQCHLPIYK 590

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RESULT 8

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US-09-188-930-185
/ Sequence 185, Application US/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Muirson, James Greg
/ TITLE OF INVENTION: Compositions Isolated from Skin Cells
/ TITLE OF INVENTION: and Methods For Their Use
/ FILE REFERENCE: 11000.1011c1
/ CURRENT APPLICATION NUMBER: US/09/188,930A
/ NUMBER OF FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 185
/ LENGTH: 536
/ TYPE: PRT
/ ORGANISM: mouse
/ US-09-188-930-185

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Query Match 55.6%; Score 2269; DB 3; Length 536;
Best Local Similarity 84.1%; Pred. No. 2.1e-193;
Matches 438; Conservative 29; Mismatches 50; Indels 4; Gaps 3;

QY 1 MEGDGGTPTWALALRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 60
DB 2 VEGEGRGHMAIGLRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 61
QY 61 RERMEILLBAKKMEAKKRYILLPVYGCIBPVGVLVMEYMETGSLKELASBPLPMDLRR 120
DB 62 RERMEILLBAKKMEAKKRYILLPVYGCIBPVGVLVMEYMETGSLKELASBPLPMDLRR 121
QY 121 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSHDLSMD 179
DB 122 ITHETAVGNMFLHGMAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSHDLSMD 181
QY 180 GLFGTIAVLPERRIREKSRFLPTDKHDVYSPFAIVMGVLTOKKPPADEKNILHIMKVVYK 239
DB 182 GLFGTIAVLPERRIREKSRFLPTDKHDVYSPFAIVMGVLTOKKPPADEKNILHIMKVVYK 241
QY 240 HRPBLPVCRRAPRACSHLIRLMORCMQGDPRVPTFOITSETEDLCEKPDDEVYKTAH 299
DB 242 HRPBLPVCRRAPRACSHLIRLMORCMQGDPRVPTFOITSETEDLCEKPDDEVYKTAH 301
QY 300 DLDVKSPPBPRSEVVP--ARLKRASAPTFDNDYSLSELSQLDSGV--SQAVGPBELSR 356
DB 302 EGGKSSLSLESKEAPRPSRKLKASAPPFNDSCSLSELSQLDSGICITLEGPELSRSS 361
QY 357 SSKSLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTDLGTTTRPEBEACGCHRV 416
DB 362 SSKSLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTDLGTTTRPEBEACGCHRV 421
QY 417 RPTSLMTKLQPDVDLALDSASLHLAABAGQEECAKMLLNANPNLNSRSGSTPLH 476
DB 422 RPTSLMTKLQPDVDLALDSASLHLAABAGQEECAKMLLNANPNLNSRSGSTPLH 481
QY 477 MAYERVRGVVELLARKISVANAKDEDOWTALHFAAONDE 517

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Db          482  MAVERKRGIVELLARKTSSVAKXDEDMTALHFAAQNQDE 522

RESULT 9
US-09-312-283C-185
; Sequence 185, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Muirson, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-185

```

Query Match	55.6%;	Score 2269;	DB 4;	Length 536;
Best Local Similarity	84.1%;	Pred. No. 2.1e-193;		
Matches 438;	Conservative 29;	Mismatches 50;	Indels 4;	Gaps 3;

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QY      _NEGDDGTPALALLRLTRFDADGEFLGMEKVSQGGQVYKVRHMYKMTWLIKCSPLSHVD 60
      : : : :
Db      2 VEGEGRGRALGLTRTFDAGEFPAKMEKVSQGGQVYKVRHMYKMTWLIKCSPLSHVD 61

QY      61 RERMELLEBAKOMEAKFRYILPVYGI CEBPVGLVMEYMETGSELEKLASEPLPMDLRFR 120
      : : : :
Db      62 RERMELLEBAKOMEAKFRYILPVYGI COEBPVGLVMEYMETGSELEKLASEPLPMDLRFR 121

QY      121 ITHETAVGNMFLHCMAPELLHDLKXANILLDNHYAV -KISDGLKKNGLSGHSHLSMD 179
      : : : :
Db      122 IYHETAVGNMFLHCMSPELLHDLKXANILLDNHYQMSRRLDGLKKNQMSHSHLSMD 181

QY      180 GLFGTIAVLPERRIREKSLPTDKHDVYSFAIYIWCVLTQKKEPADEKNIIMYEVYVG 239
      : : : :
Db      182 GLFGTIGVLPERRIREKSLPTDKHDVYSFAIYIWCVLTQNNPFADEKNIIMYEVYVG 241

QY      240 HRPBLPVOCARBPACSHILRLMORQWQODPRPRPFQOETSTEDLCERKDEVEKETHN 289
      : : : :
Db      242 HRPBLPPICRPRPRACASLIGLMORCWMADPOVRPFQOETSTEDLCERKDEVEKOLAH 301

QY      300 DLDVVSPPERPREBVPV -ARLKRAASAPTEPDNDVLSBELLSOLDGCV -SQAVEGPEELSRS 356
      : : : :
Db      302 EFGBKSSLESKSEARPESSRLKRAASAPFPDNDCSLSELSQLDSDGIFRLKPEELSRS 361

QY      357 SSESKLPSSGSGKRLSGVSSVDSAESSRGSLSLSPREBPTSBLGTTTRPEELACGCHV 416
      : : : :
Db      362 SSECKLPSSSSGGRLSGVSSVDSAFSSRSLSLSFREAESTGDLGPDLQKKLVDAIIS 421

QY      417 RDTSKLMLKLOPODVLDALDSCASLIHLAVEAQOECAKWLILNNANPNLSNRGSTPLH 476
      : : : :
Db      422 GDTSRMLKLOQPODVLDVDSASLIHLAVEAQOECAKWLILNNANPNLTNRKGSPLH 481

QY      477 MAVERRVGVVBLILARKISVNAKEDDONTALHPAANGDE 517
      : : : :
Db      482 MAVERRGVIVELLARKTSVNAKEDDONTALHPAANGDE 522

```

RESULT 10
US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:

```

? APPLICANT: Nunez, Gabriel
? APPLICANT: Inohara, Naohiro
? APPLICANT: Koseki, Takeyoshi
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
? TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
? FILE REFERENCE: UM-03333
? CURRENT APPLICATION NUMBER: US/09/069,023A
? CURRENT FILING DATE: 1998-04-27
? NUMBER OF SEQ ID NOS: 38
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 530
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-069-023-3

Query Match      13.4%   Score 545;   DB 3;   Length 530;
Best Local Similarity 33.3%   Pred. No. 9.9e-40;
Matches 150; Conservative 59; Mismatches 123; Indels 118; Gaps 17

```

ORGANISM: Homo sapiens
US-09-069-023-3

Query Match	13.4%	Score 545	DB 3	Length 530
-------------	-------	-----------	------	------------

Best Local Similarity 33.3%; Pred.No. 9.9e-40;
Matches 150; Conservative 59; Mismatches 123; Indels 118; Gaps 17;

```

QY      8 FMALLALTPTDPAGETGMEKXGSGGQVYKVRHNMKTWIALKCSPLHVD----DRBR 63
Db      5 PYKJADLR-----YLSRGSAGTVSSARHADMWQVAVK--MLHHTPLLDSEB 50
QY      64 MEILEBAKMEWAKERYILLPVYGIQREP--VGLVMEVETGSLEKTLASE----PLPWLJ 117
Db      51 KDVLREAILHKARSTYILLPIGICNEBEPFGIVTEMVNGSLNELLHKTEYEDVAVPL 110
QY      118 RFRITHEPAVGNMFLHCAPPLHLHDLPXANILLDAHYKISDPGLACNGLSHSHDS 177
Db      111 RFRITHEPALTGVNYLHNNTPPLHLHDLTQNTLLNBEFVKIADFGLSKRWMSLISQSSB 170
QY      178 M-----DGLFGTAYVLPPEIR--EKSRLPDTGHDVYSPFAIVIMGYLTOKKPEADEKNILH 231
Db      171 SKSAPBG--GTLITMPENYERGOQSRA-STGHDIYSAYVITWELYSKRQOPEDVYNPQ 227
QY      232 IMVYVVKGHRP-----ELRPVCRAPRACSHILRMORCWODPRVYRPTFOETSETBDL 286
Db      228 IMYSVGQHRPYNIEESLPYDLPBRAR---MISLIESGMANPPDERPEFLKTLILEBY 283
QY      287 CEKPDVEKETAHDLDVKSPPREBREVPARLKASAPFEDNDYSLELLSOLDGSVSOA 346
Db      284 LR-----TFE-EITFLEAVIOL-----299
QY      347 VEGPEELSRSSGSKLPSSGSGKRLGVSVSDSAFSSRGSLSLSEPERBSTDGLGTRRP 406
Db      300 -----KXTLQGVSSAIHLCDDKOME-----LSU-----NIPVHGB 331
QY      407 EBEACGCRHVRDTS-----KLMKILQPOVDY 432
Db      332 QBECSGSSQULHENSGETSPETSRELPAPOQND 361

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RESULT 11
US-09-069

Sequence 1, Application US/09069023A
Patent No. 6348573

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS-INDUCING AGENTS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILER REFERENCE: UM-0333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: patentln Ver. 2.0

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; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-1

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Query Match 13.3%; Score 541.5; DB 3; Length 531;
 Best Local Similarity 34.0%; Pred. No. 26-39;
 Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

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QY 31 GGFQGVYKVRHVMKWTWIAIKCPSLHYD---DREKMLLEBAKMEAKFRYLLPYVG 86
DB 18 GASGVSSARRHADMRQVAVK---HLHHTPLDLSERKDVLEAEILHKARFSYLLPILG 74
QY 87 ICRBP--VGLVMEYMETGSLKELKLA---PLPMDLRFRIIHTAVGMFLHCAPILL 140
DB 75 ICNEBEPFIGIVTEYMPNGSLNELHRRKTEYPDVAMPLEFRILHEIALGVNYLHNTTPILL 134
QY 141 HLDKPRANILLDAHNYKISDPGLAKCNGLSHSDLSM---DGLFGTIAVLPERRIR-- 194
DB 135 HHDLKTQNILLDNEHFVKIADFGLSKWRMWSLSQSRSSKAPDG--GTLITMPENYEPG 192
QY 195 EKSRLPDKHDVYSPFAIYWGVLTKCKPFADEKNILHIMVYVKGHRP-----ELPPYCR 249
DB 193 QKSRRA-STKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSGHRPVINEESLPYDIP 251
QY 250 APPRACSHLIRLMORCMQDPRVPRPTFOEITSETEDLCEKPDDEVKETAHDLDVXSPERP 309
DB 252 HHRAR---MISLBSGMQNPDERSFLKCLIELEPVLR----- 286
QY 310 RSEVVPARLKASAPTFDNDYSLSELSQLDSGVSAQVGEPELRSSESSEKLPSSGSGK 369
DB 287 -----TFE-EITFLEAVIQL-----KTKLQSVSSAI 312
QY 370 RLSGVSVDSAFSSRGSLSLSPFERBSTDLGTTTREPBEACGCHRVDTG---KLMTI 425
DB 313 HLCDDKKQME-----LSL-----NIPVNHGPQBSGSGSLHENSGETSRSL 355
QY 426 LQPODVD 432
DB 356 PAPQDND 362

```

RESULT 12

US-09-019-942-1
 Sequence 1, Application US/09019942

Patent No. 6033855
 GENERAL INFORMATION:
 APPLICANT: Berlin, John
 TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
 TITLE OF INVENTION: DOMAIN POLYPEPTIDES
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/019,942
 FILING DATE: 06-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/068001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 540 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-019-942-1

Query Match 13.3%; Score 541.5; DB 3; Length 540;
 Best Local Similarity 34.0%; Pred. No. 2,1e-39;
 Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

```

QY 31 GGFQGVYKVRHVMKWTWIAIKCPSLHYD---DREKMLLEBAKMEAKFRYLLPYVG 86
DB 27 GASGVSSARRHADMRQVAVK---HLHHTPLDLSERKDVLEAEILHKARFSYLLPILG 83
QY 87 ICRBP--VGLVMEYMETGSLKELKLA---PLPMDLRFRIIHTAVGMFLHCAPILL 140
DB 84 ICNEBEPFIGIVTEYMPNGSLNELHRRKTEYPDVAMPLEFRILHEIALGVNYLHNTTPILL 143
QY 141 HLDKPRANILLDAHNYKISDPGLAKCNGLSHSDLSM---DGLFGTIAVLPERRIR-- 194
DB 144 HHDLKTQNILLDNEHFVKIADFGLSKWRMWSLSQSRSSKAPDG--GTLITMPENYEPG 201
QY 195 EKSRLPDKHDVYSPFAIYWGVLTKCKPFADEKNILHIMVYVKGHRP-----ELPPYCR 249
DB 202 QKSRRA-STKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSGHRPVINEESLPYDIP 260
QY 250 APPRACSHLIRLMORCMQDPRVPRPTFOEITSETEDLCEKPDDEVKETAHDLDVXSPERP 309
DB 261 HHRAR---MISLBSGMQNPDERSFLKCLIELEPVLR----- 295
QY 310 RSEVVPARLKASAPTFDNDYSLSELSQLDSGVSAQVGEPELRSSESSEKLPSSGSGK 369
DB 296 -----TFE-EITFLEAVIQL-----KTKLQSVSSAI 321
QY 370 RLSGVSVDSAFSSRGSLSLSPFERBSTDLGTTTREPBEACGCHRVDTG---KLMTI 425
DB 322 HLCDDKKQME-----LSL-----NIPVNHGPQBSGSGSLHENSGETSRSL 364
QY 426 LQPODVD 432
DB 365 PAPQDND 371

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RESULT 13

US-09-099-041A-2
 Sequence 2, Application US/09099041A

Patent No. 6340576
 GENERAL INFORMATION:
 APPLICANT: Berlin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 TITLE OF INVENTION: PROTEIN FAMILY AND USBS THEREOF
 FILE REFERENCE: 07334-076001
 CURRENT APPLICATION NUMBER: US/09/099,041A
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 09/019,942
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 540
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-099-041A-2

Query Match 13.3%; Score 541.5; DB 3; Length 540;
 Best Local Similarity 34.0%; Pred. No. 2,1e-39;
 Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

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QY 31 GGFQGVYKVRHVMKWTWIAIKCPSLHYD---DREKMLLEBAKMEAKFRYLLPYVG 86
DB 27 GASGVSSARRHADMRQVAVK---HLHHTPLDLSERKDVLEAEILHKARFSYLLPILG 83

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|||
Db 365 PAPQDND 371

Search completed: September 17, 2005, 06:44:08
Job time : 1216.92 secs

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OM protein - protein search, using sw model

Run on: September 16, 2005, 07:27:24 ; Search time 208.039 Seconds
(without alignments)
1929.780 Million cell updates/sec

Title: US-10-658-904-2

Perfect score: 4078
Sequence: 1 MEGDGGTPTWALALRTPDAG.....SLKFGGHPATLLRSKT 784

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3976	97.5	784	2	Q9H4D1	Q9h4d1 homo sapien
2	3959	97.1	784	2	Q96T11	Q96t11 homo sapien
3	3943	96.7	832	1	R1K4_HUMAN	P57078 homo sapien
4	3628	89.0	786	2	Q9ERK0	Q9erK0 mus musculu
5	2541	62.3	720	2	Q7ZYM2	Q7zym2 xenopus lae
6	2514.5	61.7	719	2	Q6GPN2	Q6gpn2 xenopus lae
7	2389.5	58.6	820	2	Q8UH03	Q8juh3 brachydanto
8	1881	46.1	387	2	Q9NTA1	Q9nta1 homo sapien
9	1215.5	29.8	752	2	Q8NFD2	Q8nfd2 homo sapien
10	1196.5	29.3	352	2	Q9H281	Q9h281 homo sapien
11	1141.5	28.0	745	2	Q8BZ25	Q8bz25 m mus muscu
12	569	14.0	584	2	Q8JHU4	Q8jhu4 brachydanto
13	545.5	13.4	539	1	R1K2_MOUSE	P58801 mus musculu
14	541.5	13.3	540	1	R1K2_HUMAN	Q43353 h receptor-
15	541	13.3	1549	2	Q9V4B1	Q9v4b1 drosophila
16	540	13.2	1549	2	Q24241	Q24241 drosophila
17	515	12.6	1136	2	Q9N180	Q9n180 bos taurus
18	514	12.6	1159	2	Q9NCP8	Q9ncp8 drosophila
19	513.5	12.6	1571	2	Q7KJ92	Q7kjb2 drosophila
20	513.5	12.6	1726	2	Q8VC68	Q8vc68 mus musculu
21	512.5	12.6	1943	2	Q61307	Q61307 mus musculu
22	512.5	12.6	2622	2	Q70511	Q70511 rattus norv
23	509.5	12.5	1887	2	Q7Z3G4	Q7z3g4 homo sapien
24	509.5	12.5	4377	1	ANK3_HUMAN	Q12955 homo sapien
25	505	12.4	1004	2	Q7JUNZ0	Q7jun0 caenorhabdi
26	505	12.4	1786	2	Q17344	Q17344 caenorhabdi
27	505	12.4	1809	2	Q17487	Q17487 caenorhabdi
28	505	12.4	1815	2	Q17488	Q17488 caenorhabdi
29	505	12.4	1841	2	Q8MGO0	Q8mg00 caenorhabdi
30	505	12.4	1867	2	Q17486	Q17486 caenorhabdi
31	505	12.4	2039	2	Q17489	Q17489 caenorhabdi

32	505	12.4	6994	2	Q17343	Q17343 caenorhabdi
33	505	12.4	6994	2	Q17490	Q17490 caenorhabdi
34	502	12.3	1145	2	Q7PEZ8	Q7pez8 anopheles g
35	502	12.3	1501	2	Q7OKD3	Q7okd3 anopheles g
36	500.5	12.3	792	2	Q7Q172	Q7q172 anopheles g
37	500	12.3	1719	2	Q13768	Q13768 homo sapien
38	500	12.3	1856	2	Q99407	Q99407 homo sapien
39	500	12.3	1880	1	ANK1_HUMAN	P16157 homo sapien
40	499.5	12.2	1848	2	Q61302	Q61302 mus musculu
41	499.5	12.2	1862	2	ANK1_MOUSE	Q02357 mus musculu
42	485.5	11.9	1762	2	Q88521	Q88521 rattus norv
43	484.5	11.9	3924	1	ANK2_HUMAN	Q01484 homo sapien
44	483.5	11.9	1088	2	Q13484	Q13484 homo sapien
45	483	11.8	1427	2	Q6DDZ1	Q6ddz1 xenopus lae

ALIGNMENTS

RESULT 1	ID	PRELIMINARY:	PRT:	784 AA.
AC Q9H4D1	Q9H4D1			
DT 01-MAR-2001 (TREMBlrel. 16, Created)				
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)				
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)				
DN Protein Kinase.				
GN Name=dk;				
OC Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX NCBI_Taxid=9606;				
RN [1]				
RX SEQUENCE FROM N.A.				
RA MEDLINE=20549657; PubMed=10948194; DOI=10.1074/jbc.M004771200;				
RA Baehr C., Rohrer A., Stempa L., Rincke G., Marks F., Geschwendt M.;				
RT "DK, a novel protein kinase that interacts with protein kinase				
RT Cdelta. Cloning, characterization, and gene analysis.";				
RT J. Biol. Chem. 275:36350-36357(2000).				
CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.				
DR EMBL; AJ278016; CAC04247.1; -.				
DR HSSP; Q60778; 10Y3.				
DR GO; GO:0005524; F:ATP binding; NAs.				
DR GO; GO:0005515; F:protein binding; IP1.				
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.				
DR GO; GO:000468; F:protein amino acid phosphorylation; IDA.				
DR InterPro; IPR002110; ANK.				
DR InterPro; IPR011009; Kinase like.				
DR InterPro; IPR001969; Pept_Asp_AS.				
DR InterPro; IPR000719; Prot_Kinase.				
DR InterPro; IPR008271; Ser_Thr_kin_AS.				
DR InterPro; IPR001245; Tyr_kinase.				
DR Pfam; PF00023; Ank; 10.				
DR Pfam; PF00069; Pkinase; 1.				
DR PRINTS; PR01415; ANKYRIN.				
DR PRINTS; PR0109; TYRKINASE.				
DR ProDom; PD000001; Prot_Kinase; 1.				
DR SMART; SM00248; ANK; 10.				
DR PROSITE; PS50088; ANK_REPEAT; 9.				
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.				
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.				
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.				
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
KW ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;				
KW Transferase.				
SO SEQUENCE 784 AA; 86407 MW; F3C7D5D52A35AF91 CRC64;				
QY	1	MEGDGGTPTWALALRTPDAGFTGWEKVGSGFGGVYKRVHVMKWTWIALIKCSPSLHYDD	60	
Query Match	97.5%;	Score 3976;	DB 2;	Length 784;
Best Local Similarity	98.1%;	Pred. No. 2e-202;		
Matches 769;	Conservative	4;	Mismatches 11;	Indels 0;
		Gaps	0;	

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Db      1 MEGDGTWALALATTPDAGFTGMEKVGSGGFGQVYKVRHVHAKTWTALIKCSPLHADD 60
Qy      61 RERMELEBAKMEMAKFRYIIPYVGICREPVGLVMEYMETGSEKLLASEPLPMDLFR 120
Db      61 RERMELEBAKMEMAKFRYIIPYVGICREPVGLVMEYMETGSEKLLASEPLPMDLFR 120
Qy      121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHKISDPGLAKCNGLSHSDLSMDG 180
Db      121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHKISDPGLAKCNGLSHSDLSMDG 180
Qy      181 LFGTAYLPERPERIKRSKSLFTDKHGVYSFAIYIMGVLTQKKEFADENKILHIMVXVXGH 240
Db      181 LFGTAYLPERPERIKRSKSLFTDKHGVYSFAIYIMGVLTQKKEFADENKILHIMVXVXGH 240
Qy      241 REPPLPVCARAPRACSHLIRLMQRCWQDPRVRPTFOBITSTEDLCERKPDDEVETAYHD 300
Db      241 REPPLPVCARAPRACSHLIRLMQRCWQDPRVRPTFOBITSTEDLCERKPDDEVETAYHD 300
Qy      301 LDVKSPPRPRSRVVPARLKRAAPFPNDYSLSELSQLDSGVSAQVNGEPRELSSSES 360
Db      301 LDVKSPPRPRSRVVPARLKRAAPFPNDYSLSELSQLDSGVSAQVNGEPRELSSSES 360
Qy      361 KLPSGSGKRLSGVSVDSAFSSRGLSLSFEREPESTDIGTTRAPPEBACGCHRVDPDS 420
Db      361 KLPSGSGKRLSGVSVDSAFSSRGLSLSFEREPESTDIGTTRAPPEBACGCHRVDPDS 420
Qy      421 KLMKLLQPOVDLALDSGASLHLAVEAQEBCAKWLLNNANPNLSNRSGSTPLHMAVE 480
Db      421 KLMKLLQPOVDLALDSGASLHLAVEAQEBCAKWLLNNANPNLSNRSGSTPLHMAVE 480
Qy      481 BRVRGVVELLARKISVNAKDDQMTALHFAQNDDESTRLLLEKNASVNEVDEGRTP 540
Db      481 BRVRGVVELLARKISVNAKDDQMTALHFAQNDDESTRLLLEKNASVNEVDEGRTP 540
Qy      541 MHVACQHGQENIVRILRRGVDSLOGKQAWMLPLHYAMQGHPLVTKLAKOPGVSVNAQ 600
Db      541 MHVACQHGQENIVRILRRGVDSLOGKQAWMLPLHYAMQGHPLVTKLAKOPGVSVNAQ 600
Qy      601 TLDSGTPHLAAQRGHYRVARILLIDCSDVNCSLLAQPLHVAEETGHTSTARILLHRG 660
Db      601 TLDSGTPHLAAQRGHYRVARILLIDCSDVNCSLLAQPLHVAEETGHTSTARILLHRG 660
Qy      661 AKKAVTSQGTALHLAANGHLATYKILVEEKADVLARGPLNOTALHAAHGHSEVYE 720
Db      661 AKKAVTSQGTALHLAANGHLATYKILVEEKADVLARGPLNOTALHAAHGHSEVYE 720
Qy      721 ELVSADVIDLFDQGLSALHLAAQGRHAQTVETLLRHGAHINLQSLKFGQGHGPAATILLR 780
Db      721 ELVSADVIDLFDQGLSALHLAAQGRHAQTVETLLRHGAHINLQSLKFGQGHGPAATILLR 780
Qy      781 RSKT 784
Db      781 RSKT 784

RESULT 2
ID Q96T11 PRELIMINARY; PRT; 784 AA.
AC Q96T11;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14518.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

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RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yaeda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Komoto H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kinata M., Watanabe M., Hiraoa S., Chiba S., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mutsaers K., Yuuki H., Oshino H., Ichihara T., Shibata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Taehiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama H., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RT Nat. Genet. 36:40-45 (2004).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK027424; BAB5102.1; -.
DR HSSP; Q60778; 10Y3.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; ANK.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR012445; Tyr_kinase.
DR Pfam; PF00023; Ank; 10.
DR Pfam; PF00063; Pkinase; 1.
DR PRINTS; PR01415; ANKRYIN.
DR PRINTS; PR01019; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00248; ANK; 10.
DR PROSITE; PS50086; ANK_REPEAT; 9.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00144; ASP_PROTEASE; UNKNOWN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW Transferase
SQ SEQUENCE 784 AA; 86348 MW; 05B193B4EBB955AF CRC64;

Query Match 97.1%; Score 3959; DB 2; Length 784;
Best Local Similarity 97.8%; Pred. No. 1.6e-201;
Matches 767; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MEGDGTWALALATTPDAGFTGMEKVGSGGFGQVYKVRHVHAKTWTALIKCSPLHADD 60
Db 1 MEGDGTWALALATTPDAGFTGMEKVGSGGFGQVYKVRHVHAKTWTALIKCSPLHADD 60
Qy 61 RERMELEBAKMEMAKFRYIIPYVGICREPVGLVMEYMETGSEKLLASEPLPMDLFR 120
Db 61 RERMELEBAKMEMAKFRYIIPYVGICREPVGLVMEYMETGSEKLLASEPLPMDLFR 120
Qy 121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHKISDPGLAKCNGLSHSDLSMDG 180
Db 121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHKISDPGLAKCNGLSHSDLSMDG 180

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Db 121 ITHETAVGNRIHCAAPRLHLDIKPANILLDAHYHVKISDFGLAKCNGLSHSHLSMDG 180
 QY 181 IEGTIAAYPERIRREKSLFDTKHDVYSFAIYIWGLYLOKPPADKNTLIHIMVYKXH 240
 Db 181 LFGTIAAYPERIRREKSLFDTKHDVYSFAIYIWGLYLOKPPADKNTLIHIMVYKXH 240
 QY 241 REBLPVCAARRACSHLIRLMQRCMQSPRRPPTFOETSTTEPLCEPDDEVETAMD 300
 Db 241 REBLPVCAARRACSHLIRLMQRCMQSPRRPPTFOETSTTEPLCEPDDEVETAMD 300
 QY 301 LVKSPSPERSEVPARLRASAPFPDNYSLSELLSQDGSVQAVQVEPELSRSSSES 360
 Db 301 LVKSPSPERSEVPARLRASAPFPDNYSLSELLSQDGSVQAVQVEPELSRSSSES 360
 QY 361 KLPSGSGKRLSGVSVDSAFSGSLSLSPERPEPSTDLGTTTRPEEBAACGHRVDT 420
 Db 361 KLPSGSGKRLSGVSVDSAFSGSLSLSPERPEPSTDLGTTTRPEEBAACGHRVDT 420
 QY 421 KLMTIOPDVLALDGSALHLAVEAQECACAKLLNNANPNLSNRSGSTPLHMAVE 480
 Db 421 KLMTIOPDVLALDGSALHLAVEAQECACAKLLNNANPNLSNRSGSTPLHMAVE 480
 QY 481 RRVAGVVELLARKISVNAKDEDOQTALHFAAONGDESSSTRLLEKNAVNEVEEGRT 540
 Db 481 RRVAGVVELLARKISVNAKDEDOQTALHFAAONGDESSSTRLLEKNAVNEVEEGRT 540
 QY 541 MHVACQGGENTVRLIRRGVDVSLQKXAMLPHYAANQGHLPYKLLAKPGVSVNAQ 600
 Db 541 MHVACQGGENTVRLIRRGVDVSLQKXAMLPHYAANQGHLPYKLLAKPGVSVNAQ 600
 QY 601 TLDRPTPLHAAQRGYRVARILIDCSVNVCSLLAQPLHVAATGTSTARLLHNG 660
 Db 601 TLDRPTPLHAAQRGYRVARILIDCSVNVCSLLAQPLHVAATGTSTARLLHNG 660
 QY 661 AGKEATSDGYTALHAAARNGHATVYKLVYKADVLARGPLNQTALHAAAGHSEVE 720
 Db 661 AGKEATSDGYTALHAAARNGHATVYKLVYKADVLARGPLNQTALHAAAGHSEVE 720
 QY 721 ELVSADVIDLFDROGLSALHLAAQGHAAQTVELLRHGHINQSLKFGQGHGPAATLIR 780
 Db 721 ELVSADVIDLFDROGLSALHLAAQGHAAQTVELLRHGHINQSLKFGQGHGPAATLIR 780
 QY 781 RSKT 784
 Db 781 RSKT 784
 Db 781 RSKT 784

RESULT 3
 ID RIK4 HUMAN STANDARD; PRT; 832 AA.
 AC P57078; Q96RH0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Serine/threonine-protein kinase RIK4 (EC 2.7.1.37) (Receptor-
 interacting serine-threonine kinase 4) (Ankyrin repeat domain protein
 3) (PKC-delta-interacting protein kinase).
 GN Name=RIK4; Synonyms=ANKRD3, DIK;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fetal kidney, and Fetal lung;
 RA Shimizu N., Kudoh J., Shibuya K.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Tokoki Y., Choi D.-K., Soeda E.,
 RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schilhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Saeki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramer J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
 RA Wehmeyer S., Borzay K., Gardiner K., Nizetic D., Francis F.,
 RA Lehnach H., Reinhardt R., Yaspo M.-L.,
 RL "The DNA sequence of human chromosome 21.",
 RT Nature 405:311-319 (2000).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P57078-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P57078-2; Sequence=VSP_004862;
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 10 ANK repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, AB047783; BAB56136.1; -
 CC EMBL, AP001743; BAA95526.1; -
 CC HSR; Q60778; 10Y3.
 CC GeneW; HGNC:496; RIK4.
 DR MIM; 605706; -
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr Pkin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00023; Ank; 10.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00248; ANK_10.
 DR PROSITE; PS50088; ANK_REPEAT; 9.
 DR PROSITE; PS50297; ANK_REPEAT; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Alternative splicing; ANK repeat; ATP-binding; Repeat;
 KW Serine/threonine-protein kinase; Transferase;
 KW Domain
 FT DOMAIN 22 286
 FT REPEAT 485 514 ANK 1.
 FT REPEAT 518 547 ANK 2.
 FT REPEAT 551 580 ANK 3.
 FT REPEAT 584 613 ANK 4.
 FT REPEAT 617 647 ANK 5.
 FT REPEAT 651 680 ANK 6.
 FT REPEAT 684 713 ANK 7.
 FT REPEAT 717 746 ANK 8.
 FT REPEAT 750 780 ANK 9.
 FT REPEAT 782 811 ANK 10.
 FT NP_BIND 28 36 ATP (By similarity).
 FT BINDING 51 51 ATP (By similarity).
 FT ACT_SITE 143 143 Proton acceptor (By similarity).
 FT VARSPIC 278 325 Missing (in isoform 2).
 FT FTId=VSP_004862.
 FT CONFLICT 714 714 M -> V (i1n Ref. 1).
 FT SEQUENCE 832 AA; 91610 MW; 5D8FPD5F047ECB CRC64;
 Query Match 96.7%; Score 3943; DB 1; Length 832;
 Best local Similarity 92.4%; Pred. No. 1.2e-200;

Matches	769; Conservative	4; Mismatches	11; Indels	48; Gaps	1;
Qy	1	MEGGGTWALALTTFDAGETGMEKVGSGGFGVYRVHVMKTWAIKCSPSLHVD	60		
Db	1	MEGGGTWALALTTFDAGETGMEKVGSGGFGVYRVHVMKTWAIKCSPSLHVD	60		
Qy	61	RRRMLLEAKKEMAKFRYILPVYIGREPIGVMEWMSGLEKILASREPLMDLFR	120		
Db	61	RRRMLLEAKKEMAKFRYILPVYIGREPIGVMEWMSGLEKILASREPLMDLFR	120		
Qy	121	IIHETAVGNPLHCAAPPLHLDLKPANILLDAHVXISDFGLAKCNGLSHSDLSMDG	180		
Db	121	IIHETAVGNPLHCAAPPLHLDLKPANILLDAHVXISDFGLAKCNGLSHSDLSMDG	180		
Qy	181	LFGTAYIPPERIRKRSKLPFTKADYVSPALYINQVLTKQKPFADKKIILHMVKVKGH	240		
Db	181	LFGTAYIPPERIRKRSKLPFTKADYVSPALYINQVLTKQKPFADKKIILHMVKVKGH	240		
Qy	241	RPELPVCRARPRACSHILRLMQRQMGDPVRVPTFGQNGELIRQVLAALLPVTGRW	300		
Db	241	RPELPVCRARPRACSHILRLMQRQMGDPVRVPTFGQNGELIRQVLAALLPVTGRW	300		
Qy	277	-----OETSETEDLCCKPDDEVKETAHDLDVKSPPERPSE	312		
Db	301	RSPGGRFLSEVILRVTCPLSSPOEITSFTEDLCEKPDDEVKETAHDLDVKSPPERPSE	360		
Qy	313	VVPARLKRAAPFTPNNDYSLSELSQDLSGVSAQAVEGPELSRSSSESKLPSGSGSKRLS	372		
Db	361	VVPARLKRAAPFTPNNDYSLSELSQDLSGVSAQAVEGPELSRSSSESKLPSGSGSKRLS	420		
Qy	373	GVSSVDSAPSSRGSLSLSPEREPTSDGTRRPREBAOCGRVADTKMLKTILOPOVD	432		
Db	421	GVSSVDSAPSSRGSLSLSPEREPTSDGTRRPREBAOCGRVADTKMLKTILOPOVD	480		
Qy	433	LALDSGASLHLAVEAGQECACKWILLNNANPNLSNRGSTRPLHNAVERRYVVELLLA	492		
Db	461	LALDSGASLHLAVEAGQECACKWILLNNANPNLSNRGSTRPLHNAVERRYVVELLLA	540		
Qy	493	RKISVNADEDMWTALHPAONGDSSSTRLLLEKKAASVNEVDPEERTPMHVAOCHQENI	552		
Db	541	RKISVNADEDMWTALHPAONGDSSSTRLLLEKKAASVNEVDPEERTPMHVAOCHQENI	600		
Qy	553	VRIILRRGVDSLQSKDAMLPLHYAMOGHLPYVLAKKOPVSVNAOTLDORTPLHLAA	612		
Db	601	VRIILRRGVDSLQSKDAMLPLHYAMOGHLPYVLAKKOPVSVNAOTLDORTPLHLAA	660		
Qy	613	QRGHYRVARILLDCSDVNVCSLLAQTPPLHVAATGHTSTARLLHKGAKKAVTSDGYT	672		
Db	661	QRGHYRVARILLDCSDVNVCSLLAQTPPLHVAATGHTSTARLLHKGAKKAVTSDGYT	720		
Qy	673	ALHLLAARNGHLATVQLVBEKADVLRGPPLNOTALHLLAARNGHSHVVELYSADYIDLFD	732		
Db	721	ALHLLAARNGHLATVQLVBEKADVLRGPPLNOTALHLLAARNGHSHVVELYSADYIDLFD	780		
Qy	733	EOGSAHLHAAQGRHAQVETLLRHGAHINLOSLEKFGOGHGPATLLRRSKT	784		
Db	761	EOGSAHLHAAQGRHAQVETLLRHGAHINLOSLEKFGOGHGPATLLRRSKT	832		
RESULT 4					
QSERKO	PRELIMINARY;	PRT;	786 AA.		
AC	QSERKO;				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)				
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)				
DE	PKC-regulated kinase PKC (Receptor-interacting serine-threonine kinase				
DE	4).				
GN	Name=Ripk4; Synonym=Ankrd3;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				

RN	[1]	SEQUENCE FROM N.A.
RP	STRAIN=BALB/c;	
RC	MEBLINE=21293027; PubMed=11278382;	
RX	MEBLINE=21293027; PubMed=11278382;	
RA	Chen L., Halder K., Ponda M., Cariappa A., Rowitch D., Pillai S.;	
RT	"Protein kinase C-associated kinase (PKC), a novel membrane-	
RT	associated, ankyrin repeat-containing protein kinase.";	
RU	J. Biol. Chem. 276:21737-21744(2001).	
RN	[2]	SEQUENCE FROM N.A.
RP	STRAIN=BALB/c;	
RC	Chen L., Halder K., Cariappa A., Pillai S.;	
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	
RN	[3]	SEQUENCE FROM N.A.
RP	STRAIN=NMRI; TISSUE=Mammary tumor;	
RC	MEBLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603999;	
RX	MEBLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603999;	
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,	
RA	Alschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywnicki M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,	
RA	Jones S.J., Maira M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[4]	SEQUENCE FROM N.A.
RP	STRAIN=NMRI; TISSUE=Mammary tumor;	
RC	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	
DR	EMBL; AF302137; AAC30871.2; -	
DR	EMBL; BC057871; AA57871.1; -	
DR	HSSP; Q60778; 1073.	
DR	MGD; MGI:191638; Ripk4.	
DR	GO; GO:0005524; F:ATP binding; IEA.	
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0016740; F:transferase activity; IEA.	
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	
DR	InterPro; IPR002110; ANK.	
DR	InterPro; IPR011009; Kinase like.	
DR	InterPro; IPR000719; Prot kinase.	
DR	InterPro; IPR008271; Ser_Thr_kinase.	
DR	InterPro; IPR01245; Tyr_kinase.	
DR	Pfam; PF00023; Ank; 10.	
DR	PRINTS; PRO0109; TYRKINASE.	
DR	PRINTS; PRO0145; ANKYRIN.	
DR	ProDom; PD000001; Prot kinase; 1.	
DR	PROSITE; PS50088; ANK_REPEAT; 9.	
DR	PROSITE; PS50297; ANK_REPEAT; 1.	
DR	PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
KW	ANK repeat; ATP-binding; Kinase; Receptor;	
KW	Serine/threonine-protein kinase; Transferase.	
SQ	SEQUENCE 786 AA; 86612 MW; 66CE2C25EB9A40C CRC64;	
Query Match	89.0%; Score 3628; DB 2; Length 786;	
Best Local Similarity	88.9%; Pred. No. 5; Se-184;	

Matches	699;	Conservative	34;	Mismatches	51;	Indels	2;	Gaps	1;
QY	1	MEGDGTPWALALRTFDAGEFTGKVGSGGFGGVYRVHVMKWTWLAIKCPSLHAYDD							60
DB	1	MEGDEGRGMAWGLATFPDAGBFAKMEKVGSGGFGGVYRVHVMKWTWLAIKCPSLHAYDD							60
QY	61	RRRMLLEBAKMEAKRRYIIPVYGIQCEPVGLVMEWETGSLKTLASPLPMDLAFR							120
DB	61	RRRMLLEBAKMEAKRRYIIPVYGIQCEPVGLVMEWETGSLKTLASPLPMDLAFR							120
QY	121	IIHERAVGNFLHCAAPPLHDLKPANLIDAHYHVKISDGLAKCNGLSHSHDLSMDG							180
DB	121	IYHERAVGNFLHCAAPPLHDLKPANLIDAHYHVKISDGLAKCNGLSHSHDLSMDG							180
QY	181	LEGTIAYLPERIRKESRLFTDHDVYSPFAIYWGVLQKKEPADKNIHIMVYKXH							240
DB	181	LEGTIAYLPERIRKESRLFTDHDVYSPFAIYWGVLQKKEPADKNIHIMVYKXH							240
QY	241	REPLPPVCAAPRAASHILRMQRCMGDPVRPPTFOETSTEDLCERPDDEVKETAHD							300
DB	241	REPLPPVCAAPRAASHILRMQRCMGDPVRPPTFOETSTEDLCERPDDEVKETAHD							300
QY	301	LDVKSPPPEPRSEVP--ATLKASAPTPNDYSLSELSQLDSGVQAVEGPEELSRSS							358
DB	301	LDVKSPPPEPRSEVP--ATLKASAPTPNDYSLSELSQLDSGVQAVEGPEELSRSS							358
QY	359	BSKLSGSGSGKRLSGVSVDSAFSSRGSLSLSPEREPSTSDGTRRPEEAACGCHVAD							418
DB	359	BSKLSGSGSGKRLSGVSVDSAFSSRGSLSLSPEREPSTSDGTRRPEEAACGCHVAD							418
QY	419	TSKLMKILOPOVDLALDSGASLHLAVAGOECAKMLLNANPNLSNRGSTRPLHMA							478
DB	419	TSKLMKILOPOVDLALDSGASLHLAVAGOECAKMLLNANPNLSNRGSTRPLHMA							478
QY	479	VERBRVGVVELLARKISVNAKDEQWTLAHPAONGDESTRLLKKNASVNEVDFEGR							538
DB	479	VERBRVGVVELLARKISVNAKDEQWTLAHPAONGDESTRLLKKNASVNEVDFEGR							538
QY	539	TEMVAVACQHQENIVAILLRGVVSLQKQDAMLPLAVAMQGHLPYVLAKQPGSVN							598
DB	539	TEMVAVACQHQENIVAILLRGVVSLQKQDAMLPLAVAMQGHLPYVLAKQPGSVN							598
QY	599	AOTLDGRTPLHAAQGHYRVARILIDCSNVVCSLQOTPLHVAAGTGHSTARLLH							658
DB	599	AOTLDGRTPLHAAQGHYRVARILIDCSNVVCSLQOTPLHVAAGTGHSTARLLH							658
QY	601	AOTLDGRTPLHAAQGHYRVARILIDCSNVVCSLQOTPLHVAAGTGHSTARLLH							660
DB	601	AOTLDGRTPLHAAQGHYRVARILIDCSNVVCSLQOTPLHVAAGTGHSTARLLH							660
QY	659	RAGAGKAVSDGVTALHLAABNGHLATVTLVEBKADVAFRGPLNOTALHLAAAGHSEV							718
DB	659	RAGAGKAVSDGVTALHLAABNGHLATVTLVEBKADVAFRGPLNOTALHLAAAGHSEV							718
QY	719	VEELVSADYIDLFEQGLSALHLAAQGRHAQVETLLRHGAHINIQLKFGGHPAATL							778
DB	719	VEELVSADYIDLFEQGLSALHLAAQGRHAQVETLLRHGAHINIQLKFGGHPAATL							778
QY	779	LRRSKT 784							
DB	781	LRRSKT 786							

RP	SEQUENCE FROM N.A.
RC	TISUE=Embryo;
RX	MEDLINE=22368257; PubMed=12477937; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA	Ditachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Browne E.M., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA	Falley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISUE=Embryo;
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.;
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT	initiative."
RT	Dev. Dyn. 225:384-391 (2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISUE=Embryo;
RA	Klein S., Strausberg R.;
RA	Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
CC	- 1. Similarity: Belongs to the Ser/Thr protein kinase family.
DR	EMBL; BC043634; AAA43634.1; -.
DR	HSP; P42773; IB09.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR	GO; GO:0004648; F:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR011009; Kinase like.
DR	InterPro; IPR000719; Prot kinase.
DR	InterPro; IPR008271; Ser Thr Pkin_AS.
DR	InterPro; IPR001245; Tyr_kinase.
DR	Pfam; PF00023; Ank; 8.
DR	Pfam; PF00069; Kinase; 1.
DR	PRINTS; PR01415; ANKYRIN.
DR	PRINTS; PR00109; TYRKINASE.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SM00248; ANK_8.
DR	PROSITE; PS50086; ANK_REPEAT; 7.
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR	PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW	transferase.
SC	SEQUENCE 720 AA; 79853 MW; F0BB851A0B380ADB CRC64;
QY	Query Match 62.3%; Score 2541; DB 2; Length 720;
QY	Best Local Similarity 70.1%; Pred. No. 1.8e-126;
DB	Matches 491; Conservative 86; Mismatches 117; Indels 6; Gaps 3;
QY	1 MEGDGTWALALRTFDAGEFTGKVGSGGFGGVYRVHVMKWTWLAIKCPSLHAYDD 60
DB	2 VDKGASPDWMDGLRTFDGSRFCGKVGSGGFGGVYRVHVMKWTWLAIKCPSLHAYDD 61

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OY 61 RERMBLEBAKKEMAKFRYILPYVIGCREPVGVLVMEYMGTSLEKLLASEPLPMDLFR 120
DB 62 KERVLVEBAKKEMAKFRCLIPYVIGSDPVGVLVMEYMGTSLEKLLASECLPMDLFR 121
OY 121 IIHETAVGNMFLHOMAPPLHLDLKPANILLDAHVYKISDFGLAKCNGLSHSHDLSMDG 180
DB 122 IIHETAVGNMFLHOMAPPLHLDLKPANILLDGHVYKISDFGLAKCNGLSHSHDLSMDG 181
OY 181 LFGTAYLPPERRIREKSRFLDTPKHVYSFAIVYMGVLTOKKPRADENKIILHIMKVYKGH 240
DB 182 ICGTIAYLPPERFKKRCFDTKHVYSFAIVYMGVLTOKKPRADENKIILHIMKVYKGG 241
OY 241 RPELPVPCRARPRASHLIRLMQRCMGDPVRVPTFOETSTEDLCKEPPDEV--KETA 298
DB 242 RPDIGQVRVPRQOQGMILQMKCEKMDKPRPFQOETSTEDLCTKHEDETGSAQVG 301
OY 299 HDLD--VKSPPRSEVVVPAKLKRAAPFPDNDYSLSEILSQDGSQAVAGEPBLRS 356
DB 302 QELQKVGKEAPQWMTSQABGKRSPTPAFPDYSLSEILSQDGSIGQMEGPGCLSHS 361
OY 357 SSESLLPSSGSGKRLSTVSVDSAFSSRGSLSLSTFRSPSTDLGTRRPEBAAGCHRV 416
DB 362 VSEPLAS--SDKRLSGVSVDSAFSSRGSLSLSTFKDCSVLDISASDLQKKKVDALVG 419
OY 417 RDTSLKMLIOPQVDLALDGSASLHLAVEAGQECAMILLNANNPNLSNRSGSTPLH 476
DB 420 GDTALTLKILPOQVDVIVPEGSSSLHLAVESQGECKALLVYASNMNTLTKSTPLH 479
OY 477 MAVERRVGVVVELLIARKISVANAKEDQWTAHPAONGDESSSTLLLEKNAVNDPE 536
DB 480 IASDKKIKVIELLIGKKIHVNAKEDLFTALHFAONGDECTTMLLEKNAVINEVDIK 539
OY 537 GRTPEHVACQHQENIVILLRGDVSLQGDMLPLHYAMQCHLPIVYLLAKQPGVS 596
DB 540 GRTPLHVAACQHQENIVRFLRGADLTFKQGDNLALHYAMQCHLPIVYLLAKQPGAN 599
OY 597 VNAQTLDRTPPLHLAARGHYVAVAILIDLCSDVAVCSLLAQTPHLVAETGHTSTABL 656
DB 600 INAQTSIDRTPLHLAARGHYVAVAILIDVLCSDVAVCSLLAQTPHLVAETGHTSTABL 659
OY 657 LHRGAGKEAVTSDGYTALHLAARNGHLATVKLLVERKADV 696
DB 660 LSRGASINAVTTEGFTALDLASNLGHYSAVKLLMDEQSDV 699
RESULT 6
OQ6PN2 PRELIMINARY; PRT; 719 AA.
ID OQ6PN2;
AC OQ6PN2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, last annotation update)
DB MGC82765 protein.
GN Name=MGC82765;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
OC NCBI_taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22389557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheinen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Scheifer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.W., Butcherfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smaltz D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DB EMBL: BC073081; AAF73081.1; -.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR001009; Kinase like.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR008271; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00023; Ank. 8.
DR Pfam: PF00069; Kinase. 1.
DR PRINTS: PR01415; ANKTRIN.
DR PROSITE: PRO0109; TYRKINASE.
DR PRODOM: PD000001; Prot_kinase; 1.
DR SMART: SM00248; ANK. 8.
DR SMART: SM00220; S_TKC. 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS50088; ANK_REPEAT. 7.
DR PROSITE: PS50297; ANK_REPEAT_REGION. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
KW ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW transferase.
SQ SEQUENCE 719 AA; 80027 MW; CB23FE8A5CA14B77 CRC64;
Query Match 61.7%; Score 2514.5; DB 2; Length 719;
Best Local Similarity 69.7%; Pred. No. 47e-125;
Matches 487; Conservative 89; Mismatches 124; Indels 5; Gaps 2;
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QY 241 REELPPVCRAPRACSHLIRLMQRCWQDPRVRPTFOITSTEDLCEKPDDEVKETAHD 300
DB 242 REDLSQIPRVRPOOCQGMIOIMKECMNDKPRPTFOITSTETELCTHEDETSQVOTQ 301
QY 301 L---DYKSPPEERSEVVPARLKRASAPFPDNDYSISELLSQDQSGVQAVQEPPELSRSS 357
DB 302 LIQKVTQDALEKRTSQABGKRSSTPAFGKDYISELLSQDSDSGISQWEPRLCSHSV 361
QY 358 SSSKLPSSSGKRLSGVSSVDSAFSSRGLSLSFERBPSTDLGTTTRRPEERACQCHVR 417
DB 362 SRRPOLAS--SDKRLSGVSSVDSAFSSRGLSLSFERKQSVLISASDQKKLVAVIYQG 419
QY 418 DTSKMLKTIQPOVDVLLDQSGSLHLAVEAQCEBACAKLLNNANPNLSNRGSTPLM 477
DB 420 DTTKMLKTIQPOVDVLLIEGRSSLHLAVENQCEBACAKLLLYNASPMNTNKKSGSTPLM 479
QY 478 AVEERRVGVVELLARKISVNAKDEQWTAHPAAQNGESSSTRLLEKNAVNEVDPEG 537
DB 480 ASDKCLKNIVELLVKKLVNNTKDEHFTALHFSAQNGECITTRMLLEKNAVTEVDIKG 539
QY 538 RTRPVACQHQENITVIRLLRQGVDSIQKXAMPLHYAAMQGHLPVYKLAKQPGVSV 597
DB 540 RTRPVACQHQENITVIRVIRRGADLTFKQDNMLALHYAAMQGHLPVYKLAKQPGANI 599
QY 598 NQOTLDGRTPLHLAQRGHYRVARILIDCSQVNVCSLLAQTPHYAATGHTSTRALL 657
DB 600 NQOTSDGRSPHLMAQRGHYRVARILVDRCVNIIPSNLMKTPHYAATGHTSTRALL 659
QY 658 HRGAGKEAVTSDGYTALHLAARNGHATVYKLVEEKADY 696
DB 660 SRGASINALTTRGFTALDLASNLGHYSAVKLMDQSNV 698

RESULT 7
ID 08JH03 PRELIMINARY; PRT; 820 AA.
AC 08JH03,
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE Protein kinase PKK.
GN Name=PKK; ORFNames=zgc:55705;
OS Brachydanio rerio (Zebrafish).
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22191376; PubMed=12091384; DOI=10.1074/jbc.M202222200;
RA Muto A., Rutland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,
RA Chen F.F., Lin A.J., Mak T.W., Nunez G., Inohara N.,
RA "Protein kinase C-associated kinase (PKK) mediates Bcl10-independent
RT NF-kappa B activation induced by phorbol ester.",
RL J. Biol. Chem. 277:31871-31876(2002).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Smetten C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.B.,
RA Brownstein M.J., Usdin T.B., Toehyunk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skaleck U., Smalley D.E., Scherch A., Schein J.E.,
RA Jones S.U., Maitra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=AB; TISSUE=whole body;
RA Strausberg R.,
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AF487541; AAM76921.1; -
DR EMBL: BC045432; AAH45432.1; -
DR HSSP: P16157; IN11.
DR ZFIN: ZDB-GENE-040426-2042; zgc:55705.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF00023; Ank; 10.
DR PRINTS: PR01415; ANKRIN.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00248; ANK; 10.
DR PROSITE: PS50088; ANK_REPEAT; 9.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
DR ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW Transferrase.
SQ SEQUENCE 820 AA; 89985 MW; 4A53D6A99B3E8B90 CRC64;

Query_Match 58.6%; Score 2389.5; DB 2; Length 820;
Best Local Similarity 61.3%; Pred. No. 2.3e-118;
Matches 471; Conservative 110; Mismatches 168; Indels 19; Gaps 8;

QY 1 MEGDGTPEWALATRTPDAGFTGKEKVGSGFGQVYVVRHVMTWLAKCPSLSHYVD 60
DB 1 MDVPSNSGIMGLKTPFASRFGSKGSGGFGQVYVVRHMOKMTWLAKCPSLHSD 60
QY 61 BERMELEBAKMKEMAKERYILLPVYIGREBVGVLWMEYETGSLBKLIASEPLPMDLPR 120
DB 61 KERARLEBAKMKEMAKERYILLPVYIGREBVGVLWMEYETGSLBKLIASEPLPMDLPR 120
QY 121 ITHETAVGMNPLHCAAPPLHLHLDPANITLDAHNVKISDRLAKCKGSLSHSDLSMDG 180
DB 121 ITHETAVGMNPLHCAAPPLHLHLDPANITLDAHNVKISDRLAKCKGSLSHSDLSMDG 180
QY 181 LEFTAYVLPERRIREKSLPTKEDVYSFAIVYGVLTQCKPFADKNIILHIMVYVKGH 240
DB 181 FCGITAYVLPERRIREKSLPTKEDVYSFAIVYGVLTQCKPFADKNIILHIMVYVKGH 240
QY 241 REELPPVCRAPRACSHLIRLMQRCWQDPRVRPTFOITSTEDLCEKPDDEVKETAHD 300
DB 241 REDLSQIPRVRPOOCQGMIOIMKECMNDKPRPTFOITSTETELCTHEDETSQVOTQ 300
QY 301 LDVQSP-PEPRP-----EVVPAKLKRASAPFPDNDYSISELLSQDQSGVQAVQEPPELS 354
DB 301 BEPCSPCAPASSSEGTNDQKVPKPSAWLP--EKQYSLSELTQDSDGSRSLNVQV-- 356
QY 355 RSSSSKLPSSSGKRLSGVSSVDSAFSSRGLSLSFERBPSTDLGTTTRRPEERACQCH 414
DB 357 -ESLESK---DNTSRGLSGVSSVDSAFSSRGLSLSFERBPSTDLGTTTRRPEERACQCH 410
QY 415 RVRDTSKMLKTIQPOVDVLLDQSGSLHLAVEAQCEBACAKLLNNANPNLSNRGSTPLM 474
DB 411 RTEDIAKMLKTIQPOVDVLLDQSGSLHLAVEAQCEBACAKLLNNANPNLSNRGSTPLM 470

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QY 475 LHMVERKVRGVVELLARK-1SVNAKEDDQMTALHFAAONGDESSFTLLKRNASVNEV 533
DB 471 LHQAEEKLKQKSELISRKTTNVAKDEDTPTLHFAAONGDELTTLDRSSINET 530
QY 534 DFEGRTPMNVACOHQENIVRIILRGVDSLOGKDAWLPHTYAAOQHLPYVKLLAKOP 593
DB 531 DAQGRTPPHIACHHQENIVVLLSRGADVHKGDMDPTALHAAKMHGILVLLVYQA 590
QY 594 GVSVAAGTLTGRTPLHAAQRHYVARIIDLCSDVAVCSLACTPLHVAAGTGTSTA 653
DB 591 GADVAGQTSRDSRPLHLASORGQYVARILVELGANVHLTSPDLVAPLHVAAGTGTSTS 650
QY 654 RLLHRRGAKGKAVNSDGYTALHAAQRHIAATVVKLVKSKADVYLRGPILOTALHAAH 713
DB 651 RLLVHNDHDIKSRITNGCTALHAAQKGLPTVKLLAGADPESVNDHLPCHLAAQN 710
QY 714 GHSEVVEELV--SADVIDLFDEQGLSALHAAQGRHAQTVETLLRHGA 759
DB 711 GHCEVVKELLRSCSDVANAQRNGLTALHAAVSGGHKALCVLLEGGA 758

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RESULT 8

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QNTAL ID QNTAL PRELIMINARY; PRT; 387 AA.
AC Q9NTAL:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp434B2328 (Fragment).
GN Name=DKFZp434B2328;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RG The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osaenger A., Pobo G., Han M., Wiemann S.;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137448; CAB70741.2; -.
DR ANK repeat; Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 387 AA; 41831 MW; FEEBFP99A7F4E59C CRC64;

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Query Match 46.1%; Score 1881; DB 2; Length 387;
 Best Local Similarity 96.1%; Pred. No. 7, 5e-92;
 Matches 372; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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QY 388 SDLGTRRPEEACCGHVRDTSKMKITIQPDVDLADSGSLHAAVEAQSECAKWL 457
DB 1 ADLGTTDVQKKLVDAIVSGDTSKMKITIQPDVDLADSGSLHAAVEAQSECAKWL 60
QY 458 LNNANPNVSNRSGSTPLMAVERVGVVELLARKISVNAKDEDDQMTALHFAAONGDE 517
DB 61 LNNANPNVSNRSGSTPLMAVERVGVVELLARKISVNAKDEDDQMTALHFAAONGDE 120
QY 518 SSTRLLLEKNAVNEVDPEGRTPMNVACOHQENIVRIILRGVDSLOGKDAWLPHTYA 577
DB 121 SSTRLLLEKNAVNEVDPEGRTPMNVACOHQENIVRIILRGVDSLOGKDAWLPHTYA 180
QY 578 ANOQHLPYVKLLAKOPGVSVNAQTLDGRTPLHAAQRHYVARIIDLCSDVAVCSLLA 637
DB 181 ANOQHLPYVKLLAKOPGVSVNAQTLDGRTPLHAAQRHYVARIIDLCSDVAVCSLLA 240
QY 638 QTPPLHVAAGTGTSTARLILHRGAKGKAVNSDGYTALHAAQRHIAATVVKLVKSKADV 697
DB 241 QTPPLHVAAGTGTSTARLILHRGAKGKAVNSDGYTALHAAQRHIAATVVKLVKSKADV 300
QY 698 AAGPILOTALHAAHGHSEVVEELVADVIDLFDEQGLSALHAAQGRHAQTVETLLRH 757

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DB 301 ARGPILOTALHAAHGHSEVVEELVADVIDLFDEQGLSALHAAQGRHAQTVETLLRH 360
QY 758 GAHINLOSLEKPGGHPAATLLRRSKT 784
DB 361 GAHINLOSLEKPGGHPAATLLRRSKT 387

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RESULT 9

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Q9NPD2 ID Q9NPD2 PRELIMINARY; PRT; 765 AA.
AC Q9NPD2:
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE X-kinase (Protein kinase PKC) (Ankyrin repeat and kinase domain
DE containing 1).
GN Name=PKC2; Synonyms=ANKK1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14741327; DOI=10.1016/S0920-9964(03)00220-2;
RA Duberret C., Gouya L., Hanoun N., Deybach J.-C., Ades J., Hamon M.,
RA Gorwood P.;
RT "The 3' region of the DRD2 gene is involved in genetic susceptibility
RT to schizophrenia."
RL Schizophren. Res. 67:75-85(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Neville M.J., Johnstone E.C., Walton R.T.;
RT "Identification and characterization of ANKK1: a novel kinase gene
RT closely linked to DRD2 on chromosome band 11q23.1."
RL Hum. Mutat. 23:540-545(2004).
CC -1. SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF555298; AA091924.1; -.
DR EMBL; AF487542; AA009005.1; -.
DR EMBL; AJ541797; CAD62569.2; -.
DR HSSP; Q60778; 10Y3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00023; Ank; 11.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR ProDom; PD000001; Prot Kinase; 1.
DR SMART; SMO0248; ANK; 11.
DR PROSITE; PS50086; ANK_REPEAT; 11.
DR PROSITE; PS50297; ANK_REPEAT; 11.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
DR Transfasee.
SQ SEQUENCE 765 AA; 84632 MW; 549F6161B2976BPS CRC64;

```

Query Match 29.8%; Score 1215.5; DB 2; Length 765;
 Best Local Similarity 37.9%; Pred. No. 3, 2e-56;
 Matches 290; Conservative 113; Mismatches 274; Indels 89; Gaps 13;

```

QY 7 TPMLALILRTDAEFLNG-WKVGSGRGQYVKRHHWMTWLAKSPSLHVD--DRER 63
DB 6 TELRLGLIPVETRDPEGDWRLVASGSPGVQFAHRHRRTVYAKCAPCLPPDAASDV 65

```

QY 64 MELLEBAKMEMAKRYTILPVYIGICREPVGLMNETGSLKLLASRLPMDLAFRIIH 123
 DB 66 NYLIEBAKMKKIKQHIYSIYGVCKOPGLIYEMFANGSLKELVISTSLCKLFRILH 125
 QY 124 ETAVGNFLHCAVPPLHLDLKPANILLDAHYNKISDPGLAK-NGGSHSHDLSMDGLF 182
 DB 126 EYSLANFLHSHIKPPLHLDLKPANILLDAHYNKISDPGLAK-NGGSHSHDLSMDGLF 185
 QY 183 GTIAYLPPERIREKSLPDTKHDVYSFAIVIGVLTOKKPADEKNIILHIMVKKVGHHP 242
 DB 186 GMLSYIPPEMFLSNKAPGPKYDVYSFAIVIGVLTOKKPADEKNIILHIMVKKVGHHP 244
 QY 243 ELPPICRARPACSHLIRLMOCOCODPRVPRTPQELISEMDLCKKDDVYKETAHLD 302
 DB 245 SLQPVSDQWPSBAQWVDMKRCWMDPPKRCPCFDITLED- 286
 QY 303 VSPPEPRSEVVPARLKRASAPFPNDVYSLSELLQSDSGVSAVGEPELSRSSSEK 362
 DB 287 -----ILSLQSRVA-----V 298
 QY 363 PSSGSGKRLSGVSVDSAFSSRGLSLSPEREPSTSDLTGTRRPEBEACGCHRVDTSKL 422
 DB 299 PES---KALARKVSCGLSLRQPGVNEVDSQELMDSDSGNYLK-----RALQLSD- 345
 QY 423 MKILOPOVDLAL-DSGASLHLAVEAGQECATKLLNNANPNLSNRGSTPLMAVER 481
 DB 346 RKNLPVREBELCIYENKVTPLHFLVAQSGVEQRLLLAHVVDQCQASGYPLLLAOD 405
 QY 482 RRVGVVELLARKISVNAKDEQWTAHFAQNGDESTRLLLEKNASVNEVDEGRTPEM 541
 DB 406 QCPDLCALLHAGADANRVDEDEGMARLHFAQNGDDGTARLLLDIGACVDAQBERGWTPL 465
 QY 542 HVACQHQENIVRILLRGVDVSLQCKDAMPLHFAAQNGHPIYVLLAKQPGVSVNAQT 601
 DB 466 HLAQNNFENVARILVSRQADPNLHBAEGKTPHVAAYFGHVSIVYGLTSSQ-GAELDAQ 524
 QY 602 LRGTPPLHAAQGRHVRVRIILDCSDVNVCSLAQTPLHVALEHGTSTARLLHGA 661
 DB 525 RMLRTPPLHAAVERGKVRALQHLKSGAVPDALDQSGVGPLHFAARGLTKMLRYGA 584
 QY 662 GKEAVTSDGYTALHAAARGHLATVGLVBEKADVLAARPLNOTALHAAHSHSVVEE 721
 DB 585 SLRLPFGQWTPPLHAAVYGHLEIHLHLESHANMAGLAVWTPPLHAAHGERAVVSA 644
 QY 722 LV-SADVITLDFDEQGLSALHAAQGRHAAQVETLLRHGAHINLOS 765
 DB 645 LIQCGADP-NAABQSGWTPPLHAAVQGSTPLSVINLEHNAVHARY 669
 RESULT 10
 ID Q9H281 PRELIMINARY; PRT; 352 AA.
 AC Q9H281;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
 DE Serologically defined breast cancer antigen NY-BR-49 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_Taxid=9606;
 RN NCB1
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 MEDLINE=2263320; PubMed=12747765;
 RA Scanlan M.J., Gout I., Gordon C.M., Williamson B., Stockert E.,
 RA Gure A.O., Jager D., Chen Y.T., Mackay A., O'Hare M.J., Old L.J.,
 RT "Humoral immunity to human breast cancer: antigen definition and
 RT quantitative analysis of mRNA expression.";
 RL Cancer Immun. 1:4-4(2001).
 DR EMBL; AF308292; AAC48260.1; -.
 DR HSSP; Q60778; IOY3.
 DR InterPro; IPR002110; ANK.

DR InterPro; IPR001969; Pept_Asp_AS.
 DR Pfam; PF00023; Ank. 4.
 DR PRINTS; PR01415; ANKYRN.
 DR SMART; SM00248; ANK. 4.
 DR PROSITE; PS50088; ANK_REPEAT. 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION. 1.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 KM ANK repeat.
 FT NON TER 1
 SQ SEQUENCE 352 AA; 37874 MW; 3B6816C3274ECFEC CRC64;
 Query Match 29.3%; Score 1196.5; DB.2; Length 352;
 Best Local Similarity 78.7%; Pred. No. 1.2e-55;
 Matches 251; Conservative 7; Mismatches 20; Indels 41; Gaps 3;
 QY 316 ARLKRAAPFPNDVYSLSELLQSDSGVSAVGEPELSRSSSEKLPSSGSGKRLSGV 375
 DB 3 ARLKRAAPFPNDVYSLSELLQSDSGVSAVGEPELSRSSSEKLPSSGSGKRLSGV 62
 QY 376 SVDSAFSSRGLSLSPEREPSTSDLTGTRRPEBEACGCHRVDTSKMLILOPOVDLAL 435
 DB 63 SVDSAFSSRGLSLSPEREPSTSDLTGTRRPEBEACGCHRVDTSKMLILOPOVDLAL 122
 QY 436 DSGASLHLAVEAGQECATKLLNNANPNLSNRGSTPLMAVERVGVVELLARKI 495
 DB 123 DSGASLHLAVEAGQECATKLLNNANPNLSNRGSTPLMAVERVGVVELLARKI 182
 QY 496 SVNAKDEQWTAHFAQNGDESTRLLLEKNASVNEVDEGRTPEMVAQHQENIVRI 555
 DB 183 SVNAKDEQWTAHFAQNGDESTRLLLEKNASVNEVDEGRTPEMVAQHQENIVRI 242
 QY 556 LIRRGVDVSLQCKDAMPLHFAAQNGHPIYVLLAKQPGVSVNAQT 581
 DB 243 LIRRGVDVSLQCKDAMPLHFAAQNGHPIYVLLAKQPGVSVNAQT 302
 QY 582 -----HLPIVLLAKQPG 593
 DB 303 LIRRGVDVSLQCKDAMPLHFAAQNGHPIYVLLAKQPG 321
 RESULT 11
 ID Q8B225 PRELIMINARY; PRT; 745 AA.
 AC Q8B225;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
 DE Mus musculus adult female vagina cDNA, RIKEN full-length enriched
 DE library, clone:9930020N01 product:hypothetical tyrosine protein
 DE kinase/Ankyrin repeat profile/Serine/Threonine protein
 DE kinase/Bukaryotic protein kinase/Ankyrin-repeat/Ankyrin repeat region
 DE DE circular profile/Yeast DNA-binding domain containing protein, full
 DE insert sequence.
 GN Name=9930020N01R1k;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN NCB1
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 MEDLINE=99279253; PubMed=10344936; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN NCB1
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN NCB1

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RA The RANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carrinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carrinci P.,
RA Kono H., Aklyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carrinci P.,
RA Fukuda S., Futano M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirokane T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kanakawa T.,
RA Kurihara C., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Jul-2001) to the EMBL/Genbank/DBSJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK036872; BAC29613.1; -.
DR HSSP; Q60778; 10Y3.
DR MGD; MGI:3045301; 9930020N01R1K.
DR GO; GO:0005524; F:ADP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Ser kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00023; ANK; 11.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01415; ANKYRIN.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00248; ANK; 11.
DR PROSITE; PS50086; ANK_REPEAT; 11.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ANK repeat; ATP-binding; DNA-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 745 AA; 82479 MW; DDD391ECD19E84D CRC64;

Query Match 28.0%; Score 1141.5; DB 2; Length 745;
Best Local Similarity 35.9%; Pred. No. 2.6e-52;

Matches 272; Conservative 115; Mismatches 280; Indels 91; Gaps 12;
QY 11 LALLRTPDAGEP-TGWEKVGSGRGQVYKVRHVMKTKALIKGSPSLHVD--DREBEREL 67
DB 22 LGSITVTRDDPFEERWMLVASGGSKVFOARHKMRQYAIKSPCLQKETTSEVTCLEF 81
QY 68 EEAQKEMAKFRYLIPYVGI CREPVGILVMEYMETGSLLEKLASEPLPWDRFRRIHETAV 127
DB 82 EEAIVKMEKIFQGHVTSIVGCKQPLGI VMEFMA SGSL EKLTPHSLCWPMLKRIHETSL 141
QY 128 GGNFLHCMPDPLHLDLKPNALLDAHYKISDPGLAK-CNGLSHSDLSMDGLFETIA 186
DB 142 AMNPLHSIKPPLHLDLKPNALLDNNMHKISDPFGISKMEGOSTQRYERSALRGLTS 201
QY 187 YLPERIRREKSRLEFDTHGVDYSPFAIVMGVLTQKKPRADENKILHIVKVKGRPELP 246
DB 202 YLPEMFLENKKAPGPEYDVSPFAIVWEILTQKKPYAG-LNMWTTIIRAAAGRPSELQD 260
QY 247 VCRARPRACSHLIRLMQRCWQGDPRVAPTEQITSETEDLCERPDDEVKETAHDLVYSP 306
DB 261 VSDWPEBEVHQVMVLMKRCMDQDPKRPCLNVAVEITDMLSL-----FQSP 307
QY 307 -PEPRSSVPAKLKGRASAPTFNDYSLSELISQDLSGVSQAVBGPBLSRSSSESKLPSS 365
DB 308 MTPDGCALTKQV--SKPESISQPHKVSKEVNO-----EIASVSSDSL-- 349
QY 366 GSGGRSLGVSVDGSAFSSRSLSLSPFERPSTSLGTRRPEBACGHRVDTSKLMI 425
DB 350 -----KNILQSDSKSLVADVNR----- 370
QY 426 LQPDVDLALDSGASLHLAVEAGQEBACAKMLNNANPNLSNRGSTPLHMAVERVRG 485
DB 371 -----VTPHLFVAGSLEQVRLLSHDVDVQOQASGYTPLLATQDQPD 417
QY 486 VVELLARKTSVNAKEDDQWTAHPFAQNGDESTRLLEKNSVNEVDEGTPMNVAC 545
DB 418 LCALLHAGDVTNADDEGVAHPFAQNDQDHTARLLDLHGLVNAERHEGWTPLHAA 477
QY 546 OHQENIVRILRQGVDSVLSQGDWMLPLHYAAMQGHLPYVKLAKPGVSNVNAQTLDGR 605
DB 478 QNNEENARLIVSRQADLSPEHEBEGKTPLVAAVFGHIGVKLLSGQ-GAELDAQNNLR 536
QY 606 TPLHAAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGTSFARLLHRGAKKEA 665
DB 537 TPLHAAVERGVARIQGLHLKCGALPDALDSGVSPLHIAAARGKDLFKKLLRYGASLEL 596
QY 666 VTSQGYTALHAAARNGHATVVKLIVEBKADVLARGPLNQTALHAAAGHSEVVEELVSA 725
DB 597 RTQGSWTPLHATYKGLLEIHIQAKSHVDLDALGSMQWTPPLHAAFGEGVALLQOC 656
QY 726 DV-IDLFDEQSLALHAAQGRHAGVETLLRHGAHIN 762
DB 657 GANPNAAGSQWTPHLHAAVHKGTFGLGITHLLEYGADIH 694
RESULT 12
08JHU4 PRELIMINARY; PRT; 584 AA.
AC 08JHU4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase RICK.
GN Name=rick; Synonyms=rick;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98241596; PubMed=9575181; DOI=10.1074/jbc.273.20.12296;
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;

RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis."
RL J. Biol. Chem. 273:12296-12300(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22191376; PubMed=12091384; DOI=10.1074/jbc.M20222200;
RA Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamacka S.,
RA Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.,
RT "Protein kinase C-associated kinase (PKC) mediates Bcl10-independent
RT NF-kappa B activation induced by phorbol ester."
RL J. Biol. Chem. 277:31871-31876(2002).
DR EMBL: AF487540; AAM76920.1; -.
DR ZFIN: ZDB-GENE-030902-3; ripk2.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0004468; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0042981; F:regulation of apoptosis; IEA.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_kin_AS.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00069; PKINASE; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
DR KINASE.
SQ SEQUENCE 584 AA; 66124 MW; 7AAEFCB5DEB9C0 CRC64;

Query Match 14.0%; Score 563; DB 2; Length 584;
Best Local Similarity 29.5%; Pred. No. 3.9e-22;
Matches 177; Conservative 97; Mismatches 197; Indels 128; Gaps 25;

QY 21 EFTGMEKVGSGGQYKRVHMKTWLAIKC---SPSLAVDDRREMLERAKKMEVA 76
DB 27 KATDLHYIKSGGFGVYFRAQHSNKRITVAIKCKLDSF---VGERRNCLKEAEVLHKA 83
QY 77 KERYLLPVYVICRNP--VGLVMEYMTGSLKELASEPI---PMDLRPIIHTETAVGMN 130
DB 84 RFNHIIQIFGVCEPFCFICITEYVNGSLDELHKKDIPAVAWPLRIIYEIALGVN 143
QY 131 FLHCAPPLHLHLDKRANILLDAHYKISDFGLAC-NGLSHSH-DLSMDGLFTIATL 188
DB 144 FLHNSPPLHLHDLKQNTILMDGEYHVKIADPGLSKPSPALDHQRLRLQPAEMGGTVIYM 203
QY 189 PPERLR-ERSRLPDTGADVSPATVWGLTQCKPFADEKNILHIVKVGKGRPE---- 243
DB 204 PPEYEPSTKRTVDKIMSTAIIMWVLSKRIPEBEATNPQIMFSLRGARPTGID 263
QY 244 -LPVCTRAPRACSHLIRLMQRCMGDPVVRPTPOBITSETBDLCRPPD-EVKETAHDL 301
DB 264 SLIPVDIPSR---ETILNMTSGWTANPDERPFLHCLIEBPMLEBRPEIDVLEAV--L 317
QY 302 DYK-----SPPEPRSVVPAKLKRAAPFPDN-DYLSLSLLSQDSGVQAYE 348
DB 318 EYKRIKYPSPSCCSSTOSNGKIKERKCYELNVPMWDSSTGSGSCSQEARIQ--- 374
QY 349 GPRELSSRSSESLTPSSGSGKRLSVSS-----VDSAFSSRGLSLISFEREP 395
DB 375 -PEPLTIST-----PSQGA---YAGLPSSLSMLPDLPPRYLMNC--SPNNLSPEYQTA 423
QY 396 STSDLGTTTRRPEEACGCHRVDPYSKLMKLIQ-----POVDLALDSGASILLHVAE 448
DB 424 VVSDLMNIPK-----AAHPQSESEIALAIQPLTLHPHQDVTAFDD----- 465
QY 449 GQEECAKMLLNANPRLSRRGSTPLHMAVERRVAGVLELLARKISVNAKDEDMWTAL 508

DB 466 -QGPAAWIA-----ARREVVROMTEACIANSQDLSLARELLMR---EDYELIV 511
QY 509 HPAQNGDESTRLLERKMSVNVVDPEGRTPMVAOCHGENTVRLIRGVVSLQ 567
DB 512 N---QTRTAKVRLLD-----TCRHSSEECRVVVRKLQDNKMG 549

RESULT 13
AC RIK2_MOUSE STANDARD; PRT; 539 AA.
ID RIK2_MOUSE
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Receptor-interacting serine/threonine-protein kinase 2 (EC 2.7.1.37).
GN Name=Ripk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097; DOI=10.1038/416190a;
RA Chn A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
RT "Involvement of receptor-interacting protein 2 in innate and adaptive
RT immune responses."
RT Nature 416:190-194(2002).
RL -FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappa-B (By similarity).
CC -CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
CC -SUBUNIT: Binds to CLARP/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2. TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity).
CC -SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -PTM: Autophosphorylated (By similarity).
CC -SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -SIMILARITY: Contains 1 CARD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib.ch).
CC -----
DR EMBL: AF461040; AAL96436.1; -.
DR MGD: MGI:1891456; Ripk2.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_kin_AS.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00069; PKINASE; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Apoptosis; ATP-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 18 294
FT DOMAIN 431 523
FT NP_BIND 24 32 ATP (By similarity).
FT BINDING 47 47 ATP (By similarity).
FT ACT_SITE 146 146 Proton acceptor (By similarity).
SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;
Query Match 13.4%; Score 545.5; DB 1; Length 539;

Best Local Similarity 34.6%, Pred. No. 6.2e-21;
Matches 151; Conservative 60; Mismatches 134; Indels 91; Gaps 17;

QY 31 GGFQGVYKVRHVKMTLAIKCSPLHVD---DREMLLEAKKEMAKFYIILPYG 86
D 27 GASGVSSARHADRVRVAVK---HLHITPLDSESRDILREABIIHKAFSYILPLIG 83
QY 87 ICRBP--VGLVMEYMGSLSEKLASE---PLWMDLRFRIIHEYAVGMNHLHCAPPL 140
D 84 ICNPEEFGLIVETVPMGSLNELLRKTEYDPDIAMPFLRIHLHETALGVNLYHNNPPLL 143
QY 141 HLDLKPANILDAHYHVKISDFGLAKCNGL---SHSHDLMDGLFTIAYLPPERIR- 194
D 144 HHDLKTQNIILLDNHRYKADPGLSKMTMMLSSQSRYSKSAPEG--GTLIMPEENYEG 201
QY 195 EKSLRPTKVDYSPALVIGVLTQKRPADKNTLIMVYKVGHPRLPPVCRAPRA 254
D 202 OKSRA-SVKHDIYSYAVIMMEVLRSKQPFEEVTPLOIMYSVSGHRDPTSE--ENLPFD 258
QY 255 CSH--LIRLMORCKQSDPRVRP-----TFQKIT-----S 281
D 259 IPHGLMLSLIQSGAQNDRPSPFLKCLILEPVLRTFEDITLEAVIQLKAKIOSS 318
QY 282 ETEBICEKPDDEVKETAHDLVYKSPPEPRSEVVPARLKRASAPTFDNDYSLSELLSQL- 339
D 319 STIHLCDKMD---LSINIPANHPQRES-----CGSSLSLRNTG 355
QY 340 DSGVSGAVEGPEELSRSSSEKLPSSGSKRLSGVSYD-----SAPSRGSLISF 391
D 356 SPGFSRSLASAPQDKFLSGAPQDCSSLKAHRCQGNHSDGIVSVPPGAAFCDRRASCSL 415
QY 392 E-REPSTSDLTGTRP 406
D 416 AVISPEFLVEKGSERP 431

RESULT 14

RIK2_HUMAN STANDARD; PRT; 540 AA.
AC 04353;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Receptor-interacting serine/threonine-protein kinase 2 (BC 2.7.1.37)
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase)
DE (UNQ277/PRO314).
GN Name=RIPK2; Synonyms=CARDIAK, RICK, RIP2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX MEDLINE=98241596; PubMed=9575181; DOI=10.1074/jbc.273.20.12296;
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.";
RL J. Biol. Chem. 273:12296-12300(1998).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RC TISSUE=endothelial cell;
RX MEDLINE=98307936; PubMed=9642260; DOI=10.1074/jbc.273.27.16968;
RA McCarthy J.V., Ni J., Dixit V.M.;
RT "Rip2 is a novel NF-kappaB-activating and cell death-inducing
RT kinase.";
RL J. Biol. Chem. 273:16968-16975(1998).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
RX MEDLINE=98381580; PubMed=9705938; DOI=10.1016/S0960-9822(07)00352-1;
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
RA Matmann C., Tschopp J.;

RT "Identification of CARDIAK, a RIP-like kinase that associates with
RT caspase-1.";
RL Curr. Biol. 8:885-888(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Ozersky P., Holmes A., Broy M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Platzner M., Varon R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chu C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Bacon D., Foster J., Grimaldi C., Gu Q., Haas P.B., Helens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehgali S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vardlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [7]
RP SEQUENCE FROM N.A.
RP TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grzymalski M.I., Skalska U., Smalins D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schmeich A., Schein J.B., Jones S.J.W., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappa-B.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to CFLAR/CLARP and Casp1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF3 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,
CC pancreas and lymph node.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).

CC -----
 DR EMBL; AF027706; AAC34970.1; -
 DR EMBL; AF078530; AAC27722.1; -
 DR EMBL; AF064824; AAC25668.1; -
 DR EMBL; AC004003; AAC24561.1; -
 DR EMBL; AF117829; -; NOT_ANNOTATED_CDS.
 DR EMBL; AY358814; AA089173.1; -
 DR EMBL; BC004553; AA04553.1; -
 DR Genew; HGNC:10020; RIPK2.
 DR H-InVDB; HIX0007636; -
 DR MIM; 603455; -
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; IBP.
 DR GO; GO:0006915; P:apoptosis; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IBP.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR01029; DEATH_Like.
 DR InterPro; IPR01009; Kinase_Like.
 DR InterPro; IPR00719; Prot_Kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00114; CARD; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS50107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Apoptosis; ATP-binding; Phosphorylation;
 Serine/threonine-protein kinase; transferase.
 KW DOMAIN 18 294
 FT NP_BIND 432 524 CARD
 FT BINDING 47 47 ATP (By similarity).
 FT ACT_SITE 146 146 Proton acceptor.
 FT MUTAGEN 47 47 K->A: Abolishes kinase activity.
 FT MUTAGEN 146 146 K->M: Reduces FAS-mediated apoptosis.
 FT MUTAGEN 146 146 D->N: Abolishes kinase activity.
 SQ SEQUENCE 540 AA; 61194 MW; 575A69239505792 CRC64;
 Query Match 13.3%; Score 541.5; DB 1; Length 540;
 Best Local Similarity 34.0%; Pred. No. 1e-20;
 Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;
 QY 31 GGGGYYKRYHMKTKLAKSPSLHVD---DRERMELBEAKKMEAKRYTLPVYG 86
 DB 27 GASGVSSARHADMRYQVAVK---HLHHTPLDSEKQVLEAELHAKRSYILPILIG 83
 QY 87 ICREP--VGLVMEYMETGSLKELKLA---PLPMDLRRIIHTETAVGNFLHCAPLL 140
 DB 84 ICNEPEFGLIVTEYMPNGSLNELHAKTEYPPVAVMPLRRIIHEIALGVNVLHNTPTLL 143
 QY 141 HLDLKPANILLDAHYVTKISDGLAKCNGLSHSHDMS---DGLFGLTAIYPPERIR-- 194
 DB 144 HHDLTKQNLILLNDFEFTKIDFGLSKRMWMSLSQSRSSKSADEG--GTLIYMPPEYEBG 201
 QY 195 EKSRLFDTHGDVYSFAIIVGWLTOKKPPADEKNILHIMVKKVGRHP-----ELPPVCR 249
 DB 202 QKSRRA-SIHGDIVSYAVITWEVLSRKQPEEDVTNPLQINYSVSGHRPIYNESLPYDLP 260
 QY 250 AAPRACSHLIRLMQRCOGDPRVRYPTFOBITSETEDLCRKPDEVKETAHDLVKSPPRP 309
 DB 261 HBAR-----MISLESQMAQNPDRPSPFLKCLIELEPVLR----- 295
 QY 310 RSEVVPARLKRASAPFPNDYSLSELISQLDSGVSAVAGPEBELSSSSESTLPSGSGSK 369
 DB 296 -----TFE-EITLEAVIQL-----KTKIKQVSSAI 321
 QY 370 RLSGVSVDSAPSSRSLSLSPFRBSTSDLTGTRPEEBACGCHVRDTS-----KLMTKI 425
 DB 322 HLCDDKKKME-----LSL-----NIPVNHGPQEBSSCSQLHNSGSPETSRSL 364

QY 426 LQPDVD 432
 DB 365 PAPQDND 371
 RESULT 15
 Q9VAB1 PRELIMINARY; PRT; 1549 AA.
 AC Q9VAB1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE CG1651-PA (CG1651-pb)
 GN Name=Ank; ORFNames=CG1651;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot G.L.,
 RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Butts J.K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Glasner K.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laevo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Splitter B., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wesserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Myers E.W., Rubin G.M., Venter J.C., Zhu X., Smith H.O.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Fries B., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber F.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RSEBARCH0079-RSEBARCH0079(2002).

RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaneline J.S., Bergman C.M., Krommiller B., Carlson J., Svitek R.,
RA Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hildecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.D., Whitfield E.J., Bayraktaroglu U., Berman B.P.,
RA Bettemcourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AE003845; AAF59369.2; -.
DR HSSP; P16157; IN11.
DR FLYBase; FBgn011747; Ank.
DR GO; GO:0045169; C:fusome; NAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0045170; C:spectrosome; IDA.
DR GO; GO:0007016; P:cytoskeletal anchoring; IDA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR00488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; Ank; 23.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKRN.
DR SMART; SM00246; ANK; 23.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS50088; ANK_REPEAT; 21.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KM ANK repeat.
SQ SEQUENCE 1549 AA; 170167 MW; 3EECE852B1484DFF CRC64;
Query Match 13.3%; Score 541; DB 2; Length 1549;
Best Local Similarity 34.7%; Pred. No. 4.2e-20;
Matches 128; Conservative 76; Mismatches 155; Indels 10; Gaps 6;
QY 396 STSDIGTRRPEEACGCHRVADTSKIMKIIQPQ-DVDLALDSGASLIHLAVEAGQEBCA 454
DB 427 ATTESGLTPLHVASFMGCINI-----VYLLQHEASADLPTRIGETPLHLAARAOADI 481
QY 455 KMLILNANPNLSNRGSTPLHMAVERVRGVVELLARKISVNAKDQWTALHFAQN 514
DB 482 R-ILRSKAVDAIAEGQTPHVASRLNININIMILLQGARINAOISNDKXSALHIAKE 540
QY 515 GDESSTRLLEKNASVNEVDPEGRTPMHVAQHQENTVRIILRGVDVSLQKDAWPL 574
DB 541 GQENTVQVLELNGAENNAVTKGFTPLILACKYKQNVQIILONGASIDFGKNDVTP 600
QY 575 HYAAQGHLPYVKLLAKQGVSVNAQTLDGRTPLHLAAQGHYVARILIDLCSQDVNCS 634
DB 601 HVAETHNPSIYELLKRN-GSSPNCARRNGCAHIAICKNYLRTAMQLQHGADVNIIS 659

QY 635 LIAOTPLHVAEFGHTSTARLLLRGAGREAVTSDGYTALHLAARNGHLATVKLVEKA 694
DB 660 KSGSPPLHLAAQGNVDMVQLLEYGV-ISAANKGLTPLHVAQBGHVLVSQILLEHGA 718
QY 695 DVLAGPLNOTALHLAAAGHSEVEBELVSADV-IDLFDEQGLSALHLAAQGRHAQTVER 753
DB 719 NISERTNGTTPHMAAHYGHLDLVKFFIENDADIEMSNIGTTPHLQMAQGHIMINL 778
QY 754 LLRHGAHIN 762
DB 779 LLRHKANPN 787

Search completed: September 17, 2005, 02:43:22
Job time : 251.039 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 13:13:47; Search time 63.5676 Seconds
(without alignment)
1186.673 Million cell updates/sec

Title: US-10-658-904-2

Sequence: 1 MEGDGGTFWALLALRTFDAG.....SLKFGGHHGPAATLLRSKT 784

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1885.5	46.2	397	2 T46445	hypothetical prote
2	540	13.2	1549	2 T13940	ankyrin - fruit fl
3	513.5	12.6	1765	2 T42714	ankyrin 3, splice
4	513.5	12.6	1940	2 T42715	ankyrin 3, splice
5	513.5	12.6	1943	2 T42713	ankyrin 3, splice
6	513.5	12.6	1961	2 T42716	ankyrin 3, splice
7	509.5	12.5	4377	2 A55575	ankyrin 3, long sp
8	505	12.4	2039	2 T15347	ankyrin-related un
9	500	12.3	1856	2 B35049	ankyrin 1, erythro
10	500	12.3	1880	2 A35049	ankyrin 1, erythro
11	500	12.3	1881	1 SUHUK	ankyrin 1, erythro
12	499.5	12.2	1848	2 S37771	ankyrin - mouse
13	499.5	12.2	1862	2 T49502	ankyrin - mouse
14	484.5	11.9	3924	2 S37431	ankyrin 2, neuroma
15	422.5	10.4	1423	1 T37275	death-associated p
16	406.5	10.0	426	2 AE2149	hypothetical prote
17	405	9.9	791	2 T42691	hypothetical prote
18	397.5	9.7	1062	2 T14151	inv protein - mous
19	396.5	9.7	1062	2 T30255	inversin - mouse
20	389.5	9.6	1401	2 S11527	alpha-latrotoxin p
21	385	9.4	671	2 T09479	serine/threonine p
22	382	9.4	1411	2 S30355	alpha-latrotoxin p
23	380	9.3	579	2 UC5955	transforming growt
24	373.5	9.2	606	2 UC5956	transforming growt
25	370	9.1	567	2 UC5957	transforming growt
26	350.5	8.7	656	2 T49299	receptor interacti
27	350.5	8.6	2584	2 T24158	hypothetical prote
28	350.5	8.6	2606	2 T24157	hypothetical prote
29	350	8.6	1435	2 T32930	hypothetical prote

30	349.5	8.6	1031	2 T43458	hypothetical prote
31	347.5	8.4	368	2 T18184	ankyrin repeat pro
32	347.5	8.4	736	2 T05137	protein kinase hom
33	338.5	8.3	1184	2 T00253	gene Ankhzn protei
34	333.5	8.2	557	2 T46507	hypothetical prote
35	326.5	8.0	991	2 T25412	hypothetical prote
36	325.5	8.0	1188	2 T19552	hypothetical prote
37	324.5	8.0	855	2 T10655	hypothetical prote
38	323	7.9	606	2 AC2508	hypothetical prote
39	320	7.8	1166	2 B96598	protein F20N2.4 li
40	318.5	7.8	443	2 T01182	hypothetical prote
41	318	7.8	394	2 J00229	mixed-lineage prot
42	317	7.8	934	1 H71274	probable ankyrin -
43	314	7.7	656	2 T10664	serine/threonine-s
44	314	7.7	801	2 T01289	probable protein k
45	313	7.7	1196	2 T09356	brassinosteroid-in

ALIGNMENTS

```
RESULT 1
T46445
hypothetical protein DKFZP434B2328.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C.Accession: T46445
R.BioCoker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A.Reference number: Z23032
A.Accession: T46445
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-397 <AAA>
A.Cross-references: UNIPROT:Q9NTAI; EMBL:AL137448
A.Experimental source: adult testis; clone DKFZP434B2328
C.Genetics:
A.Note: DKFZP434B2328.1

Query Match          46.2%; Score 1885.5; DB 2; Length 397;
Best Local Similarity 94.5%; Pred. No. 5.3e-89;
Matches 375; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 368 SLSEFERESTSDIGTRRPEREACGCHRVDRPTSKLMTILOPOVDVLDLDSGASLHLAV 447
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 2 ALTF-ASPLPADLGTITDVQKKLVDAIVSGPTSKLMTILOPOVDVLDLDSGASLHLAV 60

QY 448 AGOEECAKMLLNANPNLSNRGSTPLHMAVERRVRGVVELLARKISVNAKDEDDQWTA 507
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db 61 AGOEECAKMLLNANPNLSNRGSTPLHMAVERRVRGVVELLARKISVNAKDEDDQWTA 120

QY 508 LHPAANGDESSSTRLLLEKNASVNEVDEEGRTPMHVAQCOHQENIVRLLRGGVVSLOG 567
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db 121 LHPAANGDESSSTRLLLEKNASVNEVDEEGRTPMHVAQCOHQENIVRLLRGGVVSLOG 180

QY 568 KDAMPLHYAAMOGHLPIVKLLAKOPGVSVNAQTLDGSTPLHLAQRGHYRVARLLIDLC 627
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db 181 KDAMPLHYAAMOGHLPIVKLLAKOPGVSVNAQTLDGSTPLHLAQRGHYRVARLLIDLC 240

QY 628 SDVNCSSLLAQTPLVAALTEGHTSTARLLLRGAKKEAVTSDGYTALHLAANGHLATVK 687
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db 241 SDVNCSSLLAQTPLVAALTEGHTSTARLLLRGAKKEAVTSDGYTALHLAANGHLATVK 300

QY 688 ILVEEKADVLARGLNQTALHLAANGHSEVEEIVSADVIDLFPBOGLSALHLAANGRH 747
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db 301 ILVEEKADVLARGLNQTALHLAANGHSEVEEIVSADVIDLFPBOGLSALHLAANGRH 360

QY 748 AQTVETLLRHGHNTILSLKFGGHHGPAATLLRSKT 784
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db 361 AQTVETLLRHGHNTILSLKFGGHHGPAATLLRSKT 397

RESULT 2
```


QY 611 AAGRGHRYVARIILDLCSNV-----VCSLLAQ----- 638
DB 522 AAREGHEVDVAAFLDHGASLITTKGFTPLHVAAGKLEVASILLQKSASPDAAGSG 581
QY 639 -TPLHVAETGHTSTARLLHHRGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVL 697
DB 562 LTPHVAAHYDNOKYVALLLDQASPHAAKNGTTPHIAAKKQMDATISLEYGADAN 641
QY 698 ARGPLNOTALHAAAGHSEVVEELVSADV-IDLPDEQGISALHIAAQGRHAQVETTLR 756
DB 642 AVTRGSIASVHLAAQEGHVDVWSLLSRANVNLNKSGLTPLHIAAQEDRVNAEVLVN 701
QY 757 HGAHINLOS 765
DB 702 QGAHVDAQT 710

RESULT 5
T42713
ankyrin 3, splice form 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42713
R:Peterson, L.L.; John, K.M.; Lu, F.M.; Blicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: 222237; MUID:95340633; PMID:7615634
A:Accession: T42713
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1943 <P>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710550; PIDN:AAB01606
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 855/1
C:Function:
A:Description: supposed to play an important role in the polarized distribution of many
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 12.6%; Score 513.5; DB 2; Length 1943;
Best Local Similarity 35.8%; Pred. No. 2.2e-18;
Matches 132; Conservative 51; Mismatches 151; Indels 35; Gaps 4;

QY 431 VDLALDSGASLHLAVEAGQEBQCAKWLNNANPNLSNRGSTPLHMAVERVGVVELL 490
DB 343 VDDVTNDVLTALHVAACGHYKAVKVLDDKASPNKALNGFTPLHIAACKKRIKRMELL 402
QY 491 LARKSVNAKDDQMTALHFAANGDESTRLLEKNASVNEVDPEGRTPMVAOCQGOE 550
DB 403 LKHGASIQVTSGLTPHVAAPMGHVNIVSQLMHGHASPTTNVREGTALHMAARSQGA 462
QY 551 NIVRILRRGVDSLQGDAMLPLHYAAMQGHLPYKLLAKOPGVSVNAQTLDDGRTPLH 610
DB 463 EVRYLVQDGAQVBAKADQTPHISRLKADIVQGLLQO-GASPNAAATTSVTPPLH 521
QY 611 AAGRGHRYVARIILDLCSNV-----VCSLLAQ----- 638
DB 522 AAREGHEVDVAAFLDHGASLITTKGFTPLHVAAGKLEVASILLQKSASPDAAGSG 581
QY 639 -TPLHVAETGHTSTARLLHHRGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVL 697
DB 562 LTPHVAAHYDNOKYVALLLDQASPHAAKNGTTPHIAAKKQMDATISLEYGADAN 641
QY 698 ARGPLNOTALHAAAGHSEVVEELVSADV-IDLPDEQGISALHIAAQGRHAQVETTLR 756
DB 642 AVTRGSIASVHLAAQEGHVDVWSLLSRANVNLNKSGLTPLHIAAQEDRVNAEVLVN 701

QY 757 HGAHINLOS 765
DB 702 QGAHVDAQT 710

RESULT 6
T42716
ankyrin 3, splice form 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42716
R:Peterson, L.L.; John, K.M.; Lu, F.M.; Blicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: 222237; MUID:95340633; PMID:7615634
A:Accession: T42716
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1961 <P>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710552; PIDN:AAB01607
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 12.6%; Score 513.5; DB 2; Length 1961;
Best Local Similarity 35.8%; Pred. No. 2.2e-18;
Matches 132; Conservative 51; Mismatches 151; Indels 35; Gaps 4;

QY 431 VDLALDSGASLHLAVEAGQEBQCAKWLNNANPNLSNRGSTPLHMAVERVGVVELL 490
DB 343 VDDVTNDVLTALHVAACGHYKAVKVLDDKASPNKALNGFTPLHIAACKKRIKRMELL 402
QY 491 LARKSVNAKDDQMTALHFAANGDESTRLLEKNASVNEVDPEGRTPMVAOCQGOE 550
DB 403 LKHGASIQVTSGLTPHVAAPMGHVNIVSQLMHGHASPTTNVREGTALHMAARSQGA 462
QY 551 NIVRILRRGVDSLQGDAMLPLHYAAMQGHLPYKLLAKOPGVSVNAQTLDDGRTPLH 610
DB 463 EVRYLVQDGAQVBAKADQTPHISRLKADIVQGLLQO-GASPNAAATTSVTPPLH 521
QY 611 AAGRGHRYVARIILDLCSNV-----VCSLLAQ----- 638
DB 522 AAREGHEVDVAAFLDHGASLITTKGFTPLHVAAGKLEVASILLQKSASPDAAGSG 581
QY 639 -TPLHVAETGHTSTARLLHHRGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVL 697
DB 562 LTPHVAAHYDNOKYVALLLDQASPHAAKNGTTPHIAAKKQMDATISLEYGADAN 641
QY 698 ARGPLNOTALHAAAGHSEVVEELVSADV-IDLPDEQGISALHIAAQGRHAQVETTLR 756
DB 642 AVTRGSIASVHLAAQEGHVDVWSLLSRANVNLNKSGLTPLHIAAQEDRVNAEVLVN 701
QY 757 HGAHINLOS 765
DB 702 QGAHVDAQT 710

RESULT 7
A55575
ankyrin 3, long splice form - human
N:Alternate names: ankyrin G
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55575
R:Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A>Title: Ankyrin-G, A new ankyrin gene with neural-specific isoforms localized at the ax
A:Reference number: A55575; MUID:95138209; PMID:7836469
A:Accession: A55575

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-4377 <KOR>
A:Cross-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
C:Genetics:
A:Gene: GDB:ANK3
A:Cross-references: GDB:424503; OMIM:600465
A:Map position: 10q21.1-10q21
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C:Keywords: alternative splicing; peripheral membrane protein
F:73-105/Domain: ankyrin repeat homology <AN01>
F:106-138/Domain: ankyrin repeat homology <AN02>
F:139-171/Domain: ankyrin repeat homology <AN03>
F:172-200/Domain: ankyrin repeat homology <AN04>
F:201-223/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>
F:597-629/Domain: ankyrin repeat homology <AN17>
F:630-662/Domain: ankyrin repeat homology <AN18>
F:663-695/Domain: ankyrin repeat homology <AN19>
F:696-728/Domain: ankyrin repeat homology <AN20>
F:729-761/Domain: ankyrin repeat homology <AN21>
F:762-794/Domain: ankyrin repeat homology <AN22>
F:795-827/Domain: ankyrin repeat homology <AN23>
Query Match 12.5%; Score 509.5; DB 2; Length 4377;
Best Local Similarity 35.2%; Pred. No. 9,46-18;
Matches 130; Conservative 52; Mismatches 152; Indels 35; Gaps 4;
QY 411 VDLALDSGASLLHLAVEAGQECATKLLNNANPMLSRKSTPLHMAVERKGVZEL 490
DB 360 VDDVTNDVLTALHVAHCGHKYKAVAVLLDKCKNPAKALNGFTPLHCKNRKIKWML 419
QY 491 LARKSVNAKQEDQDTALHFAAQNDESSTRLLEKKNASVNEVDEGRTPMHVACQHQE 550
DB 420 LKHGASIQAVTESGTLPIHVAAPFQHVNIIVSGLMHGASPMPTNVRGETALHMAARSQA 479
QY 551 NIVRLILRRGVDSLQGDAMLPILHYAAMQGLPIVKKLAKQPGVSVNAQTLDGRTPLH 610
DB 480 EVVRVLYVDGAQVEAKAKDDQTPPLHISARLGRKADIVQQLDQ-GASPMNAATTSGYTPHL 538
QY 611 AAGRGHYVARLLIDLCSDVN-----VCSLLAQ----- 638
DB 539 SARBEHEVVAFLDLHGASLSITTKKGTPLHVAAKYGLKLEVANLLDKKSASPDAAKSG 598
QY 639 -TPHVAATGHTSPARLLHRRGAKKAVTSDGYTALHAAARNGHILATVKLLVEEKADVL 697
DB 599 LTPHVAHYNQKATALLLDGASPHAAKNGYTPHIAKKNQMDATLTLLBEGADAN 658
QY 698 ARGPLNQALHIAAHGSEVEELVSAADV-IDLFEQGLSALHIAAGGRHAQVETLLR 756
DB 659 AVTROGASVHLAAQEGHVDVSLILGRVANVILSNKSGLPPLHIAAQEDRVNVAEVLVN 718
QY 757 HGAHINLOS 765
DB 719 QGAHVDAQT 727

RESULT 8
T15347
ankyrin-related unc-44 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text change 09-Jul-2004
C:Accession: T15347; T15346; T15345; A57282; B57282; C57282

R:Gatung, S.
Submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid B0350.
A:Reference number: Z18332
A:Accession: T15347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2039 <GAT>
A:Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208071; PID:g1208073; PIDN:AAA9344
A:Accession: T15346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1000, 'SKQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVBE'
32, 'S', 2034-2035, 'GSPTRSVPEERHSHQEDHEGST' <GA2>
A:Cross-references: EMBL:U50071; NID:g1208071; PID:g1208075; PIDN:AAA93445.1
A:Accession: T15344
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAESTSEQVPE', 1934-1935, 'EC'
<GA3>
A:Cross-references: EMBL:U50071; NID:g1208071; PID:g1208074; PIDN:AAA93444.1
A:Accession: T15345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVBE'
PTRRSVPEERHSHQEDHEGST' <GA4>
A:Cross-references: EMBL:U50071; NID:g1208071; PID:g1208076; PIDN:AAA93446.1
R:Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpoor
J. Cell Biol. 129, 1081-1092, 1995
A:Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Caer
A:Reference number: A57282; MUID:95263663; PMID:7744957
A:Accession: A57282
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852, 'GGG', 856-1000, 'SKQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E'
, 'SHED', 2007-2008, 'TT', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: B57282
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E'
, 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRRSVPEERHSH', 1984-1985, 'EDHEGS', 1986
A:Accession: C57282
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 194, 'F', 196, 'T', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, 'E'
, 4, 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESBS', 1944, 'REDDSTIVT', 1946
A:Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
C:Genetics:
A:Gene: CESP:unc-44
A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979/
C:Superfamily: ankyrin; ankyrin repeat homology
F:164-192/Domain: ankyrin repeat homology <AN04>
F:358-390/Domain: ankyrin repeat homology <AN11>
F:391-423/Domain: ankyrin repeat homology <AN11>
Query Match 12.4%; Score 505; DB 2; Length 2039;
Best Local Similarity 26.0%; Pred. No. 6,36-18;
Matches 188; Conservative 97; Mismatches 277; Indels 160; Gaps 20;
QY 160 SDFGLAKNGLSHSDSMGLFGTIAVL--PPERIEKSRLEPDTKDYVSFA--IWIWG 215
DB 57 TDINTSNANGLSHLASKEGHSVVAEELIKRQAVDAATRKNGTALHISLNGOSLIVT 116
QY 216 VLTQKKPFADENKILHITVAVVKGHPRLPVCARPACSHLR----- 260
DB 117 ILVE-----NCANVNVQSVNGFTPLVMAAGENHEEVVKYLLKGGANQALSTEDGFTP 168
QY 261 LMGRCMGQDRVRRTPPEITSETE-----DLCEKPDDEVKET-----AADDLVKSPPEP 309
DB 169 LAVALAQGHDRVAVVLLLENDKGRVRLPALHIAAKKDDTAAATLTLONEHNPVTS----- 224

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QY 310 RSEVVPALTKRASA.PTPFNDVYSLELISOLDPSQAWVEGEBSELSSSSSSK 369
Db 225 KSGTTPPLHIT---AAHYGHE-NVGOQL--LEKGNVNYQARHNISPLHVATKW----- 270
QY 370 RLASGVSVDSAFSSRGSLSLSFEREPSTSDIGTTRRBEBAQCHRVVDTSKMLTLOPQ 429
Db 271 ---GRTMNANULLSRGAII-----DSRTKOLLTPH-----CARSGHD-----Q 307
QY 430 DVDLALBSGSL-----LHLAV 446
Db 308 VVDLLVVOGAPI.SAKTKNGLAPLHMAAQGDHVDAAETLLYHRAVDVTVDYLTPLHVAA 367
QY 447 EAGGEBECCAKWILLNANPNLSNRBSPTPLHMAVERVRGVYELLARKISYNAKDEDMQT 506
Db 368 HCHGAVRAKULLIDPSADNPSBALNGFTPLHACKKNRIKVEYELLTKRAAEATTEGSLT 427
QY 507 ALHFAPAONGDESSRLLLEKNAVNEVD.FEGRTPMHVAQCHQENIVRILLRGVDVSLQ 566
Db 428 PLHVAFAFGALINIVYILLQGANPDVETVRGETPLHLAARANGDVVRVILIRNGAKVDAQ 487
QY 567 GKDAMLPLHYAAMQCHLP.YVKLLAKQBPQSVYNAOTLDGRTPLHLAARGHVRVARIIDL 626
Db 488 ARELOTPLHIASRLGNTDIVILL-QAGANMATTRDNYSP.LHIAAREGSEVAVGILLDH 546
QY 627 CSD-----VNVCSLALQ-----TP.LHVAEREGHSTA 653
Db 547 NADTTLTKKGFTPLHASKYGTNTE.FVVRLLERGT.PVDIBSKNOVTP.LHVAHAHNNDUKVA 606
QY 654 RLLLHRGAKBEAVTSDGYTALHLAARNGHLATVKKLVEBKADVLARGPLNOTALHLAAH 713
Db 607 MLLLENGASAAKAAKNGVTPPLHIAAKKNQMEIASTLLOFKAD.PPAKSRAGFTPLHLSAOE 666
QY 714 GHSEVVEELV-SADYIDL.FDEQGISALHLAAQGRHAQVETLTLRHGAHINIOSLKFQGH 772
Db 667 GHKEISGLIERGSDVGAKANNGLTAMHLCAQEDHVPVAQIILYNNGAIEIN---SKTNAGY 723
QY 773 GP 774
Db 724 TP 725

```

RESULT 9
 B35049
 ankryn 1, erythrocyte splice form 3 - human
 N:Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N:Contains: ankryn 2.2, erythrocyte
 C:Species: Homo sapiens (man)
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 C:Accession: B35049
 R:Clamber, S.; Yu, H.; Prehal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A:Title: cDNA sequence for human erythrocyte ankryn.
 A:Reference number: A35049; MUID:90175370; PMID:1685849
 A:Accession: B35049
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1856 <LAM>
 C:Genetics:
 A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 C:Superfamily: ankryn; ankryn repeat homology
 C:Keywords: alternative splicing
 F:2-1856/Product: ankryn 1, erythrocyte form 3 #status predicted <MAT>
 F:2-1513,1676-1856/Product: ankryn 2.2, erythrocyte #status predicted <MA2>
 F:44-76/Domain: ankryn repeat homology <AN01>
 F:77-109/Domain: ankryn repeat homology <AN02>
 F:110-142/Domain: ankryn repeat homology <AN03>
 F:143-171/Domain: ankryn repeat homology <AN04>
 F:172-204/Domain: ankryn repeat homology <AN05>
 F:205-237/Domain: ankryn repeat homology <AN06>
 F:238-270/Domain: ankryn repeat homology <AN07>
 F:271-303/Domain: ankryn repeat homology <AN08>

Query Match	Similarity	Score	DB 2;	Length
Matches 135; Conservative	12.3%;	500;	1856;	
	31.1%;	Pred. No. 1e-17;		
	52;	Mismatches 161;	Indels 86;	Gaps 5

Query Match	12.3%	Score 500;	DB 2;	Length 1856;
Best Local Similarity	31.1%	Pred. No. 1e-17;		
Matches 135;	Conservative	52;	Mismatches 161;	Indels 86; Gaps 5

QY	431	VDLALDGSASTL-----LHLAVAGOECAKWLILNANPNLSNRSGSTPLHMAVE	480
		: : : :	
DB	255	VRLLLDRAQIETKTKBELTPLHCAARGVHRISILLDHGAPIQAKTKNGLSPIHMAAQ	314
		: : : :	
QY	481	RRVGVVELLIARKI SVNAKDEDQMTALHPAAQNGDESSTKLLEKMASVNEVDEGKPT	540
		: : : :	
DB	315	GDHLDCVRLLLQYDAEIDITLDHLTPLHVAAGCHHRVAKVLTLDKGAKPNSRALNGFTP	374
		: : : :	
QY	541	MHVACQHQENIVKILRLRGYDVSIGGDAPLPLHYAMOGHRLPVTKLAKQPGVSVNAQ	600
		: : : :	
DB	375	LHACKNHVVEMLLKTGASIDAVTESGLTPLPHVASFMGHLPLPVKULL-ORQASPNVS	433
		: : : :	
QY	601	TLDDGRTPLHLAARGHYVARILLDLCDGNVVCISLTAQTPPLHVALETGHTSTABRLLHRG	660
		: : : :	
DB	434	NVKYETPLHMAARGHTEVAKYLLQNKAKVNAKAKDDPTPLHCAARIGHTNNVKKLLEN	493
		: : : :	
QY	661	AGKEAVTSDGYTALHLAARNGHLATVKLLVEBKADVLA RGPLNQTAHLHAAAHGSEVVE	720
		: : : :	
DB	494	ANPNLATTAGHTPLHIA RBGHEVEVALLLEKMSQAQMTKKGFPLHVAAKYGVKRVAE	553
		: : : :	
QY	721	ELV-----SADYIDLF-----	731
		: : : :	
DB	554	LILERDAPHNAAGKNGLTPLHVAVHHNNLIDIVKLLPRGSGPSHPAMNGYTPLHIAAKON	613
		: : : :	
QY	732	-----DBQGLSALHHLAAGRGHAQTVEITLLRHGAHNLIAOS-----	765
		: : : :	
DB	614	QVEVARSLQYCGSANAASVQGVTPPLHLAABGHAEMVALLLSKOANGNLGNKSGLTPLH	673
		: : : :	
QY	766	LKFOGSGHPAATLL 779	
		: : : :	
DB	674	LVAQBGHVFPVADVLL 687	
		: : : :	

RESULT 10
A35049
ankyrin 1, erythrocyte splice form 2 - human
N.Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N.Contains: ankyrin 2.2, erythrocyte
C.Species: Homo sapiens (man)
C.Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004
C.Accession: A35049
R.Liambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A.Title: cDNA sequence for human erythrocyte ankyrin.
A.Reference number: A35049; MUID:90175370; PMID:1689849
A.Accession: A35049
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-1880 <LAM>
A.Cross-references: UNIPROT:P16157; GB:M2880
C.Genetics:
A.Gene: GDB:ANK1; ANK
A.Cross-References: GDB:118737; OMIM:182900

[illegible]

RESULT 13

C:Accession: I49502
 Mamm. Genome 3, 281-285, 1992
 A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain
 A:Reference number: I49502; MIMD:92345717; PMID:1386265
 A:Accession: I49502
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-1862 <RES>
 A:Cross-references: UNIPROT:Q02357; GB:M84756; NID:G191939; PIDN:AAA57236.1; PID:G191940
 C:Genetics:
 A:Gene: Ank-1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:40-72/Domain: ankyrin repeat homology <AN01>
 F:73-105/Domain: ankyrin repeat homology <AN02>
 F:106-138/Domain: ankyrin repeat homology <AN03>
 F:139-167/Domain: ankyrin repeat homology <AN04>
 F:168-200/Domain: ankyrin repeat homology <AN05>
 F:201-233/Domain: ankyrin repeat homology <AN06>
 F:234-266/Domain: ankyrin repeat homology <AN07>
 F:267-299/Domain: ankyrin repeat homology <AN08>
 F:300-332/Domain: ankyrin repeat homology <AN09>
 F:333-365/Domain: ankyrin repeat homology <AN10>
 F:366-398/Domain: ankyrin repeat homology <AN11>
 F:399-431/Domain: ankyrin repeat homology <AN12>
 F:432-464/Domain: ankyrin repeat homology <AN13>
 F:465-497/Domain: ankyrin repeat homology <AN14>
 F:498-530/Domain: ankyrin repeat homology <AN15>
 F:531-563/Domain: ankyrin repeat homology <AN16>
 F:564-596/Domain: ankyrin repeat homology <AN17>
 F:597-629/Domain: ankyrin repeat homology <AN18>
 F:630-662/Domain: ankyrin repeat homology <AN19>
 F:663-695/Domain: ankyrin repeat homology <AN20>
 F:696-728/Domain: ankyrin repeat homology <AN21>
 F:729-761/Domain: ankyrin repeat homology <AN22>
 F:762-794/Domain: ankyrin repeat homology <AN23>

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